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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:41:58 ; Search time 34.2113 Seconds
(without alignments)
3179.172 Million cell updates/sec

Title: US-09-887-669-1

Perfect score: 7809

Sequence: 1 MDVAAALPAFVALWLLYPW.....EAPQYRVCYDVVALEYLESS 1457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7809	100.0	1457	2	US-08-652-971-3
2	7809	100.0	1457	2	US-08-449-644-1
3	7809	100.0	1457	2	US-08-087-244A-1
4	7809	100.0	1457	2	US-08-991-258A-3
5	7809	100.0	1457	2	US-08-769-399-3
6	7809	100.0	1457	3	US-08-991-953A-3
7	7586	97.1	1439	2	US-08-449-644-2
8	7586	97.1	1439	2	US-08-087-244A-2
9	4812.5	61.6	1452	2	US-08-449-644-8
10	4812.5	61.6	1452	2	US-08-087-244A-8
11	4793.5	61.4	1452	2	US-08-652-971-4
12	4793.5	61.4	1452	2	US-08-991-258A-4
13	4793.5	61.4	1452	2	US-08-769-399-4
14	4793.5	61.4	1452	3	US-08-991-953A-4
15	4575	58.6	1436	2	US-08-652-971-2
16	4575	58.6	1436	2	US-08-991-258A-2
17	4575	58.6	1436	2	US-08-769-399-2
18	4575	58.6	1436	3	US-08-991-953A-2
19	4063	52.0	777	4	US-09-949-016-7158
20	3732	47.8	1075	4	US-09-949-016-8308
21	1514.5	19.4	1501	2	US-08-447-464-3
22	1514.5	19.4	1501	2	US-08-716-679-3
23	1480	19.0	1911	1	US-08-348-006B-5
24	1480	19.0	1911	2	US-08-800-825A-5
25	1480	19.0	1911	3	US-09-158-657-5
26	1480	19.0	1911	5	PCT-US94-10166-5
27	1170.5	15.0	793	1	US-08-015-985-3

28	1170.5	15.0	793	4	US-09-280-597-3	Sequence 3, Appli
29	1155	14.8	802	1	US-08-015-985-1	Sequence 1, Appli
30	1155	14.8	802	4	US-09-280-597-1	Sequence 1, Appli
31	1155	14.8	807	4	US-09-949-016-7356	Sequence 7356, Ap
32	1153	14.8	538	4	US-09-743-492A-9	Sequence 9, Appli
33	1142	14.6	699	1	US-08-348-006B-7	Sequence 7, Appli
34	1142	14.6	699	2	US-08-800-825A-7	Sequence 7, Appli
35	1142	14.6	699	3	US-09-158-657-7	Sequence 7, Appli
36	1096	14.0	249	2	US-08-685-992-8	Sequence 8, Appli
37	1096	14.0	249	2	US-09-144-925-8	Sequence 8, Appli
38	1073.5	13.7	560	4	US-09-949-016-10786	Sequence 10786, A
39	1019	13.0	2314	4	US-09-816-703A-2	Sequence 2, Appli
40	1018	13.0	2308	1	US-08-015-973-1	Sequence 1, Appli
41	1018	13.0	2308	2	US-08-448-164-1	Sequence 1, Appli
42	1018	13.0	2308	3	US-08-081-929-2	Sequence 2, Appli
43	1018	13.0	2308	4	US-10-000-954-2	Sequence 2, Appli
44	1009	12.9	1442	1	US-08-015-986A-3	Sequence 3, Appli
45	1009	12.9	1442	2	US-08-446-363-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-652-971-3
; Sequence 3, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Labky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-652-971-3

Query Match 100.0%; Score 7809; DB 2; Length 1457;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDVAAALPAFVALWLLYPWLLGSAIGQPSAGCTFDDGFGACDYHQDLYDDPEWVHVS 60
Db 1 MDVAAALPAFVALWLLYPWLLGSAIGQPSAGCTFDDGFGACDYHQDLYDDPEWVHVS 60

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QY 121 TLNLLVRNKGPLANPIWNVTGFTGRDMLRAELAVSTFWPNEYQVIFAEVSGGRSGYIA 180
Db 121 TLNLLVRNKGPLANPIWNVTGFTGRDMLRAELAVSTFWPNEYQVIFAEVSGGRSGYIA 180
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QY 241 QTKNINRRFAASFRLOVTKTDQDLYRCVTSQSERGSGVSNFAQLIVREPRPTAPPOLL 300
Db 241 QTKNINRRFAASFRLOVTKTDQDLYRCVTSQSERGSGVSNFAQLIVREPRPTAPPOLL 300
QY 301 GVGPTYLLIQLNANSIIGDPTIILKEVYRMTSGSWTETHAVNAPTYKMLHLDPTDTEYEI 360
Db 301 GVGPTYLLIQLNANSIIGDPTIILKEVYRMTSGSWTETHAVNAPTYKMLHLDPTDTEYEI 360
QY 361 RVLTRPCEGGTGLPGPLITRTKCAEPMRTPTKLKIAEIQARRIAVDWESLGYNITRCH 420
Db 361 RVLTRPCEGGTGLPGPLITRTKCAEPMRTPTKLKIAEIQARRIAVDWESLGYNITRCH 420
QY 421 TFNVITICHYFRGHNESADCLDMDPKAPQHVNNHLPPTVTVSLXKMLTNPGRKESSET 480
Db 421 TFNVITICHYFRGHNESADCLDMDPKAPQHVNNHLPPTVTVSLXKMLTNPGRKESSET 480
QY 481 IIQTDDEVPVPVKSLQGTSPENKI FLNWKPELTPNGII IQEYVSYSSIRSFDPAPVPA 540
Db 481 IIQTDDEVPVPVKSLQGTSPENKI FLNWKPELTPNGII IQEYVSYSSIRSFDPAPVPA 540
QY 541 GPPQTVSNLWNSHTHVFHMLHPGTTTYFFIRASTVKFGFPATAINVTNINSAPSLPDYEG 600
Db 541 GPPQTVSNLWNSHTHVFHMLHPGTTTYFFIRASTVKFGFPATAINVTNINSAPSLPDYEG 600
QY 601 VDASLNETAATTITVLLRPAQAKGAPISAYQIIVVEQLHPHRTKREAGAMECYQVPVYQNA 660
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Db 901 EYESFFEGQSASWDVAKKQNRKNRNGNIIAYDHSRVILQPVDEDDPSSDYINANYIDI 960
QY 961 WLYRQGYQRPISHYIATQGVPHETVDFWVMWQESACIVMTNLVEGRVKCYKWPDD 1020
Db 961 WLYRQGYQRPISHYIATQGVPHETVDFWVMWQESACIVMTNLVEGRVKCYKWPDD 1020
QY 1021 TEVYGDVKVTCVEMPEPLAEBYVVRTFTLRRRGVNEIREVKQFHTGWPDHGVPHYATGLLS 1080
Db 1021 TEVYGDVKVTCVEMPEPLAEBYVVRTFTLRRRGVNEIREVKQFHTGWPDHGVPHYATGLLS 1080
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Db 1081 FIRRVKLSNPPSAGPIVWHCSAGAGRTGCIYVIDIMLDMAREGVVDIYNCVKALRSRRI 1140

QY 1141 NMVOTESQYFIHDAILEACLCGETAIPVCBFAAYFDMIRIDSQTNSSHLKDBFOTLNS 1200
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Db 1201 VTPRLQAEDECSIACLRPNHDKNRFMDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPA 1260
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QY 1321 SCSDMDCDVINRIFRICNLTRPOEGYLMVQOQFYILGWASHREVPGSKRSFLKLILOVEKWO 1380
Db 1321 SCSDMDCDVINRIFRICNLTRPOEGYLMVQOQFYILGWASHREVPGSKRSFLKLILOVEKWO 1380
QY 1381 ECEBEGEGRTIIHCLNGGSGRMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
Db 1381 ECEBEGEGRTIIHCLNGGSGRMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
QY 1441 EQRFCYDVALEYLESS 1457
Db 1441 EQRFCYDVALEYLESS 1457
RESULT 2
US-08-449-644-1
; Sequence 1, Application US/08449644
; Patent No. 5856162
; GENERAL INFORMATION:
; APPLICANT: Schlössinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,644
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/087,244
; FILING DATE: 01-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-449-644-1

Query Match 100.0%; Score 7809; DB 2; Length 1457;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDVAAALPAFVALWLLYPWLLSALGQFSGAGCTFDDGPGACDYHQDLDDFEWVHVS 60
Db 1 MDVAAALPAFVALWLLYPWLLSALGQFSGAGCTFDDGPGACDYHQDLDDFEWVHVS 60

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Db 61 AQEHPYLPPEMPOGSMYVDSNHDPEKARLQIPTWKENDTHCIDPSYLLYSOKGLNPG 120

Qy 121 TLNLTVRVNKGPLANPTWNTGTRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGVIA 180
Db 121 TLNLTVRVNKGPLANPTWNTGTRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGVIA 180

Qy 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNKWLQORNGEDIPVA 240
Db 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNKWLQORNGEDIPVA 240

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Db 241 QTKNINHRFAASPRLOEVTKTDQDLYRCVTQSERGSGVSNFAQLIVREPPRIAPPOLL 300

Qy 301 GVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKWLHLDPTYEI 360
Db 301 GVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKWLHLDPTYEI 360

Qy 361 RVLLTRPEGGTGLPGPLTRTKCAEPMRTPTKLTAEIQARRIADWESLGNITRCH 420
Db 361 RVLLTRPEGGTGLPGPLTRTKCAEPMRTPTKLTAEIQARRIADWESLGNITRCH 420

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Qy 541 GPPQTVSNLWNSTHVFMHLHPGTYQFFIRASTVKGFGPATANVTNISAPSLPDYEG 600
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Db 721 KTCQVRIATKAAATEEPEVDPAPAKOTDRVVKIAGISAGILVFTLLLVIVIVKSKLA 780

Qy 781 KKRKDMAGNTQEMTHVMVANDRSYADQSTLHAEPLSLTFMDQHNFSRPLNDPLVPTA 840
Db 781 KKRKDMAGNTQEMTHVMVANDRSYADQSTLHAEPLSLTFMDQHNFSRPLNDPLVPTA 840

Qy 841 VLDEHGAATESRLLDVPRLYLCGTSPTQGTQLHPAIRVADLLQHNLMKTSDSYGFK 900
Db 841 VLDEHGAATESRLLDVPRLYLCGTSPTQGTQLHPAIRVADLLQHNLMKTSDSYGFK 900

Qy 901 EYESPFEGOSASWDVAKQONRAKNYGNIIADHRSRVILQPVEDDPSDYNINAYIDI 960
Db 901 EYESPFEGOSASWDVAKQONRAKNYGNIIADHRSRVILQPVEDDPSDYNINAYIDI 960

Qy 961 WLVRDGYQRSHYIATQGVHETVYDFWRVWQSQSACIIVMTNLVWVGRVKCYKWPDD 1020
Db 961 WLVRDGYQRSHYIATQGVHETVYDFWRVWQSQSACIIVMTNLVWVGRVKCYKWPDD 1020

Qy 1021 TEVYDGFVKTCVEMEPLAEYVVRTFTLERRGYNEIREVKQFHTGWPDHGVPYHATGLLS 1080

Db 1021 TEVYDGFVKTCVEMEPLAEYVVRTFTLERRGYNEIREVKQFHTGWPDHGVPYHATGLLS 1080

Qy 1081 FIRRKLSNPPSAGPIVVHCSAGAGRTGCVIIVIMLMDMAEREGVVDIYNCVKALRSRI 1140
Db 1081 FIRRKLSNPPSAGPIVVHCSAGAGRTGCVIIVIMLMDMAEREGVVDIYNCVKALRSRI 1140

Qy 1141 NMVQTEQYFIHDAILEACLCGETAIPVCEFFKAAYFDMIRIDSQTNSSHLKDBFQTLNS 1200
Db 1141 NMVQTEQYFIHDAILEACLCGETAIPVCEFFKAAYFDMIRIDSQTNSSHLKDBFQTLNS 1200

Qy 1201 VTRLOAEDCSIACLPRNHDKNRPMDLPPDRCLPFLITIDGESSNYINAAALMDSYQPA 1260
Db 1201 VTRLOAEDCSIACLPRNHDKNRPMDLPPDRCLPFLITIDGESSNYINAAALMDSYQPA 1260

Qy 1261 AFIVTQYPLENTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVECM 1320
Db 1261 AFIVTQYPLENTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVECM 1320

Qy 1321 SCNMDCDVINRIFRICNLTRPQEGYLMVQOQFYVLGWAHREVPGSKRSFLKLILOVEKMQ 1380
Db 1321 SCNMDCDVINRIFRICNLTRPQEGYLMVQOQFYVLGWAHREVPGSKRSFLKLILOVEKMQ 1380

Qy 1381 ECEEGEGRTIIHCLNGGGRSGMFCATGIIVVMYKRONVVDVHAKVTLRNSKKNMVEAP 1440
Db 1381 ECEEGEGRTIIHCLNGGGRSGMFCATGIIVVMYKRONVVDVHAKVTLRNSKKNMVEAP 1440

Qy 1441 EQYRFCYDVALEYLESS 1457
Db 1441 EQYRFCYDVALEYLESS 1457

RESULT 3
US-08-087-244A-1
; Sequence 1, Application US/08087244A
; Patent No. 5863755
; GENERAL INFORMATION:
; APPLICANT: Schlensing, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ulrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,244A
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid

; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
US-08-087-244A-1									
Query Match 100.0%; Score 7809; DB 2; Length 1457;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MDVAAAALPAFVALMLLPWLLGALQGFAGGCTFDDGACDYHQDLVDDFEWVHVS	60						
Db	1	MDVAAAALPAFVALMLLPWLLGALQGFAGGCTFDDGACDYHQDLVDDFEWVHVS	60						
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Db	121	TLNIIILVRNKGKPLANPIWNVGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYIA	180						
Qy	181	IDDIQVLSYPCDKSPHFLRLGDEVNAGONATFQCIATGRDAVHNKMLQRRNGEDIPVA	240						
Db	181	IDDIQVLSYPCDKSPHFLRLGDEVNAGONATFQCIATGRDAVHNKMLQRRNGEDIPVA	240						
Qy	241	QTKNINHRERFAASFLQEVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRTIAPPQL	300						
Db	241	QTKNINHRERFAASFLQEVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRTIAPPQL	300						
Qy	301	GVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYEI	360						
Db	301	GVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYEI	360						
Qy	361	RVLTRPGEGGTGLPGPLIRTKCAEPMRTPTKLIAEIQARRIADVWSLGYNITRCH	420						
Db	361	RVLTRPGEGGTGLPGPLIRTKCAEPMRTPTKLIAEIQARRIADVWSLGYNITRCH	420						
Qy	421	TENVTCICHYFRGHNESRADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESSET	480						
Db	421	TENVTCICHYFRGHNESRADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESSET	480						
Qy	481	IIQDDEDVGPVPVKSQGTSPENKIFLNWKEPLEPNGIIQYEVSYSSIRSFDPAVPA	540						
Db	481	IIQDDEDVGPVPVKSQGTSPENKIFLNWKEPLEPNGIIQYEVSYSSIRSFDPAVPA	540						
Qy	541	GPQTVSNLWNSHTHVFVHMLHGGTTYQFFIRASTVKGFGPATAINVTNINISAPSLPYEG	600						
Db	541	GPQTVSNLWNSHTHVFVHMLHGGTTYQFFIRASTVKGFGPATAINVTNINISAPSLPYEG	600						
Qy	601	VDASLNETHATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA	660						
Db	601	VDASLNETHATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA	660						
Qy	661	LSGGAPYFAAELPPGNLPEPAPFTVGDNRITYKGFWNPPPLAPRKGYNIYFQAMSSVEKET	720						
Db	661	LSGGAPYFAAELPPGNLPEPAPFTVGDNRITYKGFWNPPPLAPRKGYNIYFQAMSSVEKET	720						
Qy	721	KTQCVRITAKAATEEPEVIPPAPKQTRVVKIAGISAGILVFILLLLVIVIVVKSKLA	780						
Db	721	KTQCVRITAKAATEEPEVIPPAPKQTRVVKIAGISAGILVFILLLLVIVIVVKSKLA	780						
Qy	781	KRKDAMGNTRQEMTHMNMDSRVADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA	840						
Db	781	KRKDAMGNTRQEMTHMNMDSRVADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA	840						
Qy	841	VLDENHSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYSGFK	900						
Db	841	VLDENHSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYSGFK	900						
Qy	901	EYESFFEQSQASWDVAKQDNRAKNRYGNIITAYDHSRVILQPVDDPSSDYINANYIDI	960						
Db	901	EYESFFEQSQASWDVAKQDNRAKNRYGNIITAYDHSRVILQPVDDPSSDYINANYIDI	960						
Qy	961	WLYRDGYQRPSHYIATQGPVHETVDFWRVMWQSQSACIVMTNLVEGVRVKYKYWPD	1020						

RESULT 4

US-08-991-258A-3
; Sequence 3, Application US/08991258A
; Patent No. 5928887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1457 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-991-258A-3

Query Match 100.0%; Score 7809; DB 2; Length 1457;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDVAAAALPAFVALLWLPWLLGSLGALQPSAGGCTFDDGPGACDYHQDLVDDPEWVHVS	60
Db	1	MDVAAAALPAFVALLWLPWLLGSLGALQPSAGGCTFDDGPGACDYHQDLVDDPEWVHVS	60
Qy	61	AOEPHYLPPEMPOGYSVWVDSNNHDPGEKARLQPTMKENDTHCIDSFYLLYSOKGLNPG	120
Db	61	AOEPHYLPPEMPOGYSVWVDSNNHDPGEKARLQPTMKENDTHCIDSFYLLYSOKGLNPG	120
Qy	121	TLNLIVRVNKGPLANPIWNVGTGRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGVIA	180
Db	121	TLNLIVRVNKGPLANPIWNVGTGRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGVIA	180
Qy	181	IDDIQVLSPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNKWLQRRNGEDIPVA	240
Db	181	IDDIQVLSPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNKWLQRRNGEDIPVA	240
Qy	241	QTKNINHRRAAASPRLOEVTKTDODLYRCVTSQSERGVSNSFAOLIIVREPPRIAPQLL	300
Db	241	QTKNINHRRAAASPRLOEVTKTDODLYRCVTSQSERGVSNSFAOLIIVREPPRIAPQLL	300
Qy	301	GVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGTETHAVNAPTYKLMHLDPDTEYEI	360
Db	301	GVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGTETHAVNAPTYKLMHLDPDTEYEI	360
Qy	361	RVLLTRPEGGTGLPGLPILTRTKCAEPMRTPKTKIAEQARRIAVDWESLGYNIIRCH	420
Db	361	RVLLTRPEGGTGLPGLPILTRTKCAEPMRTPKTKIAEQARRIAVDWESLGYNIIRCH	420
Qy	421	TENVTCIYHFRGHNESRACLDMDPKAPQVNVNHLPPYTNVSLKMLITNPEGRKSEET	480
Db	421	TENVTCIYHFRGHNESRACLDMDPKAPQVNVNHLPPYTNVSLKMLITNPEGRKSEET	480
Qy	481	IIOTDEDPGVPVVKSLQGTGFENKIFLNWKEPLEPNGIITQYEVSYSSIRSDPAVPVA	540
Db	481	IIOTDEDPGVPVVKSLQGTGFENKIFLNWKEPLEPNGIITQYEVSYSSIRSDPAVPVA	540
Qy	541	GPPTVSNLWNSHHVFMHLHPGTTYQFFIRASTVKGFGPATAINVTNNISAPSLPDYEG	600
Db	541	GPPTVSNLWNSHHVFMHLHPGTTYQFFIRASTVKGFGPATAINVTNNISAPSLPDYEG	600
Qy	601	VDASLNATATITVLLPAPQAKGAPISAYQIVVQLHPHRTKRGAMECVQVPTVYQNA	660
Db	601	VDASLNATATITVLLPAPQAKGAPISAYQIVVQLHPHRTKRGAMECVQVPTVYQNA	660
Qy	661	LSGGAPYFAELPPGMLPEPAPTVGDNRITYKGFVNPPPLAPRKGYNIYFOAMSSVEKET	720
Db	661	LSGGAPYFAELPPGMLPEPAPTVGDNRITYKGFVNPPPLAPRKGYNIYFOAMSSVEKET	720
Qy	721	KTCQVRIATKAAATEEPEVIPPDAKQDRVVKIAGISAGILVFLILLVIVIVKSKLA	780
Db	721	KTCQVRIATKAAATEEPEVIPPDAKQDRVVKIAGISAGILVFLILLVIVIVKSKLA	780
Qy	781	KKRKDAAGNTQETHMVMNMDRYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA	840
Db	781	KKRKDAAGNTQETHMVMNMDRYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA	840
Qy	841	VLDENHSAATESRLLDVPRLVLCGTSPTQGLHPAIRVADLLOHINLMKTSDSYGFK	900
Db	841	VLDENHSAATESRLLDVPRLVLCGTSPTQGLHPAIRVADLLOHINLMKTSDSYGFK	900

Qy	901	EYESFPFEGQSASWDVAKQONRAKNRYGNIAYDHSRVILQPVDEDDPSSDIYINANYIDI	960
Db	901	EYESFPFEGQSASWDVAKQONRAKNRYGNIAYDHSRVILQPVDEDDPSSDIYINANYIDI	960
Qy	961	WLYRDGYQRPSHYIATQGVHETVYDFWRWVWQSQSACIIVMTNLVVEGRVKCYKYPDD	1020
Db	961	WLYRDGYQRPSHYIATQGVHETVYDFWRWVWQSQSACIIVMTNLVVEGRVKCYKYPDD	1020
Qy	1021	TEVVGDFKVTCEMEPLAEYVVRTFTLLERRGYNEIREVKQFHFHTGWDHGVPIYHATGLLS	1080
Db	1021	TEVVGDFKVTCEMEPLAEYVVRTFTLLERRGYNEIREVKQFHFHTGWDHGVPIYHATGLLS	1080
Qy	1081	FIRRVKLSNPSPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRI	1140
Db	1081	FIRRVKLSNPSPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRI	1140
Qy	1141	NMQVTEBOYIFIHDALEACLCGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFQTLNS	1200
Db	1141	NMQVTEBOYIFIHDALEACLCGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFQTLNS	1200
Qy	1201	VTPLQAEDECSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNYINAALMDSYRQPA	1260
Db	1201	VTPLQAEDECSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNYINAALMDSYRQPA	1260
Qy	1261	AFIVTQYPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECM	1320
Db	1261	AFIVTQYPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECM	1320
Qy	1321	SCSMDCDVINRIFRINLTPQEGYLMVQOQFYVLGWSHREVPKGSFKLILQVEKQW	1380
Db	1321	SCSMDCDVINRIFRINLTPQEGYLMVQOQFYVLGWSHREVPKGSFKLILQVEKQW	1380
Qy	1381	EECEEGEGRTIIHCLNGGSGRGMFCATIGIVVMVKRQNVVDVPHAVKTLRNSKENMVEAP	1440
Db	1381	EECEEGEGRTIIHCLNGGSGRGMFCATIGIVVMVKRQNVVDVPHAVKTLRNSKENMVEAP	1440
Qy	1441	EQYRFCYDVALEYLESS 1457	
Db	1441	EQYRFCYDVALEYLESS 1457	

RESULT 5
US-08-769-399-3
; Sequence 3, Application US/08769399
; Patent No. 5976852
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Laaky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216


```

; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-953A-3

Query Match      100.0%; Score 7809; DB 3; Length 1457;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDVAAALPAFVALWLLYPWLLGSLGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHVS 60
Db 1 MDVAAALPAFVALWLLYPWLLGSLGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHVS 60
Qy 61 AOEPHYLPPMPQSGSYMVVDSSNHDGPKARLQPTMKENDTHCIDFSYLLYSOKGLNPG 120
Db 61 AOEPHYLPPMPQSGSYMVVDSSNHDGPKARLQPTMKENDTHCIDFSYLLYSOKGLNPG 120
Qy 121 TLNLIVRVNKGPLANPIWNTVGTGRDWLRAELAVSTFWPNEYOVIFEAEVSGRSGYIA 180
Db 121 TLNLIVRVNKGPLANPIWNTVGTGRDWLRAELAVSTFWPNEYOVIFEAEVSGRSGYIA 180
Qy 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNKLMWLRNGEDIPVA 240
Db 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHNKLMWLRNGEDIPVA 240
Qy 241 QTKNINRRFAASRLQEVTKTDOLYRCVTSQSRGSGVSNFAOLIIVREPPRIAPQLL 300
Db 241 QTKNINRRFAASRLQEVTKTDOLYRCVTSQSRGSGVSNFAOLIIVREPPRIAPQLL 300
Qy 301 GVGPYLLIOLNANSIIGDGPILKEVEYRMTSGSTWETHAVNAPTYSKLWHLDPDTEYI 360
Db 301 GVGPYLLIOLNANSIIGDGPILKEVEYRMTSGSTWETHAVNAPTYSKLWHLDPDTEYI 360
Qy 361 RVLLTRPEGGTGLPGPLITRTKCAEPMRTPTKTKIAEQARRIADWESLGYNIIRCH 420
Db 361 RVLLTRPEGGTGLPGPLITRTKCAEPMRTPTKTKIAEQARRIADWESLGYNIIRCH 420
Qy 421 TFNVTCIYHFRGHNESRADCLMDPKAPQHVVNHLPPYTNVSLKMLITNPEGRKESEET 480
Db 421 TFNVTCIYHFRGHNESRADCLMDPKAPQHVVNHLPPYTNVSLKMLITNPEGRKESEET 480
Qy 481 IIQTDDEVPGVPVKSLSQTSFENKI FLNWKLEPNGLITQYEVSYSSIRSDPAVPVA 540
Db 481 IIQTDDEVPGVPVKSLSQTSFENKI FLNWKLEPNGLITQYEVSYSSIRSDPAVPVA 540
Qy 541 GPPTVSNLWNSTHVFMHLHPGTYOFFIRASTVKGFGPATAINVTNINSAPSLPDYEG 600
Db 541 GPPTVSNLWNSTHVFMHLHPGTYOFFIRASTVKGFGPATAINVTNINSAPSLPDYEG 600
Qy 601 VDAISNETATTITVLLRPAQAKGAPI SAYQIVVQLPHRTRKREAGAMECVQVPTVYQNA 660
Db 601 VDAISNETATTITVLLRPAQAKGAPI SAYQIVVQLPHRTRKREAGAMECVQVPTVYQNA 660
Qy 661 LSGGAPYFAAELPPGNLPEPAPTVGDNRTYKGFWMPPPLAPRGYNIYFOAMSSVEKET 720
Db 661 LSGGAPYFAAELPPGNLPEPAPTVGDNRTYKGFWMPPPLAPRGYNIYFOAMSSVEKET 720
Qy 721 KTCQVRIATAAATEEPEVIPPDAKQTDVVKIAGISAGIIVFLLLVIVIVVKSKLA 780
Db 721 KTCQVRIATAAATEEPEVIPPDAKQTDVVKIAGISAGIIVFLLLVIVIVVKSKLA 780
Qy 781 KGRKDMGNTRQEMTHVMNAMDRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840

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RESULT 7

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US-08-449-644-2
; Sequence 2, Application US/08449644
; Patent No. 5856162
; GENERAL INFORMATION:
; APPLICANT: Schliesinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,644
; FILING DATE: 24-May-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/087,244
; FILING DATE: 01-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 FENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1439 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-644-2

Query Match          97.1%; Score 7586; DB 2; Length 1439;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1421; Conservative 12; Mismatches 5; Indels 20; Gaps 4;

QY 1 MD-VAAALPAPVALWLLPPLGSLGQFSAGGCTFDGFGACDYHQDLYDFEWHV 59
DB 1 MDTTAAALPAPVALLSPPLGSAQGSAGGCTFDGFGACDYHQDLYDFEWHV 60
QY 60 SAQEPHYLPPEMPOGQSYMVDSNDHDPGEKARLQLPTWKENDTHCIDFSYLLYSQGLNP 119
DB 61 SAQEPHYLPPEMPOGQSYMVDSSDHPGEKARLQLPTWKENDTHCIDFSYLLYSQGLNP 120
QY 120 GTNLTLVRVNGKPLANPTWNTGFGROWLRAELAVSTFWNEYOVIVPEAEVSGRSYI 179
DB 121 GTNLTLVRVNGKPLANPTWNTGFGROWLRAELAVSTFWNEYOVIVPEAEVSGRSYI 180
QY 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHKLWLRNGEDIPV 239
DB 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFOCIATGRDAVHKLWLRNGEDIPV 240
QY 240 AQTKNINRRFAASFRLEQVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPPRPTAPPOL 299
DB 241 AQTKNINRRFAASFRLEQVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPPRPTAPPOL 300
QY 300 LGVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYE 359
DB 301 LGVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYE 360
QY 360 IRVLLTRPGEQGTGLPGPLIITRTKCAEPMRTPKTLKIAEQARRIAVDWESLGYNITRC 419
DB 361 IRVLLTRPGEQGTGLPGPLIITRTKCAEPMRTPKTLKIAEQARRIAVDWESLGYNITRC 420
QY 420 HTFNVTICVHYPRGNESRADCLMDPKAPQVAVVHLLPPYTNVSLKMLITNPEGRKESSE 479
DB 421 HTFNVTICVHYPRGNESKADCLMDPKAPQVAVVHLLPPYTNVSLKMLITNPEGRKESSE 480
QY 480 TTIQTDDEVPVGVKSLQGTSEFNKIPLNWKPELPENGIITQYEVSYSSIRSPDPAPVP 539
DB 481 TTIQTDDEVPVGVKSLQGTSEFNKIPLNWKPELPENGIITQYEVSYSSIRSPDPAPVP 540
QY 540 AGPPQTVSNLWNSTHHVMHLHPGTTGYQFFIRASTVKFGFPATAINVTNITASAPLDPYE 599
DB 541 AGPPQTVSNLWNSTHHVMHLHPGTTGYQFFIRASTVKFGFPATAINVTNITASAPLDPYE 600
QY 600 GVDASINETATTITVLLRPAQAKGAPISAYQIVVQLPHRHTKREAGAMECVQVPVTVQN 659
DB 601 GVDASINETATTITVLLRPAQAKGAPISAYQIVVQLPHRHTKREAGAMECVQVPVTVQN 660
QY 660 ALSGAPYFAAELPPGNLPEPAPFTVGNRTYKGFWMNPPLAPRKGYNIFYQAMSSVEKE 719
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DB 661 AMSGAPYFAAELPPGNLPEPAPFTVGNRTYKGFWMNPPLAPRKGYNIFYQAMSSVEKE 720
QY 720 TKTCVRIATKAAATEBEVIPPDAKQTDNRVVKIAGISAGILVILLLLVIVIVKSKL 779
DB 721 TKTCVRIATK-AATEBEVIPPDAKQTDNRVVKIAGISAGILVILLLLVIVIVKSKL 779
QY 780 AKKEDAMGNTRQEMTHVMNADRSYADQSTLHAEDPLSLTFMDQHNPSRPLPNDPLVPT 839
DB 780 AKKEDAMGNTRQEMTHVMNADRSYADQSTLHAEDPLSLTFMDQHNPSRY----- 831
QY 840 AVLDEHSATAESRLLDVPRYLCCEGTESPTQTQLHPAIRVADLLQHINLMKTSDSYGF 899
DB 832 ----ENHSATAESRLLDVPRYLCCEGTESPTQTQLHPAIRVADLLQHINLMKTSDSYGF 887
QY 900 KEYESFFEGQASWDVAKQDNRAKRYGNIIDHRSRVILQPVEDDPSDDSYNANYID 959
DB 888 KEYESFFEGQASWDVAKQDNRAKRYGNIIDHRSRVILQPVEDDPSDDSYNANYI- 946
QY 960 IWLRYDGVQRPESHVATQGPVHETVDFWRMVWQEQSACIVMVTNLVEVGRVKCYKWP 1019
DB 947 -----DGYQRPESHVATQGPVHETVDFWRMVWQEQSACIVMVTNLVEVGRVKCYKWP 1001
QY 1020 DTEVYGFKVTCEMEPLAEYVVRTFTLERRGYNEIREVKQFHTGWDHGVPHYATGLL 1079
DB 1002 DTEVYGFKVTCEMEPLAEYVVRTFTLERRGYNEIREVKQFHTGWDHGVPHYATGLL 1061
QY 1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMDMAEREGVVDIYNCVKALRSRR 1139
DB 1062 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMDMAEREGVVDIYNCVKALRSRR 1121
QY 1140 INMVQTEQYIFIHDAIILEACLGCGETAIPVCEPKAAVDFMIRIDISQTNSSHLKQEFQTLN 1199
DB 1122 INMVQTEQYIFIHDAIILEACLGCGETAIPVCEPKAAVDFMIRIDISQTNSSHLKQEFQTLN 1181
QY 1200 SVTPRLQAECSIACLPRNHDKNRFDMLPPDRCLPFLITIDGSSSNYINAAALMDSYRQP 1259
DB 1182 SVTPRLQAECSIACLPRNHDKNRFDMLPPDRCLPFLITIDGSSSNYINAAALMDSYRQP 1241
QY 1260 AAFIVTQVPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVEK 1319
DB 1242 AAFIVTQVPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVEK 1301
QY 1320 MSCSMDCDVNIRIENLTPQEGYLMVQOQFYLGWASHREVPGSKESFLKLLIQVEKW 1379
DB 1302 MSCSMDCDVNIRIENLTPQEGYLMVQOQFYLGWASHREVPGSKESFLKLLIQVEKW 1361
QY 1380 QEECEGEGRITIIHCLNGGGRSGMFCALGIIVEMVKRQNVVDVFAVKTLRNSKENMVEA 1439
DB 1362 QEECEGEGRITIIHCLNGGGRSGMFCALGIIVEMVKRQNVVDVFAVKTLRNSKENMVEA 1421
QY 1440 PEQYRFCYDVALEYLESS 1457
DB 1422 PEQYRFCYDVALEYLESS 1439

RESULT 8
US-08-087-244A-2
; Sequence 2, Application US/08087244A
; Patent No. 5863755
; GENERAL INFORMATION:
; APPLICANT: Schlössinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-KAPPA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
```

COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,244A
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1439 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-087-244A-2

Query Match 97.1%; Score 7586; DB 2; Length 1439;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1421; Conservative 12; Mismatches 5; Indels 20; Gaps 4;

Qy 1 MD-VAALPAFAVALWLLYPWLLGSLGQSGAGCTFDGPGACDYHQDLYDFEWVHV 59
Db 1 MDTAAAAALPAFAVALLLSPWLLGSAQSQFSAAGCTFDGPGACDYHQDLYDFEWVHV 60
Qy 60 SAQEPHYLPMPGSGYVVDSSNHDGCEKARLQPTMKENDTHCIDFSLYLLYSQKGLNP 119
Db 61 SAQEPHYLPMPGSGYVVDSSNHDGCEKARLQPTMKENDTHCIDFSLYLLYSQKGLNP 120
Qy 120 GTNLVVRVNGKPLANPWNVTGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 179
Db 121 GTNLVVRVNGKPLANPWNVTGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180
Qy 180 AIDDIQVLSYPCDKSPHFLRGDVEVNAQONATFCIATGRDAVHNKLWLQRRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRGDVEVNAQONATFCIATGRDAVHNKLWLQRRNGEDIPV 240
Qy 240 AQTNIHNRPAASFRLOEVTKTDDLYRCVYQTSERGSVSNFAQLIVREPPRIAPPOL 299
Db 241 AQTNIHNRPAASFRLOEVTKTDDLYRCVYQTSERGSVSNFAQLIVREPPRIAPPOL 300
Qy 300 LGVGPTVLLIQLNANSIIGDGPITLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPPDTEYE 359
Db 301 LGVGPTVLLIQLNANSIIGDGPITLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPPDTEYE 360
Qy 360 IRVLLTRPGEGLTGPPLTRTKCAEPMPTKTLKIAETQARRIAVDMESLYNITRC 419
Db 361 IRVLLTRPGEGLTGPPLTRTKCAEPMPTKTLKIAETQARRIAVDMESLYNITRC 420
Qy 420 HTFNVTTCYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESSE 479
Db 421 HTFNVTTCYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESSE 480
Qy 480 TIITDDEVPQPVVKSLOGTSFNKIFLNKWEPLNPGIITQVEVSVSSIRSFDPAPVP 539
Db 481 TIITDDEVPQPVVKSLOGTSFNKIFLNKWEPLNPGIITQVEVSVSSIRSFDPAPVP 540
Qy 540 AGPPQTVSNLWNSHHVFMHLHPCGTTQFFIRASTVKGFGPATAINVTNISAPSLDYE 599
Db 541 AGPPQTVSNLWNSHHVFMHLHPCGTTQFFIRASTVKGFGPATAINVTNISAPSLDYE 600
Qy 600 GVDASLNETAITIVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 659
Db 601 GVDASLNETAITIVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 660
Qy 660 ALSGAPYFAAELPPGNLPEPAPFTYGDNRITKGFWNPPPLAPRKGNINYFOAMSSVEKE 719
Db 661 AMSGAPYFAAELPPGNLPEPAPFTYGDNRITKGFWNPPPLAPRKGNINYFOAMSSVEKE 720
Qy 720 TKTCQVRIATKAAATEPEVIPPAPKQDRVVKIAGISAGILVILLVIVIVKSKL 779
Db 721 TKTCQVRIATK-AAATEPEVIPPAPKQDRVVKIAGISAGILVILLVIVIVKSKL 779
Qy 780 AKKRDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 839
Db 780 AKKRDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 831
Qy 840 AVLDENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLQHLINIMKTSDSYGF 899
Db 832 ----ENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLQHLINIMKTSDSYGF 887
Qy 900 KEYESFEGQSASWDYAKQONRAKRYGNI IAYDHSRVILQPVDDPPSSDIYNANYID 959
Db 888 KEYESFEGQSASWDYAKQONRAKRYGNI IAYDHSRVILQPVDDPPSSDIYNANYI- 946
Qy 960 IWLRYDGVQRPSPHYIATQGPVHETVDFWRMVMQESACIWMVTLNVEGRVKCYKWPDP 1019
Db 947 ----DGYQRPSPHYIATQGPVHETVDFWRMVMQESACIWMVTLNVEGRVKCYKWPDP 1001
Qy 1020 DTEVYGDVKTCVEMEPLAEYVVRFTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLL 1079
Db 1002 DTEVYGDVKTCVEMEPLAEYVVRFTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLL 1061
Qy 1080 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIDIMLDMAREGVVDIYNCVKALRSRR 1139
Db 1062 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIDIMLDMAREGVVDIYNCVKALRSRR 1121
Qy 1140 INMVQTEEQIIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDISQTNSSHLKDFEOTLN 1199
Db 1122 INMVQTEEQIIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDISQTNSSHLKDFEOTLN 1181
Qy 1200 SVTPRLQAECDSCIACLPNRHDKNRFMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1259
Db 1182 SVTPRLQAECDSCIACLPNRHDKNRFMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1241
Qy 1260 AAFITVQYPLNTVKDFWRLVYDYGCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVEK 1319
Db 1242 AAFITVQYPLNTVKDFWRLVYDYGCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVEK 1301
Qy 1320 MSCMDCDVINRIFRICNLTRPOEGLVLMVQFQYLGHASHREVPGSKRSTFLKILQVEKW 1379
Db 1302 MSCMDCDVINRIFRICNLTRPOEGLVLMVQFQYLGHASHREVPGSKRSTFLKILQVEKW 1361
Qy 1380 QBECEGEGRITIIHCLNGGSGRMFCAIGIIVEMVKRQNVVDVFAVKTLRNSKPNMVEA 1439
Db 1362 QBECEGEGRITIIHCLNGGSGRMFCAIGIIVEMVKRQNVVDVFAVKTLRNSKPNMVEA 1421
Qy 1440 PEQYRFCYDVALEYLESS 1457
Db 1422 PEQYRFCYDVALEYLESS 1439

RESULT 9
US-08-449-644-8
Sequence 8, Application US/08449644
Patent No. 5856162
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
APPLICANT: Ulrich, Axel
APPLICANT: Vogel, Wolfgang
APPLICANT: Fuchs, Miriam
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

US-08-652-971-4

; Sequence 4, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-652-971-4

Query Match 61.4%; Score 4793.5; DB 2; Length 1452;
Best Local Similarity 61.3%; Pred. No. 0;
Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

QY 22 LIGSALGQPSAGGCTFDGPGACDYHQDLDDFEVWHVSAQPHYLPPMPGSGYMWYDS 81
DB 14 LLLTAAGETFGGCLFDEPYSTCGYSDAEDDFNEHQVNTLTKPTSDPMPGSGFWLNT 73

QY 82 SNHDPGEKARLQLPWKENDTHCIDFSYLLYSQKGLNPGTLMILVRVKNKGPIANPWNVT 141
DB 74 SKPEGORAHLLLPQKENDTHCIDFHYFVSSKNAAPGLLNVVYKVNNGPLGNPWNIS 133

QY 142 GTGRDLRAELAVSTFEMNEVQVFEAVSGRSGYTAIDDIQVLSYPCDKSPHFLRLG 201
DB 134 GQPTTRHRAELAISTFENFQVIFEV-VTSGHQGLAIDEVKVLGHPCETKTPHFLRIQ 192

QY 202 DVEVNAGQATQCIATGDAVHKLWLQRRGEDIPVAQTKNINHRRAFAASFRQEVTK 261
DB 193 NVEVNAGQATFQCSAIGTVAGDRLWLQIDVRDAPLKEIKVTSRRFIASFNVNVTK 252

QY 262 TDQDLRYCVTQSERGSGVSNFAQLIVREPPRIAPQLLGVGPTYLLIQLNANSITGDGP 321
DB 253 RDAGKYRCMCTEGGVGIGNVAELVVKPEPVIAPQLASVGATVLIWLNANSINGDGP 312

QY 322 IILKEVEYRMTSGSWTEHAVNAPTYKLMHLDPDTEYEIRVLLTRPGEGLGCPPLIT 381
DB 313 IVAREVEYCTASGSMNDQFVDSYSYKIGHLPDTEYEISVLLTRPGEGLGSPGPAURT 372

QY 382 RTKCAEPMRTPTKIAETQARRIAVDWESLGNITRCHTFNVNTICYHYFRGHNSRAD- 440
DB 373 RTKCADPMRGPKLEVVEVVKSRQIIRWEPPFGVNVTRCHSYNLTVHYGVQGGQVREE 432

[illegible]

QY 1446 CYDALEYLEL 1456
 DB 1441 CYDALEYLELNS 1451

RESULT 13
 US-08-769-399-4
 ; Sequence 4, Application US/08769399
 ; Patent No. 5976852
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheng, Jill
 ; APPLICANT: Lasky, Laurence A.
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 ; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd.
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/769,399
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: P1033
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 225-3216
 ; TELEFAX: (415) 952-9881
 ; TELEX: 910 371-7168
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1452 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-769-399-4

Query Match 61.4%; Score 4793.5; DB 2; Length 1452;
 Best Local Similarity 61.3%; Pred. No. 0;
 Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

QY 22 LIGSALGQFSAGGCTFDGPGACDYHQLDYDFWVHVSQAQPHYLPPMPGSGVMYVDS 81
 DB 14 LLTLAAGTFTSGCLFDEPYTCGYSQADEDFNMEQVNTLTKPTSDPMPGSGFVLNT 73

QY 82 SNHDPGEARLQPTMKENDTHCIDFSYLLYSQKGLNPGTLNLRVKNKGPLANPIWNT 141
 DB 74 SKPEGORALLLPOLKENDTHCIDFHYFVSKSNAPGLLNLYVKNVNGPLGNINWIS 133

QY 142 GTGDRWLRAELAVSTFWNEVQVTFEAEVSGRSGYIAIDIQVLSVPCDKSPHFLRIG 201
 DB 134 GDTTRTHRAELAISTFWNPNFYQVFEV-VTSGHQYLAIDVKVGLGHPCTRTPHFLRIQ 192

QY 202 DVEVNAQNAATQCATGEDAVHKLWLRNGEDIPVAQTKNINHRPFAASFRLOEVTK 261
 DB 193 NVEVNAQOPATTCQGAIGTAVAGRLWLGIDVDRAPLKEIKVTSRRFIASFNVVNTTK 252

QY 262 TQDLYRCVQTSRSGSVNFAQLIVREPPRIAPQLLGVGPTYLLIQLNANSITGDGP 321
 DB 253 RDAGKYRCMCTEGGVGISNYAEVLVKEPPVPIAPQLASVGATYLIQLNANSINGDGP 312

QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPDTEYEIRVLLTRPGBGGTGLPGPPLIT 381
 DB 313 IVAREVEYCTASGWNDRQPDVSTSYKIGHLDPDTEYEISVLLTRPGBGGTSGPGLART 372

QY 382 RTKCAEPMRTPKTLKIAEIQARRIAVDWESLGNITRCHTFNVITICVHYFRGHNESRAD- 440
 DB 373 RTKCADPMRGPRKLEVEVKSQITIRWEPGYNVTRCHSYNLTVHYQVGGQEQVREE 432

QY 441 -CLDMDPKAFOHVVNHLPPYTNVSLKMLITNPGRKESSEETIIQTDENVPGVPVKSLOG 499
 DB 433 VSWDTNSHPQHITITNLSPYTNVSVKILNMPGRKESQELTVQTDPLGAVPTESIQG 492

QY 500 TSFENKIFLWKEPLENGIITQVEVSVSSRSRSDPAVPVAGPPQTVSNLWNSTHHVPMH 559
 DB 493 SAFEKIFLOWREPTQYGVITLYEITYKAVSSFPDELDLSNQSGRVSUKLNETHFLFFG 552

QY 560 LHPGTTYQFFITRASTVKGFGPATAINVTNINISAPSLPDYEGVDASLNETATTITVLLRPA 619
 DB 553 LYPGTTYFTIRASTAKGFGPPATNQFTTKISAFMPAYE-FETPLNQTDNTVTVMKAPA 611

QY 620 QAKGAPISAYQIVVEQLHPHRTKREAGAMECYVPVTVYQNALSGGAPYFPAELPPGNLP 679
 DB 612 QSRGAPSVTVQIVVEEERPRRTKTKTEILKCYVPVPIHFQNASILNSQYFPAEEFPADSLQ 671

QY 680 EPAPFTVGDNRTYKGFWNPLAPRKGYNIYFQAMSSVEKETKTCQVRIATKAAATEPEV 739
 DB 672 AAQPTTIGDNKTYNGYNTPLLPKHSYRIYQAAASRANGETKIDCVRVATKAVTPKE-- 729

QY 740 IPDPAKQTDNRVVKIAGISAGILVFILLVIVIVVVKSKLAKGRKADMGNTQEMTHVN 799
 DB 730 VPEPEKQTDHTVKIAGVIAGILLVFLGVVLMKKEKLAKKRKETMSSTRQEMTMVN 789

QY 800 AMDSYADQSTLHAEDPLSLTFMDQHNPSPLNDP-----LVPTAVL-DENH 846
 DB 790 SMDKSYAEQGTNCDE--AFSFMGTHNLNGRSVSPSSFTMKTNTLSTSPNSVYPPDETH 846

QY 847 SATAESRLLDVPRY-LCEGTESPVOTGOLHAPRAVADLLOHINLMKTSVSGRKEEYES 905
 DB 847 TMSADTSLAQPHTYTKREAADVPYQGLHAPRAVADLLOHITQMKCAEGTGFKEEYES 906

QY 906 FPEGOSASWDVAKKDONRAKNRYGNIAYDHSRVILQPVEDDPSSDYINANYIDILWYRD 965
 DB 907 FPEGOSAPWDSAKDENEMKNRYGNIAYDHSRVLRVQLMLEDGNNSDYINGNYI-----D 960

QY 966 QYRPSHYIATQGPVHETVYDFWRMVWQESACIIMVTNLVEVGRVKCYKWPDPDTEVYG 1025
 DB 961 GYHRPNHYIATQGPWQETIYDFWRMVWHENTASIIIMVTNLVEVGRVKCYKWPDPDTEIYK 1020

QY 1026 DPKVTCVEMEPLAEVVRFTTLERRGYNEIREVQFHFTGHPDHGVPVYHATGLLSFIRRV 1085
 DB 1021 DIKVTLIDTELLAEYIKTFAVEKRGHIEIRIQFHTGWPDPHGVPTHTATGLLGFVQV 1080

QY 1086 KLSNPPSAGPIVHVHCSAGAGRTGCVIVIDIIMLDAEREGVVDIYNCVKALSRRIINMVT 1145
 DB 1081 KSKSPNAGPLVHCSAGAGRTGCFIVIDIIMLDAEREGVVDIYNCVRELRSRRVNVQT 1140

QY 1146 EQYFIFIHDAILEACLCGETAIPVCEFKAAVDMIRIDISQNTSSHLKDEFTQLNSVTPRL 1205
 DB 1141 EQYVFIHDAILEACLCGDTSGIPASQVRSVLYYDMNKLDPTQNTSSQIKBEFRTLNMTPTL 1200

QY 1206 QAEDCSIACLRNHDKRFDMLPDRCLPILITIDGESSNYINAAIMDSYRQPAFIVT 1265
 DB 1201 RVEDCSIALPRNHEKNKCMIDLIPDRCLPILITIDGESSNYINAAIMDSYKQPSAFIVT 1260

QY 1266 QYPLNVTVKDFWRLVYDYGCTSIYMLNEVDLSQGCPOQWPBEGMLRYGPIQVECMSCSD 1325
 DB 1261 QHPLNVTVKDFWRLVLDVHCTSVMLNDVDPALCPCQWPENGVRHGHGPIQVEFVSADLE 1320

QY 1326 CDVINRIFRIENLTPRQEGYLMVQFOYLGWASHREVPGSKRSFLKILLOVEKWQEEBCE 1385
 DB 1321 EDIISIRIFRIYNASRPQDHRMVQFOFLGMPWVRTDTPVSKRSFLKILRQVDKWQBEYNG 1380

QY 1386 GEGRTIIHCLNGGGSGMFCAGIIVEMVQRNVVDVFHAVKTLRNSKPNMVEAPEQYRF 1445

Db 1381 GEGTVHCLNGGSGTFCALISVCEMLRQRTVDVFAVKTLLRNKNPNWDLDDQYKF 1440
Qy 1446 CYDVALEYLES 1456
Db 1441 CYEVALEYLNS 1451
RESULT 14
US-08-991-953A-4
; Sequence 4, Application US/08991953A
; Patent No. 6083748
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991.953A
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-953A-4
Query Match 61.4%; Score 4793.5; DB 3; Length 1452;
Best Local Similarity 61.3%; Pred. No. 0;
Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;
Qy 22 LLGSAFGSAGGCTFDDPGACDYGHDLYDDFEMVHVSQAQEPHYLPMPQGSVMVYDS 81
Db 14 LLLTAAGETSGGCLFDEPYSTCGYSQADEDDFNEQVNTLTUKFTSDPFWMPGSGFVLVNT 73
Qy 82 SNHDPGKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGTLNILVRNKGGLANPIWNVT 141
Db 74 SKRPEGORAHLLLPOLKENDTHCIDFHYFVSSKSNAPGLLVVYKVNNGPLGNPINIS 133
Qy 142 GFTGRDLRLAELAVSTFWPNEYQVIFEAESVGGSGGYAIDDIQVLSYPCDKSPHFLRLG 201
Db 134 GDPTRTHRAELAISTFWPNFYQVIFEV-VTSGHQGYLAIDEVKVLGHPCRTTRTHFLRIQ 192
Qy 202 DVEVNAQONATFOCIATGRDAVHNKMLQRRNGEDIIPAQTKNINHRFPAAFPLOEVTK 261
Db 193 NVEVNAQOFATFQCSAIGRTVAGDRLWLQGDVDRDAFLKEIKVTSSRRFTASFNVNTTK 252

Qy 262 TDQDLXRCVTSOERSGSVSNFAQLIVREPPRIAPPQLLGVGPTYLLQLNANSINGDP 321
Db 253 RDAGKYRCMICTEGGVGISNVAELVWKPEVPVPIAPPQLASVGATVLIQLNANSINGDP 312
Qy 322 IILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYEIRVLLTRPGGCTGLDGPPLIT 381
Db 313 IVAREVEYCTASGWNDRQPDVSTSYKIGHLDPDTEYEISVLLTRPGGGTSGPGPALRT 372
Qy 382 RTKCAEPMRTPKTLKIAEIOARRIAVDWESLGYNITRCHTNVNTICVHYFRGHNESRAD- 440
Db 373 RTKCADPMRGPRLVVEVVKSRQITIRWEPGVNVTCHSYNLTVHYGVGGQEQVREE 432
Qy 441 CLDMDPKAPQHVHVLPPYTNVSLKMLINPBRKSEETIIOTDDEVPGVPVVKSLQG 499
Db 433 VSWDTNSHPQHTITNLSPYTNVSVKILMLNPEGRKESQELTVQTDDELPAGVPTESIQG 492
Qy 500 TSPENKIFLWKEPLENGIITQVEVSYSSTRSDPAVPVAGPPQTVSNLWNSHTHVPMH 559
Db 493 SAFEKIFLOWREPTQYGVITLYEITYKAVSSFPDEIDLSNQSGRVSUKGNETHFLPFG 552
Qy 560 LHPGTTYQFFIRASTVKGFGPATVNTNISAPSLPDYEGVDASLNETAATTITVLRLPA 619
Db 553 LYPGTTYFTIRASTAKFGGPPATNQFTTKISAPSPAYB-FETPLAQTDNTVIVMLKPA 611
Qy 620 QAKGAPISAYQIVVEQLHPHRTKREAGAMBCYQVPVYQNALSGGAPYFAELPPGNLP 679
Db 612 QSRGAPSVVYQIVVEEERPRRTKTKTEILKCYPPVPIHFQNASILNSQYVFAAEFPADSLQ 671
Qy 680 EPAPFTVDNRITYKGFANPPLAPRGYNIYFOAMSSVEKETKTCVRIATKAAATEPEV 739
Db 672 AAQFTTIGDNKTYNGYWNTEFLPHKSYRIYYQAAASRANGETKIDCVRVATKGVTPKP- 729
Qy 740 IPOPAKQTRVVKIAGISAGILVFILLVIVIVVKSKLAKKRDAMGNTRQEMTHVN 799
Db 730 VPPEKQTDHTVKIAGVIAGILLFVILFGLVLMKKKLLAKKXKETMSSTRQEMTVVN 789
Qy 800 AMDRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDP-----LVPTAVL-DSNH 846
Db 790 SMDKSYAEQGTNCDE--AFSPMGTHNLSRVSVPSSFTMTKTNTLSTSVNSVYVPDETH 846
Qy 847 SATAESRLLDVPRY-LCEGTSPYQGLHPAIRVADLLQHLINLMKTSIDSYGKEEYES 905
Db 847 TMASDTSSLAQPHYTKKREAADVPYQGLHPAIRVADLLQHLITQMKCAEGYKKEEYES 906
Qy 906 FFEGQSASWVAKDONRAKNRYNIIAYDHSRVILOPVEDDPSSDYKNYINIDWLVRD 965
Db 907 FFEGQSAPWSAKKDONRAKNRYNIIAYDHSRVLQWLEGDNNSDINGNYI-----D 960
Qy 966 GYQRPSHYIATQGPVHETVYDFWRMVMQESACIVMVVNLVVEGRVKCYKWPDDTEVYG 1025
Db 961 GYHRPNHYIATQGPVHETVYDFWRMVMHENTASIIIMVNLVVEGRVKCYKWPDDTEVYG 1020
Qy 1026 DFKVTCTVMEPLAEYVVRTTLERRGVNREVKQFHTGPDHGVPHATGLLSFRVRV 1085
Db 1021 DIKVTLLDTELLAEYVIRTEFAVEKRGHIREIRIQFHTGPDHGVPHATGLLGFVRQV 1080
Qy 1086 KLSNPPSAGPIVHCSAGAGRTGCVIVIDMLDMABREGVVYIYNCVKALRSRRINMVQT 1145
Db 1081 KKSPPNAGPLVHCSAGAGRTGCVIVIDMLDMABREGVVYIYNCVKALRSRRINMVQT 1140
Qy 1146 EEQVFIHDAILEACLGETAIIPVCEPKAAYFDMIRIDSQTNSSHLKDEFTQLNSVTPRL 1205
Db 1141 EEQVFIHDAILEACLGETAISIPASQVRSYLYDMNKLDPQTNSSQIKKEEFTLNWVPTL 1200
Qy 1206 QABDCSIACLPNRHDKNRNFMMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVT 1265
Db 1201 RVEDCSIALLPNRHDKNRNFMMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVT 1260
Qy 1266 QYPLPNTVKDFWRLVVDYDGYCTSIUMLNEVDLSQCGQYQWEEGMRLRGVPTQVECKSCSD 1325
Db 1261 QHPLPNTVKDFWRLVLDVHCTSVVMLNDVDPAQLCPQYWPENGVRHHRGPIQVEFVSADLE 1320

Qy	1342	QEGYLMVOQFOYLGWASHREVPGSKRSPLKLILOVEKQWEECEGEGETIIHCLNGGGRS	1401
Db	1320	QEGHLLVRHFQFLWSAYRDTPTDSRKAFLLHLLAEVDKWQ--AESGDGRVTVVHCLNGGGRS	1377
Qy	1402	GMFCAIGIVVEMVKRQNVVDEHAKVTLRNSKPNMVEAPEQYRFCYDVALEYLES	1456
Db	1378	GTFCACTVLEMIRCHSLVDVFFAAKTLRNYKPNNVETMDQYHFCYDVALEYLEA	1432

Search completed: June 1, 2005, 13:57:37
Job time : 41.2113 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:31:52 ; Search time 147.411 Seconds
(without alignments)
3822.724 Million cell updates/sec

Title: US-09-887-669-1
Perfect score: 7809
Sequence: 1 MDVAALPAFVALMLLPW.....EAPQYRFCYDVALEYLESS 1457

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7809	100.0	1457	5	ABB57308 Mouse isc
2	7762	99.4	1457	2	AAR63633 Murine re
3	7586	97.1	1439	2	AAR63632 Human rec
4	7582	97.1	1439	7	ADJ68478 Human hea
5	7567.5	96.9	1440	2	AAJ29591 Human pro
6	7567.5	96.9	1440	8	ADI23886 Human PTP
7	7412	94.9	1407	2	AAR63631 Murine re
8	4823.5	61.8	1452	4	AAJ79159 Human pro
9	4812.5	61.6	1452	6	ABR58629 Human can
10	4812.5	61.6	1452	8	ADI80761 Human pro
11	4789.5	61.3	1452	7	ADJ68277 Human hea
12	4783	61.2	1455	4	AAJ80143 Human pro
13	4591	58.8	1436	7	ADB79775 Rat putat
14	4577	58.6	1499	4	AAJ25768 Human pro
15	4575	58.6	1436	2	AAW41361 Receptor
16	4545	58.2	1462	5	ABB97521 Human hum
17	4542.5	58.2	1463	6	ABJ37035 Human bre
18	4542.5	58.2	1463	7	ADB75519 Prostate
19	4542.5	58.2	1520	5	ABJ05584 Breast ca
20	4359	55.8	1442	7	ADJ68999 Human hea
21	4271	54.7	1430	2	AAW49907 Human pan
22	2471.5	31.6	623	4	AAJ25675 Human pro
23	2216	28.4	815	4	AAJ25875 Human pro
24	1514.5	19.4	1501	2	AAJ72858 Rat recep
25	1495.5	19.2	1948	7	ADD18742 Human dis

26	1494.5	19.1	1796	6	AAE37971	AAE37971 Human kin
27	1494.5	19.1	1949	7	ADE57117	ADE57117 Human pro
28	1494.5	19.1	1949	7	ADE57121	ADE57121 Human pro
29	1494.5	19.1	1949	7	ADD47019	ADD47019 Human pro
30	1494.5	19.1	1949	7	ADD47015	ADD47015 Human pro
31	1492.5	19.1	1897	3	AAJ81785	AAJ81785 Human pro
32	1492.5	19.1	1897	3	AAJ56100	AAJ56100 LAR tyros
33	1492.5	19.1	1897	3	AAJ59712	AAJ59712 Human pro
34	1492.5	19.1	1897	7	ADD18740	ADD18740 Human dis
35	1492.5	19.1	1897	8	ADJ33670	ADJ33670 Human leu
36	1492.5	19.1	1907	8	ADP18674	ADP18674 Human pro
37	1490	19.1	1266	8	ADQ66041	ADQ66041 Novel hum
38	1488.5	19.1	1907	4	AAJ41443	AAJ41443 Human nov
39	1485.5	19.0	1254	8	ADN02662	ADN02662 Liver dis
40	1482.5	19.0	1912	8	ADR40183	ADR40183 Human pro
41	1480	19.0	1911	2	AAJ71726	AAJ71726 Human PTP
42	1480	19.0	1911	2	AAJ27225	AAJ27225 Human pro
43	1480	19.0	1911	2	AAJ94027	AAJ94027 Human pro
44	1476	19.0	1911	4	AAU01459	AAU01459 Human pro
45	1476	18.9	1495	5	ABB57380	ABB57380 Rat mucoc

ALIGNMENTS

RESULT 1

ABB57308
ID ABB57308 standard; protein; 1457 AA.
XX ABB57308;
XX
XX 07-MAR-2002 (first entry)
XX
XX
XX Mouse ischaemic condition related protein sequence SEQ ID NO:862.
XX
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
XX Mus musculus.
XX
XX WO200188188-A2.
XX
XX 22-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-JP004192.
XX
XX 18-MAY-2000; 2000JP-00145977.
XX
XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
XX WPI; 2002-034733/04.
XX N-PSDB; ABI99774.
XX
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.
XX
XX Claim 2; Page 2155-2161; 2690pp; English.
XX
XX The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or

CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
SQ Sequence 1457 AA;

Query Match 100.0%; Score 7809; DB 5; Length 1457;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVAAAALPAFVALWLLYPWLLGALGQFAGGCTFDDGACADYHQDLYDDFEWVHS 60
DB 1 MDVAAAALPAFVALWLLYPWLLGALGQFAGGCTFDDGACADYHQDLYDDFEWVHS 60
QY 61 AOEPHYLPEMPQGSYMWVDSNHDGPKARLQLPTMKENDTHC1DPSYLLYSQKGLNPG 120
DB 61 AOEPHYLPEMPQGSYMWVDSNHDGPKARLQLPTMKENDTHC1DPSYLLYSQKGLNPG 120
QY 121 TLNILLVRNKGFLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESVGGSGYIA 180
DB 121 TLNILLVRNKGFLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESVGGSGYIA 180
QY 181 IDDIQVLSYPCDKSPHFLRLGDEVEYNAGONATFQCIATGRDAVHNKMLQRRNGEDI PVA 240
DB 181 IDDIQVLSYPCDKSPHFLRLGDEVEYNAGONATFQCIATGRDAVHNKMLQRRNGEDI PVA 240
QY 241 QTKNINHRRAASFLQEWTKTDQLYRCVQTSERGSVSNPAQLIVREPPRPPIAPPOLL 300
DB 241 QTKNINHRRAASFLQEWTKTDQLYRCVQTSERGSVSNPAQLIVREPPRPPIAPPOLL 300
QY 301 GVGPTYLILQLNANSIIGDGPITLKEVEYRMTSGSWTETHAVNAPTYKMLHLDPPDTEYI 360
DB 301 GVGPTYLILQLNANSIIGDGPITLKEVEYRMTSGSWTETHAVNAPTYKMLHLDPPDTEYI 360
QY 361 RVLTRPGEGETGLPGPLITRTKCAEPMRTPTKLIKIAEQARRIAVDWESLGYNITRCH 420
DB 361 RVLTRPGEGETGLPGPLITRTKCAEPMRTPTKLIKIAEQARRIAVDWESLGYNITRCH 420
QY 421 TPNVTICVHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESBET 480
DB 421 TPNVTICVHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESBET 480
QY 481 IIOQTDEDVPGPVVKSLOGTSPENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVA 540
DB 481 IIOQTDEDVPGPVVKSLOGTSPENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVA 540
QY 541 GPPQTVSNLWNSHTRHVFVHLHPGTTYYQFFIRASTVKFGFPATAINVTNISAPSLPDYEG 600
DB 541 GPPQTVSNLWNSHTRHVFVHLHPGTTYYQFFIRASTVKFGFPATAINVTNISAPSLPDYEG 600
QY 601 VDASLNETAATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA 660
DB 601 VDASLNETAATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA 660
QY 661 LSGGAPYFAAELPPGNLPEPAPFTVGNRTYKGFNPNPLAPRKGYNIYFOAMSSVEKET 720
DB 661 LSGGAPYFAAELPPGNLPEPAPFTVGNRTYKGFNPNPLAPRKGYNIYFOAMSSVEKET 720
QY 721 KTCQVRIATKAAATEBEPEVDPKQTDORVVKIAGISAGILVFILLLLVIVVVKSKLA 780
DB 721 KTCQVRIATKAAATEBEPEVDPKQTDORVVKIAGISAGILVFILLLLVIVVVKSKLA 780
QY 781 KKRKDMAGNTRQEMTHVNMNDRSADOSTLHAEDPLSLTFMDQNFSPRLPNDPLVPTA 840
DB 781 KKRKDMAGNTRQEMTHVNMNDRSADOSTLHAEDPLSLTFMDQNFSPRLPNDPLVPTA 840
QY 841 VLDEHNSATAESRLLDVPYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYGFK 900
DB 841 VLDEHNSATAESRLLDVPYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYGFK 900
QY 901 EYESFFEGQSASWDVAKKQNRKNRYGNIITAYDHSRVILQPVEDDDPSSDYINANYIDI 960
DB 901 EYESFFEGQSASWDVAKKQNRKNRYGNIITAYDHSRVILQPVEDDDPSSDYINANYIDI 960

QY 961 WLYRDGYQRSHYIATQGPVHETVYDFWRMTWQSQSACIVMTNLVEYGVKCYWPD 1020
DB 961 WLYRDGYQRSHYIATQGPVHETVYDFWRMTWQSQSACIVMTNLVEYGVKCYWPD 1020
QY 1021 TEVTGDFKVCVEMEPLAEYVVRTFTLERRGYNEIREVKQFHFTCWPDHGVYPYHATGLLS 1080
DB 1021 TEVTGDFKVCVEMEPLAEYVVRTFTLERRGYNEIREVKQFHFTCWPDHGVYPYHATGLLS 1080
QY 1081 FIRVKLSNPPSAGPIVVHCSAGAGRTGCIYIVDIMLDMABREGVVDIYNCVKALRSRI 1140
DB 1081 FIRVKLSNPPSAGPIVVHCSAGAGRTGCIYIVDIMLDMABREGVVDIYNCVKALRSRI 1140
QY 1141 NMVQTESQYIFIHDAIILEACLCEGTAIPVCEFKAAAFDMIRIDQTSNSSLKDEFQTLNS 1200
DB 1141 NMVQTESQYIFIHDAIILEACLCEGTAIPVCEFKAAAFDMIRIDQTSNSSLKDEFQTLNS 1200
QY 1201 VTPRLQAEDECSIACLPRNHDKNRMDMLPPDRCLPFLITIDGESNYINAALMDSYRPA 1260
DB 1201 VTPRLQAEDECSIACLPRNHDKNRMDMLPPDRCLPFLITIDGESNYINAALMDSYRPA 1260
QY 1261 AFIVTQVPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCQYWPPEGMLRYGPIQVECM 1320
DB 1261 AFIVTQVPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCQYWPPEGMLRYGPIQVECM 1320
QY 1321 SCSNDCDVINRIFRICNLTRPOEGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKWQ 1380
DB 1321 SCSNDCDVINRIFRICNLTRPOEGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKWQ 1380
QY 1381 ECEGEGRTIHCINGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
DB 1381 ECEGEGRTIHCINGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
QY 1441 EQYRFCYDVALEYLESS 1457
DB 1441 EQYRFCYDVALEYLESS 1457

RESULT 2
AAR63633
ID AAR63633 standard; protein; 1457 AA.
XX AAR63633;
AC AAR63633;
DT 21-OCT-2004 (revised)
DT 25-MAR-2003 (revised)
DT 08-JUN-1995 (first entry)
XX
DE Murine receptor-type protein tyrosine phosphatase precursor protein.
XX Receptor-type protein tyrosine phosphatase protein; cellular signal;
KW RPTase-kappa; enzyme.
XX Mus musculus.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= signal
FT Region 33..189
FT /label= A5 surface protein homology
FT Domain 733..774
FT /label= Transmembrane
FT Domain 926..1158
FT /label= PTPase I
FT Domain 1218..1455
FT /label= PTPase II
XX
PN WO9424161-A1.
XX
PD 27-OCT-1994.
XX
PF 20-APR-1994; 94WO-US004377.

XX 21-APR-1993; 93US-00049384.
 PR 01-JUL-1993; 93US-00087244.
 XX (UNY-) UNIV NEW YORK MEDICAL CENT.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;
 PI WPI; 1994-341769/42.
 XX N-PSDB; AAO72914.
 DR Mammalian receptor-type protein tyrosine phosphatase-kappa (RTP-k)
 XX protein and DNA - useful to identify cpds. which bind to RTP-k and
 PT modulate enzymatic activity. Also inhibition of type II RTP homo:phili
 PT binding (Engl).
 XX Claim 2; Fig 1; 144pp; English.
 PS The novel receptor-type protein tyrosine phosphatase protein or
 XX Glycoprotein is termed RTP kappa (also known as Rptase-kappa). The first
 CC approx. 170AAs of RTP kappa show similarity (26% overall identity) to a
 CC region in the Xenopus cell surface protein A5 with features of Ig-like
 CC domains. There are four putative fibronectin type III-like repeats
 CC (residues 236-681). The tandem repeat of two Fipase homologies is typical
 CC for most RPTases. A feature of RTP kappa is the extended distance
 CC between its transmembrane domain and the start of the first phosphatase
 CC homology domain. The RTP kappa cDNA sequence comprises a 5' UTR of 1072
 CC bps and a 3' UTR of 388 bps. The translational initiation codon is
 CC identified by a std. environmtn for initiation of translation (Kozak)
 CC and by the existence of an upstream in-frame stop codon, and is followed
 CC by a hydrophobic region that may serve as a signal peptide. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 CC Revised record issued on 21-OCT-2004 : Correction to feature table key
 XX Sequence 1457 AA;

Query Match 99.4%; Score 7762; DB 2; Length 1457;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1449; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDVAAALPAFVALWLLYPWLLGSLGQFSAGCTPDDGFGACDHYHQDLYDDPFWVHVS 60
 DB 1 MDVAAALPAFVALWLLYPWLLGSLGQFSAGCTPDDGFGACDHYHQDLYDDPFWVHVS 60

QY 61 AQSPHYLPPEMPOGSMVVDSSNHDGCEKARLQLPTMKENDTHCIDPSYLLYSQKGLNPG 120
 DB 61 AQSPHYLPPEMPOGSMVVDSSNHDGCEKARLQLPTMKENDTHCIDPSYLLYSQKGLNPG 120

QY 121 TLMILVRVNGKPLANPIWNTGTGRDMLRAELAVSTFWPNEYQVIFEAEVSGRSGYIA 180
 DB 121 TLMILVRVNGKPLANPIWNTGTGRDMLRAELAVSTFWPNEYQVIFEAEVSGRSGYIA 180

QY 181 IDIQVLSYPCDKSPHFLRGDVEVNAQONATFCIATGRDAVHKNLWLRNGEDIPVA 240
 DB 181 IDIQVLSYPCDKSPHFLRGDVEVNAQONATFCIATGRDAVHKNLWLRNGEDIPVA 240

QY 241 OTKNINHRRAAASFRLOEVTKTDQDLYRCVYQTSERGSGVSNFAQLIVREPPRIAPQLL 300
 DB 241 OTKNINHRRAAASFRLOEVTKTDQDLYRCVYQTSERGSGVSNFAQLIVREPPRIAPQLL 300

QY 301 GVGPYLLIQLNANSIIGDGPILIKVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYEI 360
 DB 301 GVGPYLLIQLNANSIIGDGPILIKVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYEI 360

QY 361 RVLLTRPEGGTGLPGPPLITRTKCAEPMRTPTKTKIAEQARRIAVDWESLGYNITRCH 420
 DB 361 RVLLTRPEGGTGLPGPPLITRTKCAEPMRTPTKTKIAEQARRIAVDWESLGYNITRCH 420

QY 421 TFWNTICYHYFRGHNESRACLDMDPKAPOHVNVNHLPPYTNVSLKMLITNPEGRKSEET 480
 DB 421 TFWNTICYHYFRGHNESRACLDMDPKAPOHVNVNHLPPYTNVSLKMLITNPEGRKSEET 480

RESULT 3
 AAR63632
 ID AAR63632 standard; protein; 1439 AA.

QY 481 IIQTDEBVPGPVPVKSLQGSTFENKIFLNWKEPLEPNGIIITQYEVSVSSIRSDPAVPVA 540
 DB 481 IIQTDEBVPGPVPVKSLQGSTFENKIFLNWKEPLEPNGIIITQYEVSVSSIRSDPAVPVA 540

QY 541 GPPQTYSNLWNSTHVVFMHLHPCGTYQFFIRASTVKGFGPATAINVTNTISAPSLPYEG 600
 DB 541 GPPQTYSNLWNSTHVVFMHLHPCGTYQFFIRASTVKGFGPATAINVTNTISAPSLPYEG 600

QY 601 VDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQNA 660
 DB 601 VDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQNA 660

QY 661 LSGGAPYFAAEELPPGNLPEPAPFTVGDNRTYGFNPPPLAPRKGYNIYFOAMSSVKEKET 720
 DB 661 LSGGAPYFAAEELPPGNLPEPAPFTVGDNRTYGFNPPPLAPRKGYNIYFOAMSSVKEKET 720

QY 721 KTCQVRIATKAAATEBEVIPPDAKQTDVRVKIAGISAGILVFTLLLVIVIVKSKLA 780
 DB 721 KTCQVRIATKAAATEBEVIPPDAKQTDVRVKIAGISAGILVFTLLLVIVIVKSKLA 780

QY 781 KKKKDANGNTRQEMTHVWNAADRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840
 DB 781 KKKKDANGNTRQEMTHVWNAADRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840

QY 841 VLDENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLINLMKTSDSYGFK 900
 DB 841 VLDENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLINLMKTSDSYGFK 900

QY 901 EYESFFEGQASADVAKQDNRAKRYGNIIDYHSRVILQVDEDDPSSDIYANVIDI 960
 DB 901 EYESFFEGQASADVAKQDNRAKRYGNIIDYHSRVILQVDEDDPSSDIYANVIDI 960

QY 961 WLVRDGYQPSHVIATQGPVHETVYDFWRMWQEQSACIWMVTNLVEVGRVKCYKWPDD 1020
 DB 961 WLVRDGYQPSHVIATQGPVHETVYDFWRMWQEQSACIWMVTNLVEVGRVKCYKWPDD 1020

QY 1021 TEYVGDPKVTCVEMPLAEYVVRTFTLRRGYNEIREVKQFHTGPDHGVPHATGLLS 1080
 DB 1021 TEYVGDPKVTCVEMPLAEYVVRTFTLRRGYNEIREVKQFHTGPDHGVPHATGLLS 1080

QY 1081 FIRRKLNSPPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRI 1140
 DB 1081 FIRRKLNSPPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRI 1140

QY 1141 NMVQTEEQYIFHDAILEACLCGETAIPVCEFKAAVFDIMIRIDISQTNSSHLKDEFOFLNS 1200
 DB 1141 NMVQTEEQYIFHDAILEACLCGETAIPVCEFKAAVFDIMIRIDISQTNSSHLKDEFOFLNS 1200

QY 1201 VTPRLQAECDCSIACLPRNHDKNRFDMDLPPDRCLPFLITIDGESSNYINAALMDSYRQPA 1260
 DB 1201 VTPRLQAECDCSIACLPRNHDKNRFDMDLPPDRCLPFLITIDGESSNYINAALMDSYRQPA 1260

QY 1261 AFITVQYPLPNTVKDFWRLVYDYGCTSIVMNEVDLSQGCPOQYWPBEGMLRYGPIQVECM 1320
 DB 1261 AFITVQYPLPNTVKDFWRLVYDYGCTSIVMNEVDLSQGCPOQYWPBEGMLRYGPIQVECM 1320

QY 1321 SCSDMCDVNRIFRIENLTPQEGYLMVQOQFQYLGWASHREVPGSKESFLKLILQVEKMQ 1380
 DB 1321 SCSDMCDVNRIFRIENLTPQEGYLMVQOQFQYLGWASHREVPGSKESFLKLILQVEKMQ 1380

QY 1381 EECBEGEGRTIHCINGGGRSGMFCFCAIGIVEMVKGQNVVDVFAVKTLSKNSKNMVEAP 1440
 DB 1381 EECBEGEGRTIHCINGGGRSGMFCFCAIGIVEMVKGQNVVDVFAVKTLSKNSKNMVEAP 1440

QY 1441 EQYRFCYDVALEYLESS 1457
 DB 1441 EHYRFCYDLPDLEYLESS 1457

Db 1062 SFIRVKLSPPSAGPIVHCSAGAGRTGCVIIDMLDAERGVDYIYNCVKALRSR 1121
Qy 1140 INMQTEEQYIFIHDAILEACLCGETAIPVCEFAAAYFDMIRIDSQTNSSHLKDEFOFLN 1199
Db 1122 INMQTEEQYIFIHDAILEACLCGETAIPVCEFAAAYFDMIRIDSQTNSSHLKDEFOFLN 1181
Qy 1200 SVTPRLQAECSIACLPRNHDKNRFDMLPPDRCLPLITIDGSSNYINAALMDSYRQP 1259
Db 1182 SVTPRLQAECSIACLPRNHDKNRFDMLPPDRCLPLITIDGSSNYINAALMDSYRQP 1241
Qy 1260 AAFITVQYPLPNTVKDFWRLVYDGYCTSIWMLNEVDLSQCPQYWPEEGLRYGPIQVEK 1319
Db 1242 AAFITVQYPLPNTVKDFWRLVYDGYCTSIWMLNEVDLSQCPQYWPEEGLRYGPIQVEK 1301
Qy 1320 MSCSMDCDVINRIFRICNLTRPQBYGLMVQOQFYLGWASHREVPGSKRSFLKILLOVEKW 1379
Db 1302 MSCSMDCDVINRIFRICNLTRPQBYGLMVQOQFYLGWASHREVPGSKRSFLKILLOVEKW 1361
Qy 1380 QEBCEGEGRITIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILRNSKPNMVEA 1439
Db 1362 QEBCEGEGRITIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILRNSKPNMVEA 1421
Qy 1440 PEQYRFCYDVALEYLESS 1457
Db 1422 PEQYRFCYDVALEYLESS 1439

RESULT 4
ADJ68478
ID ADJ68478 standard; protein; 1439 AA.
XX ADJ68478;
AC
CC
DT 06-MAY-2004 (first entry)
XX Human heat mitochondrial protein as a therapeutic target SeqID284.
DE
XX mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN W02003087768-A2.
XX
XX 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DB;
XX
XX WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 284; 180pp; English.
PS
XX

CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 1439 AA;

Query Match 97.1%; Score 7592; DB 7; Length 1439;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1420; Conservative 13; Mismatches 5; Indels 20; Gaps 4;

Qy 1 MD-VAAALPAFVALWLLYEPWLLGSAFGSAGGCTFDDGPGACDYHQDLYDDFEWVHV 59
Db 1 MDTTAAALPAFVALLLSPWLLGSAQGFAGGCTFDDGPGACDYHQDLYDDFEWVHV 60

Qy 60 SAQEPHYLPPEMQGSSYMWVDSNNDHDPGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 119
Db 61 SAQEPHYLPPEMQGSSYMWVDSNNDHDPGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120

Qy 120 GTNLILVRNKGPIANPIMNVGTGTGRDMLRABLAIVTFWPNVEYQVTFEAEVSGRSGYI 179
Db 121 GTNLILVRNKGPIANPIMNVGTGTGRDMLRABLAIVTFWPNVEYQVTFEAEVSGRSGYI 180

Qy 180 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAQONATFOCIATGRDAVHKLWQRRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAQONATFOCIATGRDAVHKLWQRRNGEDIPV 240

Qy 240 AQTKNINHRFAAFRLQEVTKTDQDLYRCVTSQSGSVSNFAQLIVRPPRIAPPOL 299
Db 241 AQTKNINHRFAAFRLQEVTKTDQDLYRCVTSQSGSVSNFAQLIVRPPRIAPPOL 300

Qy 300 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPPDTEYE 359
Db 301 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPPDTEYE 360

Qy 360 IRVLLTRPGEAGTGLPGPLITITKCAEPMRTPTKTKIAEIQARRIAVDHESLGYNTTRC 419
Db 361 IRVLLTRPGEAGTGLPGPLITITKCAEPMRTPTKTKIAEIQARRIAVDHESLGYNTTRC 420

Qy 420 HTFNVTICVHYFRGHNESRADCLMDPKAPQHVHNLPPYTNVSLKMLTNPEGRKESEE 479
Db 421 HTFNVTICVHYFRGHNESRADCLMDPKAPQHVHNLPPYTNVSLKMLTNPEGRKESEE 480

Qy 480 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKEPLFNGIITQVEYSYSSIRGFPDPAVPV 539
Db 481 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKEPLFNGIITQVEYSYSSIRGFPDPAVPV 540

Qy 540 AGPPQTVSNLWNSHTHVFHMLHFGTYTQFFIRASTVKGFGPATAINVTNISAPSLDYE 599
Db 541 AGPPQTVSNLWNSHTHVFHMLHFGTYTQFFIRASTVKGFGPATAINVTNISAPSLDYE 600

Qy 600 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQON 659
Db 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQON 660

Qy 660 ALSGGAPYFAAEPLPGNLPPEPAPFTVGDNRITKGFNPNPLAPRKGNINIFQAMSSYEKE 719
Db 661 AMSGGAPYFAAEPLPGNLPPEPAPFTVGDNRITKGFNPNPLAPRKGNINIFQAMSSYEKE 720

Qy 720 TKTQCVRATKAATBEPEVIPPAPKQTRDVKIAGISAGILVPIILLVIVIVKSKL 779
Db 721 TKTQCVRATKAATBEPEVIPPAPKQTRDVKIAGISAGILVPIILLVIVIVKSKL 779

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QY 780 AKKRDAMGNTROETHMUNAMDRSYADOSTLHAEDPLSLTFMDOHNFSPRLPNDPLVPT 839
Db 780 AKKRDAMGNTROETHMUNAMDRSYADOSTLHAEDPLSLTFMDOHNFSPRY----- 831
QY 840 AVLDEHNSATAESSRLLDVPRYLCGTESPYQTQLHPAIRVAIDLQHLINLMKTSDSYGF 899
Db 832 ----ENHSATAESSRLLDVPRYLCGTESPYQTQLHPAIRVAIDLQHLINLMKTSDSYGF 887
QY 900 KEEVESFEGQSASWDVAKQONRAKRYGNIAYDHSRVLQPVEDDPSSDIYANAYID 959
Db 888 KEEVESFEGQSASWDVAKQONRAKRYGNIAYDHSRVLQPVEDDPSSDIYANAYI- 946
QY 960 IWLVDGYORSHYIATGPHVETVYDFRWVWQESACIWMVTNLVEGVKCKYKWD 1019
Db 947 -----DGYORSHYIATGPHVETVYDFRWVWQESACIWMVTNLVEGVKCKYKWD 1001
QY 1020 DTEVYGFKVCVENEPALAEYVVRTFTLLRRGYNEIREVKQFHFPTGWDHGVPHATGLL 1079
Db 1002 DTEVYGFKVCVENEPALAEYVVRTFTLLRRGYNEIREVKQFHFPTGWDHGVPHATGLL 1061
QY 1080 SFIRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIMDMAEREGVVDIYNCVKALRSRR 1139
Db 1062 SFIRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIMDMAEREGVVDIYNCVKALRSRR 1121
QY 1140 INMVQTESQYIFIHDAILEACLCEGTALPVCEFAAYEDMIRIDISQTNSSHLKDFQTLN 1199
Db 1122 INMVQTESQYIFIHDAILEACLCEGTALPVCEFAAYEDMIRIDISQTNSSHLKDFQTLN 1181
QY 1200 SVTPRLQAECDSCIACLRNHDKNRPMWMLPPDRCLPFLITIDGESSNINAAALMDSYRQP 1259
Db 1182 SVTPRLQAECDSCIACLRNHDKNRPMWMLPPDRCLPFLITIDGESSNINAAALMDSYRQP 1241
QY 1260 AAFIVTQYPLNVTXDFWRLVYDYXCTSIIVMLNEVDLSQGGCPQYWPEBGLRYGPIQVEK 1319
Db 1242 AAFIVTQYPLNVTXDFWRLVYDYXCTSIIVMLNEVDLSQGGCPQYWPEBGLRYGPIQVEK 1301
QY 1320 MSCSMDCDVINRIFRICNLTRPQEGYLMVQFOYLGWASHREVPGSKSFLKILLOVEKW 1379
Db 1302 MSCSMDCDVINRIFRICNLTRPQEGYLMVQFOYLGWASHREVPGSKSFLKILLOVEKW 1361
QY 1380 QEBCEGEGRTIIHCLNGGSGMFCAGIVVEMVKRONVVDVFAVKTLRNSKPNMVEA 1439
Db 1362 QEBCEGEGRTIIHCLNGGSGMFCAGIVVEMVKRONVVDVFAVKTLRNSKPNMVEA 1421
QY 1440 PEQYRFCYDVALEYLESS 1457
Db 1422 PEQYRFCYDVALEYLESS 1439

RESULT 5
AA29591
ID AA29591 standard; protein; 1440 AA.
XX AC
XX AA29591;
DT 14-OCT-1999 (first entry)
XX DE
XX Human protein phosphatase k.
XX Human; protein phosphatase k; HPTPK.
XX Homo sapiens.
XX KR98026246-A.
XX 15-JUL-1998.
XX 08-OCT-1996; 96KR-00044614.
XX 08-OCT-1996; 96KR-00044614.
XX (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
PA
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XX Hah HJ, Kil MC, Yang Y, Byun GH;
XX WPI; 1999-335582/28.
XX N-ESDB; AA208539.
XX Human protein phosphatase, base sequence thereof and amino acid sequence
XX thereof.
XX Disclosure; Fig 1a-d; 14pp; Korean.
XX The present sequence represents human protein phosphatase k (HPTPK)
XX Sequence 1440 AA;
QY Query Match 96.9%; Score 7567.5; DB 2; Length 1440;
Db Best Local Similarity 97.0%; Pred. No. 0;
QY Matches 1414; Conservative 16; Mismatches 9; Indels 19; Gaps 3;
QY 1 MD-VAAALPAFVALMLLYPWLILGSLGALGQSGAGCTFDDGPGACDYHODLYDDPEWVHV 59
Db 1 MDTTAAALPAFVALMLLYPWLILGSLGALGQSGAGCTFDDGPGACDYHODLYDDPEWVHV 60
QY 60 SAQEPHYLPPMPGSGYMWVDSNHDPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 119
Db 61 SAQEPHYLPPMPGSGYMWVDSNHDPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120
QY 120 GTLNLVRVNGKPLANPINWVTGTRDMLRAELAVSTFWPNEYQVIFPEAEVSGRSGYI 179
Db 121 GTLNLVRVNGKPLANPINWVTGTRDMLRAELAVSTFWPNEYQVIFPEAEVSGRSGYI 180
QY 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFCIATGTRDAVHNKMLQRRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFCIATGTRDAVHNKMLQRRNGEDIPV 240
QY 240 AQTKNINHRFAASFRLOEVTKTDQDLYRCVTVQSERGSGVSNFAQLIVREPPRPIAPQL 299
Db 241 AQTKNINHRFAASFRLOEVTKTDQDLYRCVTVQSERGSGVSNFAQLIVREPPRPIAPQL 300
QY 300 LGVGFTYLLIQLNANSIIGDGPILKEVEYMTSGSWTETHAVNAPTYKJLWHLDPDTEYE 359
Db 301 LGVGFTYLLIQLNANSIIGDGPILKEVEYMTSGSWTETHAVNAPTYKJLWHLDPDTEYE 360
QY 360 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKTLKIAEIOARRIADVMSLGNITRC 419
Db 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKTLKIAEIOARRIADVMSLGNITRC 420
QY 420 HTFNVTICYHYFRGHNESRADCLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESSE 479
Db 421 HSFNVTICYHYFRGHNESKADCLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESSE 480
QY 480 TTIQTDSDVPGVVVKSLQGTSTFENKIPLNWKPELPNGIITQYEVSVSSIRSFDPAPVP 539
Db 481 TTIQTDSDVPGVVVKSLQGTSTFENKIPLNWKPELPNGIITQYEVSVSSIRSFDPAPVP 540
QY 540 AGPQTVSNLWNSTHVVFMHLHPGTYQFFTRASTVKGFGPATAINVTNINSAPSLDPE 599
Db 541 AGPQTVSNLWNSTHVVFMHLHPGTYQFFTRASTVKGFGPATAINVTNINSAPSLDPE 600
QY 600 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 659
Db 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 660
QY 660 ALSGGAPYFAELPPGNLPEPAPFTVGDNRNTPYKGFWMNPPPLAPRGYNYIYFOAMSVEKE 719
Db 661 AMSGGAPYFAELPPGNLPEPAPFTVGDNRNTPYKGFWMNPPPLAPRGYNYIYFOAMSVEKE 720
QY 720 TKTCVRIATKAAATEEPEVDPKAKOTDRVVVKTAGISAGILVFTLLLVIVIVKSKL 779
Db 721 TKTCVRIATKAAATEEPEVDPKAKOTDRVVVKTAGISAGILVFTLLLVIVIVKSKL 780
QY 780 AKKRDAMGNTROETHMUNAMDRSYADOSTLHAEDPLSLTFMDOHNFSPRLPNDPLVPT 839
Db 780 AKKRDAMGNTROETHMUNAMDRSYADOSTLHAEDPLSLTFMDOHNFSPRLPNDPLVPT 839
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Db      781 AKRKDAMGNTRQEMTHWVAMDRSYADQSTLHAEDPLSITFMDOHNFSPRY----- 832
Qy      840 AVLDENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLINLMKTSYGF 899
Db      833 ---ENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLINLMKTSYGF 888
Qy      900 KEVESFFEGQSADWVAKKQDNRAKRYGNIITAYDHSRVLQPVEDDPSDDYINANYID 959
Db      889 KEYESFFEGQSADWVAKKQDNRAKRYGNIITAYDHSRVLQPVEDDPSDDYINANYI- 947
Qy      960 IWLRYDQYQPSHYIATQGPVHETVDFWVRWQESACIVMTNLVEGRVKCYKWPD 1019
Db      948 -----DGYQPSHYIATQGPVHETVDFWVRWQESACIVMTNLVEGRVKCYKWPD 1002
Qy      1020 DTEVYGDVKVTCVEMEPLASYVVRFTFLRRGYNEIREVKQHFHTGHPDHGVPYHATGLL 1079
Db      1003 DTEVYGDVKVTCVEMEPLASYVVRFTFLRRGYNEIREVKQHFHTGHPDHGVPYHATGLL 1062
Qy      1080 SFTRRVKLSNPPSAGPIVHCHSAGAGRTGCVIIVIDIMLMAEREGVVDIYNCVKALBSRR 1139
Db      1063 SFTRRVKLSNPPSAGPIVHCHSAGAGRTGCVIIVIDIMLMAEREGVVDIYNCVKALBSRR 1122
Qy      1140 INNVQTEEQYIFTHDAILEACLCETAIPVCEPKAAVFDIMIRIDQSNSSHLKDEFOFOTLN 1199
Db      1123 INNVQTEEQYIFTHDAILEACLCETAIPVCEPKAAVFDIMIRIDQSNSSHLKDEFOFOTLN 1182
Qy      1200 SVTPRLQAECDSCIACLRNHDKNRPFMDLPPDRCLPELITIDGESSNYINAALMDSYRQP 1259
Db      1183 SVTPRLQAECDSCIACLRNHDKNRPFMDLPPDRCLPELITIDGESSNYINAALMDSYRQP 1242
Qy      1260 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQVWPBEGMLRYGPTQVEC 1319
Db      1243 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQVWPBEGMLRYGPTQVEC 1302
Qy      1320 MSCMCDVNLNRFICNLNTRPOEGLMWQOFOYLGWASHREVPGSKRSFLKLILOVEKW 1379
Db      1303 MSCMCDVNLNRFICNLNTRPOEGLMWQOFOYLGWASHREVPGSKRSFLKLILOVEKW 1362
Qy      1380 QEECEGEGRITIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILRNSKPNMVEA 1439
Db      1363 QEECEGEGRITIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILRNSKPNMVEA 1422
Qy      1440 PEQYRCYDVALEYLESS 1457
Db      1423 PEQYRCYDVALEYLESS 1440

RESULT 6
ADI23886
ID      ADI23886 standard; protein; 1440 AA.
XX
AC      ADI23886;
XX
AC      ADI23886;
XX
DT      22-APR-2004 (first entry)
XX
DE      Human PTPRK protein SEQ ID NO:4.
XX
KW      antisense oligonucleotide; human;
KW      protein tyrosine phosphatase receptor type K; PTPRK; cytostatic;
KW      antiinflammatory; antidiabetic; antisense gene therapy; diabetes;
KW      inflammation; hyperproliferative disorder; cancer; chromosome 6.
XX
OS      Homo sapiens.
XX
PN      WO2004005312-A1.
XX
PD      15-JAN-2004.
XX
PF      27-JUN-2003; 2003WO-US016237.
XX
PR      03-JUL-2002; 2002US-00189429.
XX
PA      (ISIS-) ISIS PHARM INC.

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XX      Cowsert LM, Freier SM;
PI      WPI; 2004-083493/08.
XX      DR      N-PSDB; ADI23748.
XX      PT      New antisense oligonucleotide, having a sequence targeted to a nucleic
PT      acid encoding PTPRK, useful for preparing a composition for treating
PT      diabetes, inflammation or hyperproliferative disorder, e.g., cancer.
XX      XX      Example 13; SEQ ID NO 4; 150pp; English.
PS      The present invention describes an antisense oligonucleotide (I), having
PS      a sequence comprising 8-80 base pairs, targeted to a nucleic acid
CC      encoding protein tyrosine phosphatase receptor type K (PTPRK), that
CC      specifically hybridizes with the nucleic acid encoding PTPRK and inhibits
CC      expression of PTPRK. Also described: (1) a composition comprising the
CC      compound and a carrier or diluent; (2) a method of inhibiting the
CC      expression of PTPRK in cells or tissues; (3) a method of treating an
CC      animal having or suspected of having a disease or condition associated
CC      with PTPRK; and (4) a method for screening for an antisense compound. (I)
CC      has cytostatic, antiinflammatory and antidiabetic activities, and can be
CC      used in antisense gene therapy. The antisense oligonucleotide (I) can be
CC      used for preparing a composition for treating diabetes, inflammation or
CC      hyperproliferative disorder, e.g., cancer. The present sequence
CC      represents human PTPRK, which is used in an example from the present
CC      invention. The human PTPRK gene is located on chromosome 6, more
CC      specifically to 6q22.2-23.1.
XX      SQ      Sequence 1440 AA;

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Query Match      96.9%; Score 7567.5; DB 8; Length 1440;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 1414; Conservative 16; Mismatches 9; Indels 19; Gaps 3;

Qy      1 MD-VAANLPAFVALWLLYFWPLLSALGQFSAGGCTFDDGACDQHLYDDFEWVHV 59
Db      1 MDTAAAAVPAFVALLLLSPWLLLSAQQFSAGGCTFDDGACDQHLYDDFEWVHV 60
Qy      60 SAQEPHYLPPEMQSGYVMVVDSSNHPDGEKARLQPLTKENDTHCIDFSYLLYSQKGLNP 119
Db      61 SAQEPHYLPPEMQSGYVMVVDSSDHPDGEKARLQPLTKENDTHCIDFSYLLYSQKGLNP 120
Qy      120 GTNLILVRVNGKPLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFAEVSGRSGYI 179
Db      121 GTNLILVRVNGKPLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFAEVSGRSGYI 180
Qy      180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKMLQRRNGEDIPV 239
Db      181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKMLQRRNGEDIPV 240
Qy      240 AQTKNINHRRAFAAFRLQEVTKTDQDLRYRCVTSERGSVSNFAQLIVREPPRPIAPPQL 299
Db      241 AQTKNINHRRAFAAFRLQEVTKTDQDLRYRCVTSERGSVSNFPQLIVREPPRPIAPPQL 300
Qy      300 LGVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 359
Db      301 LGVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 360
Qy      360 IRVLLTRPGEGGTGLPGPPLITTKCAEPNRTKTLKIAIRRAVADVHESLYGNITRC 419
Db      361 IRVLLTRPGEGGTGLPGPPLITTKCAEPNRTKTLKIAIRRAVADVHESLYGNITRC 420
Qy      420 HTFNVTICVHYFRGHNESRADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPEGRKESEE 479
Db      421 HSNVTICVHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPEGRKESEE 480
Qy      480 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKSEPLEPNGIITQYEVSYSSIRSFDPAPVP 539
Db      481 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKSEPLEPNGIITQYEVSYSSIRSFDPAPVP 540
Qy      540 AGPPQTVSNLWNSHTHVFMHLHGGTYTQFPPIRSTVKGFGPAPATINVTTHISAPSLDYE 599

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Db 541 AGPQTQVNLNNSTHVHMLHPGTTGYQFFIRASTVKGFGPATAINVTNNTISAPTLDPYE 600
QY 600 GVDASLNSTATITVLLRPAQAKGAPISAYQIVBQLHPHRTKRBAGAMECYQVPVYQN 659
Db 601 GVDASLNSTATITVLLRPAQAKGAPISAYQIVBQLHPHRTKRBAGAMECYQVPVYQN 660
QY 660 ALSGGAPYFAELPPGNLPAPAPFTVGDNRITKGFWMNPPLAPRGYNIYFQAMSSVEKE 719
Db 661 AMSGGAPYFAELPPGNLPAPAPFTVGDNRITKGFWMNPPLAPRGYNIYFQAMSSVEKE 720
QY 720 TKTCQVRIATKAAATEEPEVDPDPKQTDVVVKIAGISAGILVFLILLVIVIVKSKL 779
Db 721 TKTCQVRIATKAAATEEPEVDPDPKQTDVVVKIAGISAGILVFLILLVIVIVKSKL 780
QY 780 AKKRKDMGNTROEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPT 839
Db 781 AKKRKDMGNTROEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPT 840
QY 840 AVLDEHNSATAESSLLDVPVRLCEGTSPYOTGOLHGAIRVADLLOHINLMKTSYGF 899
Db 841 AVLDEHNSATAESSLLDVPVRLCEGTSPYOTGOLHGAIRVADLLOHINLMKTSYGF 900
QY 900 KEEYESFEGQSASMDVAKDONAKRNYGNIIAVDHSRVLQPVEDDPSDDYINANYID 959
Db 901 KEEYESFEGQSASMDVAKDONAKRNYGNIIAVDHSRVLQPVEDDPSDDYINANYID 960
QY 960 IWLRYGQRPESHYIATQSPVHETVYDFWRMVQESACIWMVNTLVEGRVKCYKYPWD 1019
Db 961 IWLRYGQRPESHYIATQSPVHETVYDFWRMVQESACIWMVNTLVEGRVKCYKYPWD 1020
QY 1020 DTEVYGDQKVTQVMEPLAEYVVRTFLERGGYNEIREVKQPHFTGWPDPVPHATGLL 1079
Db 1021 DTEVYGDQKVTQVMEPLAEYVVRTFLERGGYNEIREVKQPHFTGWPDPVPHATGLL 1080
QY 1080 SFIRRVKLSNPSPAGFIVVHCSAGAGRTGCIYIVDMLDMAEREGVDIYNCVKALRSR 1139
Db 1081 SFIRRVKLSNPSPAGFIVVHCSAGAGRTGCIYIVDMLDMAEREGVDIYNCVKALRSR 1140
QY 1140 INNVQTEQYIFIHDAILEACLCGETAIPVCFFKAAAYFDMIRIDISQTNSSHLKDBFQTLN 1199
Db 1141 INNVQTEQYIFIHDAILEACLCGETAIPVCFFKAAAYFDMIRIDISQTNSSHLKDBFQTLN 1200
QY 1200 SVTPRLQAEDECSIACLPRNHDKNRMDFMLPPDRCPLFLITIDGESSNYINAAALMDSYRQ 1259
Db 1201 SVTPRLQAEDECSIACLPRNHDKNRMDFMLPPDRCPLFLITIDGESSNYINAAALMDSYRQ 1260
QY 1260 AAFIVTQYPLPNTVDFWRLVYDYGCTSIWMLNEVDLSQGCPCQYWPBEGMLRYGPIQVE 1319
Db 1261 AAFIVTQYPLPNTVDFWRLVYDYGCTSIWMLNEVDLSQGCPCQYWPBEGMLRYGPIQVE 1320
QY 1320 MSCMDCDVINRIFRICNLTRPOEGYLMVQOYQYILGWASHREVPGSKSFLKLIQVEKW 1379
Db 1321 MSCMDCDVINRIFRICNLTRPOEGYLMVQOYQYILGWASHREVPGSKSFLKLIQVEKW 1380
QY 1380 QBECEGEGRTIHCINGGREGMFCAGIVVEMVKRQNVVDVFAVKTLRNKNMVEA 1439
Db 1381 QBECEGEGRTIHCINGGREGMFCAGIVVEMVKRQNVVDVFAVKTLRNKNMVEA 1440
QY 1440 PEQYRFDVDALEYLESS 1457
Db 1441 PEQYRFDVDALEYLESS 1458
QY 1457 PEQYRFDVDALEYLESS 1457
Db 1458 PEQYRFDVDALEYLESS 1458

RESULT 7

ID AAR63631
XX AAR63631 standard; protein; 1407 AA.

AC AAR63631;

XX 21-OCT-2004 (revised)

DT 25-MAR-2003 (revised)

DT 08-JUN-1995 (first entry)

DB Murine receptor-type protein tyrosine phosphatase protein (RPTP-kappa).
XX Receptor-type protein tyrosine phosphatase protein; cellular signal;
KW RPTPase-kappa; enzyme.
XX Mus musculus.
OS Unidentified.
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= signal
FT Region 210..270
FT /label= Ig-like repeat
FT Domain 703..724
FT /label= Transmembrane
FT Domain 877..1108
FT /label= PTPase 1
FT Domain 1168..1404
FT /label= PTPase 2
XX WO9424161-A1.
PN 27-OCT-1994.
XX 20-APR-1994; 94WO-US004377.
XX 21-APR-1993; 93US-00049384.
PR 01-JUL-1993; 93US-00087244.
XX (UNY-) UNIV NEW YORK MEDICAL CENT.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;
PI WPI; 1994-341769/42.
XX Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)
PT protein and DNA - useful to identify cpds. which bind to RPTP-k and
PT modulate enzymatic activity. Also inhibition of type II RPTP homo:phili
XX binding (Eng).
PS Claim 2; Fig 3; 144pp; English.
XX NB: It appears that one line, comprising 50AAs is missing from Figure 3
CC (cf AAR63631). The novel receptor-type protein tyrosine phosphatase
CC protein or glycoprotein is termed RPTP kappa (also known as RPTase-
CC kappa). The first approx. 170AAs of RPTP kappa show similarity (26%
CC overall identity) to a region in the Xenopus cell surface protein A5 with
CC features of Ig-like domains. There are four putative fibronectin type III
CC -like repeats (residues 296-681). The tandem repeat of two PTPase
CC homologues is typical for most RPTases. A feature of RPTP kappa is the
CC extended distance between its transmembrane domain and the start of the
CC first phosphatase homology domain. (Updated on 25-MAR-2003 to correct PN
CC field.)
CC Revised record issued on 21-OCT-2004 : Correction to feature table key
XX Sequence 1407 AA;
Query Match 94.9%; Score 7412; DB 2; Length 1407;
Best Local Similarity 95.6%; Pred No. 0;
Matches 1393; Conservative 5; Mismatches 9; Indels 50; Gaps 1;
QY 1 MDVAAAALPAFVALWLLYPWLLGSLALQGFAGGCTFDDGPGACDYHQDLYDDFEWVHVS 60
Db 1 MDVAAAALPAFVALWLLYPWLLGSLALQGFAGGCTFDDGPGACDYHQDLYDDFEWVHVS 60
QY 61 AQEPHYLPPEMPQGSYMWVDSNNHDPGEKARLQPTMKENDTHCDFSLLYSQGLNPG 120
Db 61 AQEPHYLPPEMPQGSYMWVDSNNHDPGEKARLQPTMKENDTHCDFSLLYSQGLNPG 120
QY 121 TLNILRVNKGFLANPIWNVTGFTGRDWLRALAVSTFWPNEYQVIFAEVSGSGSYIA 180
Db 121 TLNILRVNKGFLANPIWNVTGFTGRDWLRALAVSTFWPNEYQVIFAEVSGSGSYIA 180

Db 121 TLNLLVRVNGKPLANFIWNTGTFGRDWLRABEAVSTFWNEVQVIFEAESVGRSGYIA 180
Qy 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATQCIATGRDAVHNKMLQRRNGEDIPVA 240
Db 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATQCIATGRDAVHNKMLQRRNGEDIPVA 240
Qy 241 QTKNIHRRFAASFRLOEVTKTDODLYRCVYQTSERGSVSNFAQLIVREPPRIAPOLL 300
Db 241 QTKNIHRRFAASFRLOEVTKTDODLYRCVYQTSERGSVSNFAQLIVREPPRIAPOLL 300
Qy 301 GVGPYLLIQLNANSIGDGPPIILKEVEYRMTSGSWTETHAVNAPTVKMLHLPDPTYEI 360
Db 301 GVGPYLLIQLNANSIGDGPPIILKEVEYRMTSGSWTETHAVNAPTVKMLHLPDPTYEI 360
Qy 361 RVLLTRPGEGTGLPGPPLITRTKCAEPMTPTKTKIAETQARRIAVDMESLGNITRCH 420
Db 361 RVLLTRPGEGTGLPGPPLITRTKCAEPMTPTKTKIAETQARRIAVDMESLGNITRCH 420
Qy 421 TFNVITCYHYFRGHNSRADCLDMDPKAPQHVVNHLPPYTNVSLKMLITNPGKSEET 480
Db 421 TFNVITCYHYFRGHNSRADCLDMDPKAPQ----- 450
Qy 481 IIQTDEDPGVPVKSLQGSFENKIFLANKPELEPNGLITTOYEVSVSSIRSFDPAPVA 540
Db 451 -----SPEHKIFLHWKPELEPNGLITTOYEVSVSSIRSFDPAPVA 490
Qy 541 GPPQTVSNLWNSHHVFMHLHPTGTYQFFIRASTVKGFGPATAINVTNISAPSLPDYEG 600
Db 491 GPPQTVSNLWNSHHVFMHLHPTGTYQFFIRASTVKGFGPATAINVTNISAPSLPDYEG 550
Qy 601 VDASLNETATTIVLLRPAQAKAPISAYQIVVEQLHPHRTKREAGMECYQVPTVYQNA 660
Db 551 VDASLNETATTIVLLRPAQAKAPISAYQIVVEQLHPHRTKREAGMECYQVPTVYQNA 610
Qy 661 LSGGAPYFAAEPLPGNLPAPPTGDNRTYKGFNPPPLAPKGYNIYFOAMSSVEKET 720
Db 611 LSGGAPYFAAEPLPGNLPAPPTGDNRTYKGFNPPPLAPKGYNIYFOAMSSVEKET 670
Qy 721 KTCQVRIATKAAATEBEVPIPDPAKQTDVVKIAGISAGILVFILLVIVIVVKSKLA 780
Db 671 KTCQVRIATKAAATEBEVPIPDPAKQTDVVKIAGISAGILVFILLVIVIVVKSKLA 730
Qy 781 KKKDAMGNTRQEMTHVNMNDRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840
Db 731 KKKDAMGNTRQEMTHVNMNDRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 790
Qy 841 VLDENHSATAESRLIDVPRYLCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGFK 900
Db 791 VLDENHSATAESRLIDVPRYLCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGFK 850
Qy 901 EYESPFEQOSASWDVAKKQONRAKNRYGNI IAYDHSRVILQPVDDPSSDIYNANVIDI 960
Db 851 EYESPFEQOSASWDVAKKQONRAKNRYGNI IAYDHSRVILQPVDDPSSDIYNANVIDI 910
Qy 961 WLVRDGYQRPSHYIATQGPVHETVYDFWRMVWQEQSACIWMVTLNVEVGRVKCYKWPDD 1020
Db 911 WLVRDGYQRPSHYIATQGPVHETVYDFWRMVWQEQSACIWMVTLNVEVGRVKCYKWPDD 970
Qy 1021 TEYVGFVKTCVMEPLAEVYVFTFLRRGYNEIREVKQFHTGPDHGPVPHATGLLS 1080
Db 971 TEYVGFVKTCVMEPLAEVYVFTFLRRGYNEIREVKQFHTGPDHGPVPHATGLLS 1030
Qy 1081 FIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNVCVKAISRRI 1140
Db 1031 FIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNVCVKAISRRI 1090
Qy 1141 NMVQTEEQYIFIHDAILEACLGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFQTLNS 1200
Db 1091 NMVQTEEQYIFIHDAILEACLGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFQTLNS 1150
Qy 1201 VTPRLOAEDCSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGSSSNYINAAALMDSTRQPA 1260
Db 1151 VTPRLOAEDCSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGSSSNYINAAALMDSTRQPA 1210

RESULT 8

AAM79159

ID AAM79159 standard; protein; 1452 AA.

XX AC AAM79159;

XX AC AAM79159;

XX DT 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 1821.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;

XX KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX XX WO200157190-A2.

XX PD 09-AUG-2001.

XX XX 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PR 20-JUN-2000; 2000US-00598075.

XX PR 19-JUL-2000; 2000US-00620325.

XX PR 01-SEP-2000; 2000US-00654936.

XX PR 15-SEP-2000; 2000US-00663561.

XX PR 20-OCT-2000; 2000US-00693325.

XX PR 30-NOV-2000; 2000US-00728422.

XX (HYSB-) HYSEQ INC.

XX PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

XX PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX XX WPI: 2001-476283/51.

XX DR N-PSDB; AAK52292.

XX XX Nucleic acids encoding polypeptides with cytokine-like activities, useful

XX PT in diagnosis and gene therapy.

XX PS Claim 20; Page 4196-4199; 6221pp; English.

XX XX The invention relates to polynucleotides (AAK51456-AAK53435) and the

XX CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to

XX CC cytokine, cell proliferation or cell differentiation or which may induce

XX CC production of other cytokines in other cell populations. The

XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

XX CC peptide therapy. The polypeptides have various cytokine-like activities,

XX CC e.g. stem cell growth factor activity, haematopoiesis regulating

XX CC activity, tissue growth factor activity, immunomodulatory activity and

XX CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW8020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1452 AA;

Query Match	61.8%;	Score	4823.5;	DB	4;	Length	1452;
Best Local Similarity	61.5%;	Pred. No. 0;					
Matches	892;	Conservative	210;	Mismatches	320;	Indels	29;
Gaps	9;						
Qy	22	LLGSALGFGSAGGCTFDDPGACDXYHDLXDDFEWVHVSAQBPVLPPEMPOGSMVYVDS	81				
Db	14	LLLTAAGTFSGGCLFDEPYTCGYSQSEGDDFNWEQVNTLTKPTSDPWFMSGFMLVNA	73				
Qy	82	SNHDGKARLQPLTKMENDTHCIDFSYLLYSQKGLNPGTNILVRVKNKGPLANPINVT	141				
Db	74	SGRPEGORAHLLLPOLKENDTHCIDFHYFVSSKSNPPCLLVYKVNNGPLGNPINWIS	133				
Qy	142	GFTGRDWLAELAVSTFWPNEVQVITFEAEVSGRSYTAIDDIQVLSYPCDKSPHFLRLG	201				
Db	134	GDPTRTWNAELALSTFWPNFYQVIFEV-ITSGHQGYLAIDEVKVLGHPCTRTTHFLRLQ	192				
Qy	202	DVEVNAGQATFOCIATGRDAVHKNLWLRQNGEDIIPVAQTKNINHRFAAFSLRLOEYTK	261				
Db	193	NVEVNAGQATFOCSAIGRTVAGDRMLWQDVRDAPLKEIKVTSRRFIASFVNVVTTK	252				
Qy	262	TDQDLRYCVTOSERGSVSNFAQLVREPPRIAPPQLLGVGPTYLLIQLNANSIIGDGP	321				
Db	253	RDAGKYRCWIRTEGGVGISNAELVVKPPVPIAPPQLASVGATYMLIQLNANSINGDGP	312				
Qy	322	IILKEVEVMTSGSWTEHNAVAPYKJLWHLDPDTEYEIRVULLTRPGEGGTGLPGPPLIT	381				
Db	313	IVAREVEYCTAGSNDWDRQPVDSYKYGHLDPDTEYEISVULLTRPGEGGTGSPGALRT	372				
Qy	382	RTKCAEPMRTPTKLIABIQARRIADWESLGYNTTRCHTFNVTICYHYFRGHNSRAD-	440				
Db	373	RTKCADPMRGPKLEVEVKSRQIIRWEPFGVNVTRCHSYNLTVHYCYQVGGQGVQVRE	432				
Qy	441	-CLDMDPKAPQHVNVNHLPPYTNVLSKMLITNPEGRKSEETIIQTDDEDVPGVPVKSLOQ	499				
Db	433	VSDTENSHPQHTITNLSPYTNVSVKLLILMNPGRKESQELLVQTDDELPGAVPTESIQ	492				
Qy	500	TSFENKIFLNWKEPLENGIITQYEVSYSRSRFPDPAVPVAGPPQTVSNLWNSTHRVFMH	559				
Db	493	STFEKIFLOWREPTQTYGVITLYEITYKAVSSFPDEIDLNSQGRVSKLGNETHFLPFG	552				
Qy	560	LHPGTYTOFFIRASTVKGFPATAINVTNINISAPSLPDYEGVDASINETATTITVLLRPA	619				
Db	553	LYPGTYSFTIRASTAKGFGPATNOFTTKISAPMPAYE-LETPLNQDNTVTVWLKPA	611				
Qy	620	QAKGAPISAYQIVBQLPHRTKREAGAMECYQVPVTVQNALSGGAPYFAAELPPGNLP	679				
Db	612	HSRGAPSVYQIVVEERPRRTKTEILKCYVPVFIHQNASLLNSQYVFAAEFPADSLQ	671				
Qy	680	EPAPFTVGDNRTYKGFNPPLAPRGYNIYFOAMSSVEKETQCVRIATKAAATESEPV	739				
Db	672	AAQPTTIGDNKTYGWNTPLLPYKSYRIYFOAASRANGETKIDCVQVATKGAATPKP--	729				
Qy	740	IPDPAKQDTRVVVKIAGISAGILLVILLVIVVVKSKLAKRKDAMGNTRQEMTMVN	799				
Db	730	VPEPEKQDHTVKIAGVAGILLFVILFGLVVLVWKKRKLAKRKETMSSSTRQEMTMVN	789				
Qy	800	AMDRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDP-----LVPTAVL-DENH	846				
Db	790	SMDKSYAEQGTNCDE--AFSPMDTHNLNRSVSSPSFTMTKNTLSTSVPSNYPDETH	846				
Qy	847	SATRESSRLLDVPRY-LCEGTESPYQTQQLHPAIRVADLLQHLNLMKTSDSYGFKEYES	905				
Db	847	TWASDTSSLVQSHTYKKEPADVPYQTQQLHPAIRVADLLQHLITQMKCAEGYGFKEYES	906				
Qy	906	FFEGQSASWDAKQDNRAKNRYGNIAYDHSRVLQPVDEDDPSDYINANYIDIWLYRD	965				

Db	907	FFEGQSAPWDSAKDKNRMKNRYGNIAYDHSRVLRLQTIEGDITNSDYINGNYI-----D	960
Qy	966	GYQRPSEHYIATQGPVHTVVDVFWVMVQESACIWMTNLVEGRVKCYKWPDDTEYVG	1025
Db	961	GYHRPNHYIATQGPVHTVVDVFWVMVQESACIWMTNLVEGRVKCYKWPDDTEYVG	1020
Qy	1026	DFKVTVCVMEPLAEBYVVRTFTLERRGYNEIREVQKQFHTGMPDGPVPHATGLLSFIRRV	1085
Db	1021	DIKVTLTETELLAEYVIRTFVAKRGKGVHREIRIQFHTGMPDGPVPHATGLLGFRQV	1080
Qy	1086	KLNSPPSAGTIVVHCSAGAGRTGCIYIVIDIMLMAEREGVVVDIYNCVKALRSRRINMYQT	1145
Db	1081	KSKSPPSAGPLVHCSAGAGRTGCFIVIDIMLMAEREGVVVDIYNCVRELSSRRVNYQT	1140
Qy	1146	BEQYIFHDAILEACLGCTETAI PVCBFKAAAYFDMIRDSQTNSSHLDKDEFOTLNSVTPRL	1205
Db	1141	BEQYVFIHDAILEACLGCTSVPASQVRSYLYDMNKLDPQTNSSQIKEEPFTLNMVTPTL	1200
Qy	1206	QAEPCSTACLPNRHDKNRFMDMLPPDRCLPPLITIDGESSNYINAAALMDSYRQPAFIYT	1265
Db	1201	RVEDCSALLPRNHEKRCMDILPPDRCLPPLITIDGESSNYINAAALMDSYKQPSAFIYT	1260
Qy	1266	QYPLNTVKDFWRLVYDYGCTSIYMLNEVDLSQCGPQYWPBEGMLRYGPIQVECMSCSMD	1325
Db	1261	QHPLNTVKDFWRLVYDCHTSVVMNLNDVDPALCPQYWPENGVRHGHGPIQVEFPVSADLE	1320
Qy	1326	CDVNRIFRNLTRPOEGYLMWQOQYVLGWSHREVPKSRFLKLILQVEKQWEECEE	1385
Db	1321	EDIISRIFRINYAARPDQGYRMVQOQFPLGMPMYRDTFVSKRSFLKLIRQVDRKQEEYNG	1380
Qy	1386	GEGRTHICLNGGSGRMFCAIGIVVMVKRQNVVDVFAVKTLRNSKPNMVEAPEQYRF	1445
Db	1381	GEGRTHVCLNGGSGRTFCAISIVCEMLRQRTVDVFAVKTLRNNKPNWDLDDQYKF	1440
Qy	1446	CYDVALEYLES 1456	
Db	1441	CYEVALEYLS 1451	
RESULT 9			
ABR58629			
ID	ABR58629	standard; protein; 1452 AA.	
XX	ABR58629;		
AC	ABR58629;		
XX			
DT	09-JUL-2003	(first entry)	
XX		Human cancer related protein SEQ ID NO:286.	
DE		Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;	
KW		heart disease; atherosclerosis; endometriosis.	
XX		Homo sapiens.	
OS		WO2003025138-A2.	
PN		27-MAR-2003.	
PD			
XX		17-SEP-2002; 2002WO-US029560.	
PF			
XX		17-SEP-2001; 2001US-0323469P.	
PR		20-SEP-2001; 2001US-0323887P.	
PR		13-NOV-2001; 2001US-0350666P.	
PR		08-FEB-2002; 2002US-0355145P.	
PR		08-FEB-2002; 2002US-0355257P.	
PR		12-APR-2002; 2002US-0372246P.	
XX		(EOSB-) EOS BIOTECHNOLOGY INC.	
PA		Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;	
PI		Zlotnik A;	
XX		WPI; 2003-354600/33.	
DR			

KW protein tyrosine phosphatase receptor type mu; PTPRM; cytosolic;
 KW antidiabetic; gene therapy; expression pattern;
 KW hyperproliferative disorder; cancer; metabolic disorder; diabetes;
 KW infection; inflammation; tumour formation; human.
 XX
 OS Homo sapiens.
 OS Unidentified.
 XX
 PN US2004014699-A1.
 XX
 XX 22-JAN-2004.
 XX
 XX 18-JUL-2002; 2002US-00200293.
 XX
 XX 18-JUL-2002; 2002US-00200293.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Cowsert LM, Dobie KW;
 XX
 DR WPI; 2004-121596/12.
 XX N-PSDB; ADI80645.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT protein tyrosine phosphatase receptor type mu, useful for treating cancer
 PT or diabetes or modulating expression of protein tyrosine phosphatase
 PT receptor type mu.
 XX
 XX Example 13; Page 33-38; 56pp; English.
 XX
 CC This invention relates to a novel compound with an oligonucleotide 8-80
 CC nucleotides in length targeted to a nucleic acid molecule encoding
 CC protein tyrosine phosphatase receptor type mu (PTPRM) which specifically
 CC hybridises with the nucleic acid molecule encoding PTPRM and inhibits the
 CC expression of PTPRM or specifically hybridises with at least 8-nucleotide
 CC portion of a preferred target region on a nucleic acid molecule encoding
 CC PTPRM. The invention may be useful for the production of compositions
 CC with a cytostatic or antidiabetic activity. In addition, the disclosed
 CC sequences may be useful for gene therapy. The compound, particularly the
 CC antisense oligonucleotide is useful in modulating the function of nucleic
 CC acid molecules encoding PTPRM. The antisense compound can also be used as
 CC research tools and diagnostics. It can also be used as tools in
 CC differential and/or combinatorial analyses to elucidate expression
 CC patterns of a portion or the entire complement of genes expressed within
 CC cells and tissues. The compound can also be used for treating diseases or
 CC conditions associated with PTPRM, preferably hyperproliferative disorder,
 CC for example cancer or metabolic disorders, for example diabetes. The
 CC compound can also be used as prophylaxis, for example to prevent or delay
 CC infection, inflammation or tumour formation. The present sequence is that
 CC of the human protein tyrosine phosphatase receptor type mu (PTPRM) which
 CC is related to the invention.
 XX
 SQ Sequence 1452 AA;

Query Match 61.6%; Score 4812.5; DB 8; Length 1452;
 Best Local Similarity 61.4%; Pred. No. 0;
 Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;

QY 22 LLGSALGQPSAGGCTFDDGPGACDYHQLYDDFEVWHVYSAQEPHYLPPEMPOGYSVMYVDS 81
 DB 14 LLLTAAGETFSGGCLFDEPYSTCGYSQSEGDDFNWEQVNTLTPTSDPMPSPGSLMLVNA 73
 QY 82 SNHDPGEKARLQPTMKENDTHCIDFYSLLYSQKGLNPGTLNILVRVKNKGPANIPWNT 141
 DB 74 SGRPEGORAHLLLPOLKENDTHCIDPHYFVSXKSNPPGLLVVYKVNNGPLGNPINWIS 133
 QY 142 GTFGDMLRAELAVSTFWNEVQVIFAEVSGRGYTAIDDIQVLSYPCDKSPHFLRLG 201
 DB 134 GDPTFTWNAELAISTFWNFYQVIFEV-ITSGHQGYLAIDKVKVLGHFCTRTPHFLRIQ 192
 QY 202 DVEVNAQNAATQCIATGDAVHKLWLQRRNGEIDIPVAQTKNINHRFAASFRLOEVTK 261
 DB 193 NVEVNAQNAATQCSAIGRTVAGDRLMLQIDVRDAPLKEIKVTSRRFIASFNVNTTK 252

QY 262 TDQDLYECVTQSBGSGVSNFAQLIVREPPRIAPPOLLGVGPTVLLIQLNANSIIGDGP 321
 DB 253 RDAGKYECMIRTEGGVGISNVAELVKEPVPVFIAPPOLLASVATYLIQLNANSIIGDGP 312
 QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPTTEYRIRVLLTRPGEGGTGLPGPLIT 381
 DB 313 IVAREVEYCTASGSWDRQPDVSTSYKIGHLDPTTEYRISVLLTRPGEGGTGSGPALRT 372
 QY 382 RTKCAEPMRTPKTLKIAEIQARRIADVWESIGYNNITRCHTENVITCYHYFHHNESRAD- 440
 DB 373 RTKCADPMRGPRKLEVVVEVKSQITIRWEPGYNVTRCHSYNLTAVHYCYQVGGQEQVREE 432
 QY 441 -CLDMDPKAQHVNVHLPPTYNSLKMILLTPEGRKSEETIIOTDEDPGVPVKSLQG 499
 DB 433 VSWDTENSHFQHTITNLSPTYNVSKLILMPEGRKESQELIVQTDPLGAVPTESIQG 492
 QY 500 TSPENKIFLWNKPELENGIITQVEVSYSIRSDDPAVPVAGPPQTYSNLMNSHTHVPMH 559
 DB 493 STFEKIFLQWREPTQYGVITLYEITYKAVSSDFDPEIDLNSQSGRVSKLGNETHFLPFG 552
 QY 560 LHPGTTYQFFIRASTVKGFGPATAINVTNISAPSLPDYEGVDASLNATATTITVLLRPA 619
 DB 553 LYPGTTYFTIRASTAKGFGPPATNQFTTKISAPSDPAYE-LETPLAQTDNTVTVMLKPA 611
 QY 620 QAKGAPISAVQIVVEQLHPHRTKREAGAMECYQVPTYQNALSGGAPYFAELPPGNLP 679
 DB 612 HSRGAPSVYQIVVEBERPRRTKTTILKCYPIIHFQNASLLNSQYFFAAEFPAADSLQ 671
 QY 680 BPAPFTVDNRTYKGFWNPLAPRKGYNIYFOAMSSVEKETKTCVRIATKAAATEEPEV 739
 DB 672 AAQPTTIGDNKTYNGYNTPLPYKSVRIYFOAASRANGETKIDCVQVATKGAATPKP-- 729
 QY 740 IPDPAKQTRVVKIAGISAGILVIFILLVIVIVKSKLAKKRKADMGNTQREMTWVN 799
 DB 730 VPEPEKQTDHTVKIAGVIAGILLFVIFLVVLMKKRKLAKRKETMSSTRQEMTVVN 789
 QY 800 ANDRSYADQSTLHAEDPLSLTFMDQHNPSPLNDP-----LVPTAVL-DENH 846
 DB 790 SMDKSYAEQGTNCDE---AFSMDTHNLNGRSVSPSFTMTKNTLTLSVNSVYYPDETH 846
 QY 847 SATAESRLLDVPRY-LCEGTSPVQTGOLHPAIRVADLLQHLINLMKTSDSYGFKEEYES 905
 DB 847 TMSDTSLSVOSHYYKREPADVYQGLHPAIRVADLLQHLITQMKCAEGYGFKEEYES 906
 QY 906 FFEGQSASWDVAKDQNRKNRYGNI IAYDSHRVILQPVEDDPPSSDYINANYIDILWYRD 965
 DB 907 FFEGQSAPWDSAKKDNRMKNRYGNI IAYDSHRVRLQTIEGDTNSDYINGNYI-----D 960
 QY 966 GYQRPISHYIATQGPVHETVDFWMMWQESACIVMTNLVEYGVKCYKWPDDTEVYG 1025
 DB 961 GYHRPNHYIATQGPMEQTIYDFWRMWHENTASIIIMVTNLVEYGVKCKYWPDDTEIYK 1020
 QY 1026 DFKYTCVEMEPLAEVYVVRFTFLRRGYNEIREVKQFHTGWPDPHGVYPYHATGLLSFIRRV 1085
 DB 1021 DIKVTILTELLAEVIRTPAVEKRGVHEIREIRQFHTGWPDPHGVYPYHATGLLGFVRQV 1080
 QY 1086 KLSPPSAGPIVWHCHSAGAGRTGCVIVIDIMLMAEREGVVDIYNCVKALSRRRINMVQT 1145
 DB 1081 KSKSPSAGPLVHCHSAGAGRTGCVIVIDIMLMAEREGVVDIYNCVKALSRRRINMVQT 1140
 QY 1146 BEQYFIHDAILEACLCGETAIPVCEFKAAATFDMIRIDISQTNSSHLKDEQFQTLNSVTPL 1205
 DB 1141 BEQYFIHDAILEACLCGETSPASQVRSYLDYDMNKLDPTQTNSSQIKBEFRTLNMTPTL 1200
 QY 1206 QAEDCSIACLPRNHDKNRFMDMLPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT 1265
 DB 1201 RVDCSIALPRNHEKNRKMIDILPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT 1260
 QY 1266 QYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCQPYWPBEGMLRYGP IQVECMSCSD 1325
 DB 1261 QHPLPNTVKDFWRLVLDVHCTSVVMLNDVDAQLCPQYWPENGVRHHRGPIQVEFVSADLE 1320

Qy	1326	CDVNRIFR CNLRTPOEYV MWQFOYL GWSHREVP GSKBSFLK LLOVEK WOBEC EE	1395
Db	1321	EDII SR FR YNAARPOD GYEMWQO FOLGWP MYRTPV SKRSP LKLI QVDR KQ E Y N G	1380
Qy	1386	GEGRTH H C N G G R S M F C A I G I V M E K R O N V V F H A V K T L R N S K P N N V E A P E Q Y R F	1445
Db	1381	GEGRV V H C N G G R S G T F C A I S V C E N L R H Q R T V D V F H A V K T L R N N K P N N V D L L D Q Y K F	1440
Qy	1446	CYDVALE YLE S	1456
Db	1441	CYEVALE Y L N S	1451

RESULT 11
ADJ68277

ID ADJ68277 standard; protein; 1452 AA.

XX
AC

DT 06-MAY-2004 (first entry)

DE Human heat-mitochondrial protein as a therapeutic target SeqID83.

XX mitochondrial; human; screening assay; diabetes mellitus;
KW

KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acids
KW myoclonic epilepsy ragged red fibre syndrome
KW neuroprotective; neurotropic; antidiabetic;
KW osteoprotective; ophthalmological; cystostatic.

OS Homo sapiens.

XX
PN
WO2003087768-A2.

PD 23-OCT-2003.

PF 04-APR-2003; 2003WO-US010870.

PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;

DR WPI; 2003-845369/78.

Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.

PS Claim 1: SEO ID NO 83: 180pp: English:

This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, neurotropic, antidiabetic, anticonvulsant, antiarrhythmic, osteopathic, ophthalmological and cyostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

Db 961 GYHRENHYIATQGPQMETIYDFWRVMWHENTASIIIMVTNLVVEGVRKCKYWPDDTEIYK 1020
QY 1026 DKVTCVEMEPLEAVVTFILRRGYNEIREVKQFHTGPDHGVPHATGLLSFIRRV 1085
Db 1021 DIKVTLEIETELAEVIRTFVAVKRGVHEIREIQFHTGPDHGVPHATGLLGFVRQV 1080
QY 1086 KLSNPSPAGPIVHCSAGAGRTGCYIVIDIMDMAEREGVVDIYNCVKALRSRRINMVQT 1145
Db 1081 KSKSPSAGPLVHCSAGAGRTGCYIVIDIMDMAEREGVVDIYNCVRELRSRRINMVQT 1140
QY 1146 EEQYIFIHDAILEACLCGETAIPVCEFAKAYFDMIRIDSQTNSSHLKDEFTQLNSVTPRL 1205
Db 1141 EEQYVFHDAILEACLCGDTSPASQVRSLYYDNMKLPQTNSSQIKKEFRTLNMVPTL 1200
QY 1206 QAEDCSIACLPRNHKNRPMMLPPDRCLPLITITIDGESSNYINAAIMDSYRQPAAFIVT 1265
Db 1201 RVEDCSIALPRNHKNRPMMLPPDRCLPLITITIDGESSNYINAAIMDSYRQPSAFIVT 1260
QY 1266 OYPLPNTVKDFWRLVVDYGCYSIVMLNEVDSQGPCQYWPBEGMLRYGPIQVCEMCSMD 1325
Db 1261 QHPLPNTVKDFWRLVVDYHCTSVMLNDVDPQALCPQYWPBEGMLRYGPIQVCEMCSMD 1320
QY 1326 CDVINRIFRICNLTRPQGYLMVQOQYLGWASHREVPCKSRFLKILQVEKMOBCEE 1385
Db 1321 EDIISKIFRIYNAARPDQHRMVQOQFLGWPMYRDTVPVSKSALLIRQVDKQOEYNG 1380
QY 1386 GEGRTIICLNGGSGMFCAGIIVEMVKRQNVVDVFAVKTILNSKPNMVEAPEQYRF 1445
Db 1381 GEGRTVHCLNGGSGSGTFCATSIIVCEMLRHQRTVDVFAVKTILNRNKNPMVLLDQYKF 1440
QY 1446 CYDVALEYLES 1456
Db 1441 CYEVALEYLNS 1451

RESULT 12
AAM80143
ID AAM80143 standard; protein; 1455 AA.
XX AC AAM80143;
XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3789.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200157190-A2.
XX PD 09-AUG-2001.
XX PF 05-FEB-2001; 2001WO-US004098.
XX PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX

DR WPI; 2001-476283/51.
DR N-PSDB; AAK53276.
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX Claim 20; Page 437-438; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX Sequence 1455 AA;
SQ Query Match 61.2%; Score 4783; DB 4; Length 1455;
Best Local Similarity 61.0%; Pred. No. 0;
Matches 887; Conservative 210; Mismatches 326; Indels 30; Gaps 10;
QY 22 LLGSAAGQFSAGGCTFDDPGACDYHQDLVYDDFEWVHVSQAQEPHYLPPEMPOGSMVYDS 81
Db 14 LLTAAGETFSGGCLFDEPYSTCGYSQSEGGDFNWEQVNTLTKTSDPMPGSGFMLVNA 73
QY 82 SNHDPGEKARLQPLTKMENDTHCIDFSYLLYSQKGLNPGTLNILVRNKGPLANINWVT 141
Db 74 SGRPEGORAHLLLPQKENDTHCIDFHYFVSKSNPGLLVVYKVNNGPLGNPINIS 133
QY 142 GFTGRDLRAELAVSTFWPNEYQVIFEAEGVGGSGYIAIDDIOLVSPCKSPHFLRLG 201
Db 134 GDFRTWNRAELASTFWPNFYQVIFEV-ITSGHGHAIADBEVKVLGHPCFTRTPHRLIQ 192
QY 202 DVEYNAGQATFQCIATGRDAVHNKMLQRRNGEDIIPAQTKNINHRHFAASFRLOEVTK 261
Db 193 NVEYNAGQATFQCSAIGRTVAGDRLMLQGDVDRDAPLKEIKVTSSRRFIASFNVNTTK 252
QY 262 TDQLYRCVTOSESGSVSNFAQLIVREPPPIAPPOLLGYGPTVLLQLNANSIIGDGP 321
Db 253 RDAGKYRCMIRTEGGVSGISNVAELVWKEPPPIAPPQLASVGATYLTQLNANSINGDGP 312
QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYEIRVLLTRPGGGTGLPGPPLIT 381
Db 313 IVAREVEYCTAGSNDNDQPDVSTSYKIGHLDPDTEYEISVLLTRPGGGTGLPGPALRT 372
QY 382 RTKCAEPMRTPTKLIKIAIARIAVDWESIGYNTIRCHTFNVTICYHYFRGHNSRAD- 440
Db 373 RTKCADPMRGPRLKEVVEKSRQITIRWEFGYNTIRCHSYNLTIVHYCYVGGQGVAREE 432
QY 441 -CLDMDPKAPQHVNNHLPPTYNVSLKMLITNPGEKSEETIIQTDDEVPGVVPVKSQ 499
Db 433 VSWDTENSHPQHTITNLSPYTNVSVKILMMPGKESQELIVQTDDELPGAVPTESIQ 492
QY 500 TSFENKIFLNWKEPLEPNGIITQYEVSYSSIRSDPAPVPVAGPPQTVNLNWSHVFHFMH 559
Db 493 STFEKIFLOWREPTQTVGVTILYEITYKAVSSDPEDDLNQSQRVSKLGNETHFLPFG 552
QY 560 LHPGTTYOFFIRASTVKGFGPATINVTNISAPSLPDYEGVDASLNATATTITVLLRPA 619
Db 553 LYPGTTYFTIRASTAKGFGPATNQFTTKISAPSPAYE-LETPLNQTNDNTVTVMKPA 611
QY 620 QAKGAPISAYQIVVQLPHPTKREAGAMECVQVPTVYQNALSGCAPYFAELPPGNLP 679
Db 612 HSRGAPVSVYQIVVEEERPRTKTKTEILKCYVPVIFHFNASLLNSYYYFAAEFPADSIIQ 671
QY 680 EPAPFTVGDNRTYKGFWMNPPLAPRGYNIYFQAMSSVEKETKTQCVRATKAAATEEPV 739

Db 672 AAQFTTGDKNTGYWNTFLPYKSYRIYFQAASRANGETKIDCVQVATKGAATPKP-- 729
Qy 740 IPQPAKQTDVWVIAGISAGILVIFILLVIVIVVKSKLAKKRDAMGNTROBMTWVN 799
Db 730 VPRPEKQTDHTVIAGVIAGILVIFILVIVIVVKSKLAKKREKETSRTQDEIDLWIG 789
Qy 800 AMD--RSYAOQSTLHAEADPISLTFMDQHNPSPLPNDP-----LVPTAVL-DE 844
Db 790 ELNGPRSYAEQGTKLATRAFS--FMDTHNLNGRSVSPSSFTMTKNTLSTSVNYSYPDE 847
Qy 845 NGSATAESSRLLDVPRY-LCEGTHSPYQGTQLHPAIRVADLLQHLINIMKTSDSYGFKEEY 903
Db 848 THMASDTSSLSVQSHTYKKEPADVPYQGTQLHPAIRVADLLQHTQMKCAEGYGFKEEY 907
Qy 904 ESFPEGQASMDVAKQDNRAKRYGNI IAYDSRSVILQVDEDDPSDDYINANYIDILWLY 963
Db 908 ESFPEGQASMDVAKQDNRAKRYGNI IAYDSRSVILQVDEDDPSDDYINANYIDILWLY 962
Qy 964 RDGVRPSHYIATQGPVHETVYDFWRMVQEQSACIVMTNLVEVGRVKCYKVPDDTEV 1023
Db 963 -DGYHRPNHYIATQGPVHETVYDFWRMVQEQSACIVMTNLVEVGRVKCYKVPDDTEI 1021
Qy 1024 YGDFKTCVSEMEPLAEVYVTFETLEREGYNEIREVKQFHETGPDHGVPHATGLLSFIR 1083
Db 1022 YKDIKVLIETELAEYVIRTFEVEKRGVHEIREIQFHTGPDHGVPHATGLLSGFVR 1081
Qy 1084 RVKLSNPSPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALSRINMV 1143
Db 1082 QVKSPPSAGPLVWHCSAGAGRTGCFIVIDIMLDMAREGVVDIYNCVRELSSRRVNV 1141
Qy 1144 QTEQYIFIHDAILEACLCEGTALPVCEFAKAAYPDMIRIDSQNSSHLKDEPOTLNSVTP 1203
Db 1142 QTEQYIFIHDAILEACLCEGTALPVCEFAKAAYPDMIRIDSQNSSHLKDEPOTLNSVTP 1201
Qy 1204 RLQAECSIACLRNDKRFMDLPDRCLPELITIDGESSNYINAAIMDSYQPAFI 1263
Db 1202 TLREDCSIALPRNHEKRCMDLTPDRCLPELITIDGESSNYINAAIMDSYQPSAFI 1261
Qy 1264 VTQVPLNTVKDFWRLVYDYGCTSI VMLNEDLSQGCPOYWPBEGMLRYGPIOVCEMCS 1323
Db 1262 VTQVPLNTVKDFWRLVYDYGCTSI VMLNEDLSQGCPOYWPBEGMLRYGPIOVCEMCS 1321
Qy 1324 MDCDVINRIFRINLTPQEGYLMVQOQYLYGWASHREVFGSKRSFLKLIQVEKMQECC 1383
Db 1322 LEEDIIISRIYNAARSPQDGRVWQOQYLYGWASHREVFGSKRSFLKLIQVEKMQECC 1381
Qy 1384 BEGERTIIHCLNGGSGHMFCAIGIVEMVKQNVVDVFAHVKTLNSKPNVVEAPEQY 1443
Db 1382 NGEGRTVHCLNGGSGHMFCAIGIVEMVKQNVVDVFAHVKTLNSKPNVVEAPEQY 1441
Qy 1444 RFCYDVALEYLES 1456
Db 1442 KFCYDVALEYLES 1454

RESULT 13

ADB79775

ID ADB79775 standard; protein; 1436 AA.

AC ADB79775;

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XX 26-JUL-2002; 2002EP-00255249.
XX 27-JUL-2001; 2001GB-00018354.
PR 07-FEB-2002; 2002GB-00002910.
XX (WARN) WARNER LAMBERT CO.
XX Brookesbank RA, Dixon AK, Lee K, Pinnock RD;
PI WPI; 2003-395407/38.
XX N-PSDB; ADB79775.
DR
DR
XX
PT Use of isolated gene sequences and encoded polypeptides that are
PT upregulated in the spinal cord in response to streptozocin-induced
PT diabetes for screening compounds for the treatment of pain, or for
PT diagnosing pain.
XX
XX
PS Claim 1; Page 59-64; 334pp; English.
XX The present invention relates to nucleotide sequences which are useful in
CC the screening of compounds for the treatment of pain, or for the
CC diagnosis of pain. The nucleotide sequences are up-regulated in the
CC spinal cord in response to streptozocin-induced diabetes. The present
CC sequence was used to illustrate the invention.
XX
SQ Sequence 1436 AA;
Query Match 58.8%; Score 4591; DB 7; Length 1436;
Best Local Similarity 59.9%; Pred. No. 0;
Matches 859; Conservative 210; Mismatches 330; Indels 36; Gaps 12;
Qy 32 AGCTTDDGPG---ACDYHQDLYDDFEWVHVSAQEPHYLPPEPQGSYMVVDSNNHPGE 88
Db 24 AAGCTTEASDPVPCFESQAQYDDFQWEQVRIHPGTRTPEDLPHGAYLMVNASQHTPGQ 83
Qy 89 KARLQPTWKENDTHCIDFSYLLYSOKGLNPGTILNLRVKNKGLANPINNVGTGORDW 148
Db 84 RAHIITQTLSENDTHCQFSYFLYSRDGHSPGTGLGVYRVNNGPLGSAVNMVMTGSHGRQW 143
Qy 149 LRALAVSWFNPWEYOVIFEAESVSGRSYVIAIDDIQVLSYPCDKSPHFRLGDEVEYNAG 208
Db 144 HQELAVSTWPNFQVLPFALISPDHKGIVIGLDDILLFSPYCAKAPHFRLGDEVEYNAG 203
Qy 209 QNATFOCIATGRDAVHNKMLWQRNGEDIPVAOTKININHRFAASFRLOVTKTDQDLYR 268
Db 204 QNASFQCMAGRAAEAEHFLOQSGVLYVPAAGVRHLSHRFLATPLASVGRSEQDLYR 263
Qy 269 CVTQSERGSGVSNFAQLIVREPPRIAPOLLGVGPTYLLIQNLANSIIGDGPILKEVE 328
Db 264 CVSQAPRGAGVSNFAELIVKEPPTIAPOLLRAAGPTYLLIQNLANSIIGDGPILKEVE 323
Qy 329 YRMTSGSWTETHAVNAPTYKLVHLDPTVEYEVLLTRPGCGGTGLPGPLITRTKCAEP 388
Db 324 YRMARGEAEVHAVNLQTYKLVHLDPTVEYEVLLTRPGCGGTGLPGPLITRTKCAEP 383
Qy 389 MRTPKTLKIAEIQARRIADWESIGYNTIRCHTFNVTICYHYPRG--HNESRADCLMDMP 446
Db 384 TRAPKGLAFIAEQARQLTQWEPGLYNTVTRCHTYAVSLCYRYTLGSSHNQITRECVQWR 443
Qy 447 KAPQHVNVNHLPPYTNVSLKMLNPNBGRKESEETIIQTDEDPVGPVVKSLQGTSTFNKI 506
Db 444 GASRYTIKNLLPPRNTHVRLILTNBGRKEKEVTFQTDDEDPGGAABSLTPTLEDMI 503
Qy 507 FLNWKPELPENGLITQYEVSYSSIRSDRAVPVAGPQTVSNLWNSHTHVFMHLHPCTTY 566
Db 504 FLKWEPPQEPENGLITQYEVSYSSIRSDRAVPVAGPQTVSNLWNSHTHVFMHLHPCTTY 563
Qy 567 QFFIRASTVKGFGFATAINVTNINISAPSLPDYEGVDASLNENATATTIVLLRPAQAKAPI 626
Db 564 LFSVRARTSKFGQAALTEITTNISAPSP-DYADMPSPGISESENTIIVLRPAQGRAPI 622
Qy 627 SAYQIVVEQLHPHRTKREAGAMECYQVPVTVYQNALSGGAPYFAAELPPGNLPEPAPPTV 686

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Db 623 SVYQVVEERPRRLRRPGQDCFSVPLTFETALARGLVHYFGAELAASSILLEAMPTV 682
Qy 687 GDNRYKGFNPPPLAPRGYNYIYFOAMSVEKETTKQCVRIATKAAATEEDEVIPDPKQ 746
Db 683 GDNQYTFGNPPPLPRKAYLIYFOAASHLKGELTNCIRIARKAAKESKRPL-EVSQR 741
Qy 747 TDRVVKIAGISA-GILVFLLLVVIVAVKSKLAKKBDKANGNTRQEWTHWVWMDRSY 805
Db 742 SEEMGLIIGICAGGLAVILLGALVIRKGPVNMWK-ATVNYRQEKTHMSAVDRSF 800
Qy 806 ADQSTLHAEDPLSLTFMDQHNSPRLPNPDLVPTAVLDENHSATAESSRL--DVPRYLCE 864
Db 801 TDQSTLQEDERLGLSMDAPGVSPR-----GDQRSGVTEASSLGGSPRRPG 849
Qy 865 GTESPYQTQLHPAIRVADLQHINLMKTSYSGFKEBYEFEGQSASVAVKQDNRA 924
Db 850 RKGSYPHTGQLHPVRVADLQHINQMKTAEYGFKEBYEFEG----WDATKKDKLK 905
Qy 925 KNRVNIITAYDHSRVIQVDEDDPSDDYNINAYIDILYRDGYQRPQSHYIATQGPVHTV 984
Db 906 GGRQPVSAVDRHHVKHPLADPADYISANYI-----DGYHRSNFIATQGPKEMI 959
Qy 985 YDFRMVWQEOSACIVMVTNLVVEGRVKCYKYKVPDDTEVYGFVKTCVEMEPLEAYVVRT 1044
Db 960 YDFRMVWQEQACASIVMTKLVEGRVKCSRWPEDSMDYGDIKITLVKTETLAEYVVRT 1019
Qy 1045 FTLERRGYNEIREVQFHTGPHDGHGVPYHATGLLSFIRRVKLSNPPSAGPIVHCSAGA 1104
Db 1020 FALERGYSARHEVRQFHTAMPERGVPYHATGLLAFIRRVKASTPPDAGPIVHCSAGT 1079
Qy 1105 GRTGCVIIVIDMLDMAEBSGVVDIYNCVKALBSRINNVQTEEOVIFTHDAILEACLGE 1164
Db 1080 GRTGCVIIVDVMLDMAEBSGVVDIYNCVKTLCSRRVNIQTEEOVIFTHDAILEACLGE 1139
Qy 1165 TAIPVCEFAAIFDMIRIDSOTNSHLKDEFOTLNSVTPRLOAEBDCSIACLPNRHDKNRF 1224
Db 1140 TTIPTNEFATYREMRIDPQNSQLREEFQTLNSVTPPLDVECSIALLPNRHDKNRS 1199
Qy 1225 MDMLPPDRCLPLIITIDGESSNYINAAIMDSYRQPAAFITVQYPLPNTVKDFWRLVYDYG 1284
Db 1200 MDVLPDRCLPLISSDGPNNYINAAITDSYTRSAAFTVLHLPLQSTTPDFWRLVYDYG 1259
Qy 1285 CTSIVMLNEVDLSQ---CPQWPBEGMLRYCPIQVECMSCMDCDINRIFRICNLTRP 1341
Db 1260 CTSIVMLNQLNQSNAWPCLOQWPPEGRQQYGLMEVFVSGTANBDLSRVFRVQNSRL 1319
Qy 1342 QBGYLMVQOQFYLGWASHREVPGSKRSFLKLILQVEKQWEECEGEGRTIICHLNGGGRS 1401
Db 1320 QBGHLVLRHFQFLRSAYRDTDSRKAFHLHLLAEVDKQW--AESDGRITVHCLNGGGRS 1377
Qy 1402 GMFCAIGIVEMKRNQVVDVPHAVKTVLRNSKNMVEAPEQYRVCYDVALEYLES 1456
Db 1378 GTFCACATVLEMIRCHSLVDVFFAAKTLRNYKPNMVTMDQYHFCYDVALEYLEA 1432
```

RESULT 14

AA25768

ID AA25768 standard; protein; 1499 AA.

XX AC

XX AA25768;

XX DT 16-OCT-2001 (first entry)

XX DE Human protein sequence SEQ ID NO:1283.

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
genetic disease; haematopoietic disorder; platelet disorder; asthma;
thrombocytopenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
neurological disorder.

XX Homo sapiens.

XX WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000WO-US035017.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI, 2001-457603/49.

XX N-FSDB; AAH99709.

Isolated human polynucleotides encoding polypeptides, useful for the
treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX Claim 20; Page 267; 1217pp; English.

AAH99166 to AAH99904 encode the human proteins given in AA25225 to
AA25963. The proteins can have activities based on the tissues and cells
they are expressed in, such as: antiinflammatory; antirheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
central nervous system; virucide; anti-HIV; fungicide; antimutagen;
cardiovascular; antianemic; antiaggregant; haemostatic; vulnerary;
antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antiparkinsonian; and immunostimulant. The proteins and polynucleotides
encoding them can be used in gene therapy, antisense therapy and vaccine
production. The proteins and polynucleotides are useful for screening for
agonists or antagonists of a protein and for the treatment and diagnosis
of disorders associated with the activity of a protein e.g. inflammation,
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
infections, autoimmunity, genetic diseases, haematopoietic disorders,
anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
osteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
Alzheimer's disease, Parkinson's disease, neurodegenerative and
neurological disorders

XX Sequence 1499 AA;

XX Query Match

XX Best Local Similarity 58.6%; Score 4577; DB 4; Length 1499;

XX Matches 862; Conservative 206; Mismatches 331; Indels 48; Gaps 14;

Qy 34 GCTFDDPG---ACDYHQDLYDDFEWHVHSAQEPHYLPPEMPQSGSYMVVDSNHPDGEKA 90

Db 71 GCTFEESDPAVPCEYSQAQYDDDFQWEQVRTHPGTRAPADLPHGSYLVMTVSQAPGORA 130

Qy 91 RLQPLTKMKENDTHCIDFSYLLYSQGLNPGTLNITLVRNKGPLANPIWNVTGFTGRDWLR 150

Db 131 HVIQSLSENTHCVQFSYFLYSRDSHSPGTLGVYRVNGPGLGSVAVNMTVHSGHGMHQ 190

Qy 151 AELAVSTFWPNEYQVIFPAEVSGRSGVYIADDIQVLSPYPCDKSPHFRLGLGVFNAGON 210

Db 191 AELAVSTFWPNEYQVLFALISPPRRGYMGDLDDILLSPYCAKAPHFRLGLGVFNAGON 250

CC tissues, as a reagent in an assay for identifying pTP (ant) agonists, and
CC as a molecular weight marker in protein gels. The Ab is used in
CC diagnosis, tissue-typing and purification of pTP lambda, also it may
CC crosslink the receptor, resulting in its upregulation. pTP lambda is a
CC mediator of cell adhesion and may be involved in development of
CC epithelial and neuronal structures (neuronal pathfinding)
XX
SQ Sequence 1436 AA;

```
Query Match          58.6%; Score 4575; DB 2; Length 1436;
Best Local Similarity 59.8%; Pred. No. 0;
Matches 858; Conservative 209; Mismatches 332; Indels 36; Gaps 12;

QY 32 AGGCTFDGPG---ACDTHQDLYDDFEWVHVAQAEPHYLPPEMPOGSMYVDDSSNHDGCE 88
DB 24 AAGCTFEASDFVVPVCEQAYDDQFQWEQRIHFGTRTPEDLPAGAYLVNASHQTFGQ 83
QY 89 KARLQPTMKENDTHCIDPSYLLYSQKGLNPOTLILVRVNGKPLANIPVNTGTGRDW 148
DB 84 RAHIIFFQILSENDTHCVQSFYLSRDSGSPOTLGVYVRVNGGPGLSAVNMTGSHGQW 143
QY 149 LRAELAVSTFWFNEYQVIFAEVSGRSGYIAIDDIQVLSYPCDKSPHFLRLGDVEVNAG 208
DB 144 HQAELAVSTFWENEXQVLFALISPDHKGYIGLDDILLFSYPCAKAPHFSRLGDVEVNAG 203
QY 209 QNATQCTATGRDAVHNKWLORNGEDI PVNQTKNVHRRFAASFRLOEVTKTDDLYR 268
DB 204 QNASQCMAGAAEAEHFFLQROSGVLVPAAGVRHISHRRFLATFFPLASVGRSQDLYR 263
QY 269 CVTQSERGSVSNFAQLVREPPRIAPPLGVGPTVLLIQLNANSIIGDGPILKKEVE 328
DB 264 CVSQPRGAGVSNFAELIVKEPTTIAPPOLLARAGPTVLLIQLNANSIIGDGPVVKKEIE 323
QY 329 YNMTSGSWTETHAVNAPTYKMLHLPDTEYEIRVLLTRPGEQGTGLPGPPLITRTKCAEP 388
DB 324 YEMARGPWAHVHVNLYKMLHLPDTEYEISVLLTRPGDGTGRPGPPLISRTKCAEP 383
QY 389 MPTPTKLIAEIQARRIADVWESLGNITRCHTFNWTTCYHYFRG--HNESRADCLMDP 446
DB 384 TRAPKGLFAETQARQLTLQWBPGLYNVTRCHTYAVSLCYRYTLGGSHNQITRECVKMER 443
QY 447 KAPOHVNVHLPYTVNLSKMLTNPGRKESBETIIQTDDEVPVGPVVKSLQGTSEFKI 506
DB 444 GASRTYIKLLPFRNHHVRLIITNPEGRKEGKEVTFQDDEVPGGIAESLTFPLEDMI 503
QY 507 FLNWKPELEPNGLIITQYEYSYSIRSFDPAVPVAGPQPTVSNLMNSTHVFHMLHPGTTY 566
DB 504 FLKWEPEQEPNGLIITQYEISYQSISSDDPAVNVPGPRRTISKLRNETHYVFSNLHPGTTY 563
QY 567 QFFIRASTVKGPGDATAINTVNTNISAPLDPYEGVDASLNETAHTIITVLLRPAQAKGAPI 626
DB 564 LFSVRARTSKGFGQAALTEITNII SAPSF-DYADMPSPGLGESENITITVLLRPAQGRGAPI 622
QY 627 SAYQIWEQLHPHRTKREAGAMECYQVPVTVYNALSGGAPYFAAELPGLNLPPEAPFTV 686
DB 623 SYQVQVVEERPRRLRREPGACDQCVLPTFTALARGLVHYFGAELASSLLEAMPTTV 682
QY 687 GDNRTYKGFNPPPLAPRGKYNITFOAMSSVEKETKTQCVRATKAAATEEPEVIPPAPAK 746
DB 683 GDNQTYRGFWNPPLPRKAYLIYFQAASHLKGTELRNLCIRIARKAAKESKRPL-EVSQR 741
QY 747 TRRVVKIAGISA-GILVFTILLVIVIVKVKSLAKKAKDKAMGNTRQETHMNVANDRSY 805
DB 742 SEEMGLILGICAGGLVILLGALIIIVIRKGPVNMTK-ATVNYRQEKTHMMSVADRSEF 800
QY 806 ADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTAVLDENHSATAESSRLL-DVPRYLCE 864
DB 801 TDQSTLQEDERLGLSFMADPGISPR-----GDQRSGVTEASSLLGSPRPPCG 849
QY 865 GTSPTYQTQLHPAIRVADLLQHLINLMKTSDSYGFKEYESPFEGQASWDVAKKDQNR 924
DB 850 RKGSPVHTQLHPAVRVADLLQHLINQMKTAEGYGFKEYESPFEG-----WDATKKDKDLK 905
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QY 925 KNRYNIIAYDHSRVLIQPVEDDPSDYINANYIDIWLYRDGYQORPSHYIATQGPVHETV 984
DB 906 GGRQEPVSAADRHHVKUHPMLADPDADYIISANYI-----DGYHRSNHFIATQGPKEMI 959
QY 985 YDFWRMVQBSQACIIVMTNLVEVGRVKCYKYNPDDTEVYGDGDFKVTCEMEPLAEYVVRT 1044
DB 960 YDFWRMVQBSQACIIVMTNLVEVGRVKCYKYNPDDTEVYGDGDFKVTCEMEPLAEYVVRT 1019
QY 1045 FTLERRGYNEIREVKQFHFTGWDHGVPHYATGLLSFIRRVKLSNPPSAGIVVHCSAGA 1104
DB 1020 PALERRGYNEIREVKQFHFTGWDHGVPHYATGLLSFIRRVKLSNPPSAGIVVHCSAGT 1079
QY 1105 GRTCYIVIDIMLDMAEREGVVDIYNCVKALRSRRINNVQTEQVIFTHDAILEACLCE 1164
DB 1080 GRTCYIVDVLMDMAEREGVVDIYNCVKALRSRRINNVQTEQVIFTHDAILEACLCE 1139
QY 1165 TAIPTVCEFAAYFDMIRIDSQTNSSHLKDEFQTLNSVTPLRQAEDCSACIACLRNHDKNRF 1224
DB 1140 TTIPVNEFRATYREMIKIDPQSNSSQLREBFQTLNSVTPLRQAEDCSACIACLRNHDKNRF 1199
QY 1225 MDMLPPDRCLPPLITIDGESSNYINAAIMDSYRQPAAFIVTYQPLPNTVKDFWRLVVDYG 1284
DB 1200 MDVLPDRXLPLPFLISSDGDPPNNYINAAITDSYTSAAAFIVTLHPLOSTTPDFWRLVVDYG 1259
QY 1285 CTSIVMLNEVDLSQ---CPQYWPEEGMLRYGPIQVECMSCMDCDVINRIFRICNLTRP 1341
DB 1260 CTSIVMLNQLNQSNSAWPCLQYWEPRGQQYGLMEVEFVSGTANEDLVSRVFRVQNSRL 1319
QY 1342 QEGYLMVQQFOYLGWASHREVPGSKRSFLKLILOVEKQWQECBEGEGRTIIHCLNGGGRS 1401
DB 1320 QEGHLLVVRHQFLAWSAYRDTFDSRKAFLLHLLAEVDKQW--AESGDGRTVVHCLNGGGRS 1377
QY 1402 GMFCAIGIVEMVKRQNVVDVHFAVKTLRNSKPNWKEAPEQYRQYCYDVALEYLES 1456
DB 1378 GTFCACATVLEMIRCHSLVDVFFAAKTLRNYKPNWVETMDQYHFCYDVALEYLEA 1432
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Search completed: June 1, 2005, 13:49:19
Job time : 156.411 secs

Qy 1 MDVAAALPAFVALWLLYPWLLGSALGQFSAGGCTFDDGPGADYHQDLYDDFEWVHVS 60
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Db 1 MDVAAALPAFVALWLLYPWLLGSALGQFSAGGCTFDDGPGADYHQDLYDDFEWVHVS 60

QY 61 AQEPHYLPPEPQSGVMVVDSSNDHDPGEKARLQLPTMKENDTHCIDFSYLLYSOKGLNPG 120
DB 61 AQEPHYLPPEPQSGVMVVDSSNDHDPGEKARLQLPTMKENDTHCIDFSYLLYSOKGLNPG 120
QY 121 TLNIIILVRNKGPLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYIA 180
DB 121 TLNIIILVRNKGPLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYIA 180
QY 181 IDDIQVLSYPCDKSPHFRLRLGDEVNAGNATFQCIATGRDAVHNKMLQRRNGEDIPVA 240
DB 181 IDDIQVLSYPCDKSPHFRLRLGDEVNAGNATFQCIATGRDAVHNKMLQRRNGEDIPVA 240
QY 241 QTKNINHRFAASFRLOEVTTKDQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOL 300
DB 241 QTKNINHRFAASFRLOEVTTKDQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOL 300
QY 301 GVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKMLHLDPPDTEYEI 360
DB 301 GVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKMLHLDPPDTEYEI 360
QY 361 RVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADVWSLGYNITRCH 420
DB 361 RVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADVWSLGYNITRCH 420
QY 421 TENVTICVHYFRCHNESRADCLMDPKAPOHVNHLPPTYNVSLKMLTNEGRKESSET 480
DB 421 TENVTICVHYFRCHNESRADCLMDPKAPOHVNHLPPTYNVSLKMLTNEGRKESSET 480
QY 481 IIQTDDEVPGPVVKSLQTSFENKI FLNWKLEPNGLITQYEVYSIRSIFDPAVPA 540
DB 481 IIQTDDEVPGPVVKSLQTSFENKI FLNWKLEPNGLITQYEVYSIRSIFDPAVPA 540
QY 541 GPPQTVSNLWNSHTHVFHMLHGGTTYQFFIRASTVKFGPATAINVTNINSAPSIPDYEY 600
DB 541 GPPQTVSNLWNSHTHVFHMLHGGTTYQFFIRASTVKFGPATAINVTNINSAPSIPDYEY 600
QY 601 VDASLNETATITVLLRPAQAGAPISAYQIIVVEQLHPHRTKREAGMECYQVPVYQNA 660
DB 601 VDASLNETATITVLLRPAQAGAPISAYQIIVVEQLHPHRTKREAGMECYQVPVYQNA 660
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DB 661 LSGGAPYFAELPPGNLPEPAPFTVGDNRITKGFNPNPLAPRKGNINYIFQAMSSVEKET 720
QY 721 KTQCVRIATKAAATEBEVPIPDPAKQTDVRVKIAGISAGILVFIILLLLVVIIVVKSKLA 780
DB 721 KTQCVRIATKAAATEBEVPIPDPAKQTDVRVKIAGISAGILVFIILLLLVVIIVVKSKLA 780
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DB 781 KKKDKAMGNTRQEMTHMVNMDRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA 840
QY 841 VLDEHNSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLNLMKTSYSGFK 900
DB 841 VLDEHNSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLNLMKTSYSGFK 900
QY 901 EYESFFEGQSASWDVAKQDNRAKNRYGNIITAYDHSRVILQVDEDDPSSDYINANYIDI 960
DB 901 EYESFFEGQSASWDVAKQDNRAKNRYGNIITAYDHSRVILQVDEDDPSSDYINANYIDI 960
QY 961 WLYRDGYQRPSPHYIATQGPVHETVDFWRMVWQESQACIWMVNLVEGRVKCYKYWDD 1020
DB 961 WLYRDGYQRPSPHYIATQGPVHETVDFWRMVWQESQACIWMVNLVEGRVKCYKYWDD 1020
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DB 1021 TEVYGDVKVTCVMEPELAEYVVRFTFLRRGNYNEIREVKQFHTGWPDPHGVPHYATGLLS 1080
QY 1081 FIRRVKLSNPPSAGPIVWHCSAGAGRTGCIYVIDIMLDMAREGVVDIYNCVKALRSRRI 1140
DB 1081 FIRRVKLSNPPSAGPIVWHCSAGAGRTGCIYVIDIMLDMAREGVVDIYNCVKALRSRRI 1140
QY 1141 NNVQTEEQYIFIHDAILEACLCGETAI PVCEFKAAVFDIMRIDSQTNSSHLKDEFTQLNS 1200

DB 1141 NNVQTEEQYIFIHDAILEACLCGETAI PVCEFKAAVFDIMRIDSQTNSSHLKDEFTQLNS 1200
QY 1201 VTPRLQAEDCSIACLPRNHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA 1260
DB 1201 VTPRLQAEDCSIACLPRNHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA 1260
QY 1261 AFIVTQVPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCCPQYWPBEGMLRYGPIQVECM 1320
DB 1261 AFIVTQVPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCCPQYWPBEGMLRYGPIQVECM 1320
QY 1321 SCSDMCDVINRIFRICNLTRPEQGYLMVQOQFOYLGMASHREVPGSKSFLKLILOVEKQW 1380
DB 1321 SCSDMCDVINRIFRICNLTRPEQGYLMVQOQFOYLGMASHREVPGSKSFLKLILOVEKQW 1380
QY 1381 ECEBEGEGRTIIHCLNGGSGRMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
DB 1381 ECEBEGEGRTIIHCLNGGSGRMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
QY 1441 EQYRFCYDVALEYLESS 1457
DB 1441 EQYRFCYDVALEYLESS 1457
RESULT 2
US-10-408-765A-284
; Sequence 284, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1439
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-408-765A-284
Query Match 97.1%; Score 7582; DB 16; Length 1439;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1420; Conservative 13; Mismatches 5; Indels 20; Gaps 4;
QY 1 MD-VAAALPAFVALWLLYPMPLIGSALGQFSAGSCTFDDGPGACDYHQDLYDDPEWHVH 59
DB 1 MDTTAAALPAFVALWLLYPMPLIGSALGQFSAGSCTFDDGPGACDYHQDLYDDPEWHVH 60
QY 60 SAQSPHYLPPEPQSGVMVVDSSNDHDPGEKARLQLPTMKENDTHCIDFSYLLYSOKGLNP 119
DB 60 SAQSPHYLPPEPQSGVMVVDSSNDHDPGEKARLQLPTMKENDTHCIDFSYLLYSOKGLNP 120
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DB 120 GTLNIILVRNKGPLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180
QY 180 AIDDIQVLSYPCDKSPHFRLRLGDEVNAGNATFQCIATGRDAVHNKMLQRRNGEDIPV 239
DB 180 AIDDIQVLSYPCDKSPHFRLRLGDEVNAGNATFQCIATGRDAVHNKMLQRRNGEDIPV 240
QY 240 AQTKNINHRFAASFRLOEVTTKDQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOL 299
DB 240 AQTKNINHRFAASFRLOEVTTKDQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOL 300

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Qy 300 LGVGTPLLIIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359
Db 301 LGVGTPLLIIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
Qy 360 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMTPTKTLIAEQARRIADWESLGYNITRC 419
Db 361 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMTPTKTLIAEQARRIADWESLGYNITRC 420
Qy 420 HTFNVTTCYHYFRGHNSRADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESEE 479
Db 421 HTFNVTTCYHYFRGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESEE 480
Qy 480 TTIOTDEDVGPVVKSIQGTFSFNKJFLANKKEPLENGIITQYEVSSYRSRSDPAVPV 539
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Qy 540 AGPQTQVSNLWNSHHVFMHLHPGTQYFFIRASTVKGFGPATAINVTNISAPSLDYE 599
Db 541 AGPQTQVSNLWNSHHVFMHLHPGTQYFFIRASTVKGFGPATAINVTNISAPSLDYE 600
Qy 600 GVDASLNETATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVTVQN 659
Db 601 GVDASLNETATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVTVQN 660
Qy 660 ALSCGAPYYFAAELPPGNLPEPAPFTVGDNRKYKGFNPPPLAPRGNYIYFQAMSSYEKE 719
Db 661 AMSCGAPYYFAAELPPGNLPEPAPFTVGDNRKYKGFNPPPLAPRGNYIYFQAMSSYEKE 720
Qy 720 TKTCVRIATKAAATEPEVTPAKQTDNRVVKIAGISAGILVFILLVLLVIVKSKL 779
Db 721 TKTCVRIATKAAATEPEVTPAKQTDNRVVKIAGISAGILVFILLVLLVIVKSKL 779
Qy 780 AKKRDAMGNTRQWTHVNMADRSYADQSTLHAEDPLSLTFMDQHNPSRLNDPLVPT 839
Db 780 AKKRDAMGNTRQWTHVNMADRSYADQSTLHAEDPLSLTFMDQHNPSRY ----- 831
Qy 840 AVLDEHNSATAESRLLDVRYLCGCTESPQYQTLHPAIRVADLLOHINLMKTSDSYGF 899
Db 832 -----ENHSATAESRLLDVRYLCGCTESPQYQTLHPAIRVADLLOHINLMKTSDSYGF 887
Qy 900 KEEYESFEGQSADWDVAKDQNKAKRYGNI IAYDHSRVLQVDEDPSSDIYANAYID 959
Db 888 KEEYESFEGQSADWDVAKDQNKAKRYGNI IAYDHSRVLQVDEDPSSDIYANAYI - 946
Qy 960 IWLRYDGYQRPISHYIATQGPVHETVDFWRVMQESACIWMVNLVEVGRVKCYKWPD 1019
Db 947 -----DCYQRPISHYIATQGPVHETVDFWRVMQESACIWMVNLVEVGRVKCYKWPD 1001
Qy 1020 DTEVYGFKVTCEMEPLAEYVVRFTFLRRGYNEIREVKQFHTGWPDRGVPYHATGLL 1079
Db 1002 DTEVYGFKVTCEMEPLAEYVVRFTFLRRGYNEIREVKQFHTGWPDRGVPYHATGLL 1061
Qy 1080 SFTIRVKLSNPPSAGPIVHVCAGAGTGCYIVIDIMLDAEREGVVDIYNCVKALRSR 1139
Db 1062 SFTIRVKLSNPPSAGPIVHVCAGAGTGCYIVIDIMLDAEREGVVDIYNCVKALRSR 1121
Qy 1140 INMVQTEBQIFIHDAILEACLCGETAIPVCEFAAAYFDMIRIDSQTNSSHLKDEFOFLN 1199
Db 1122 INMVQTEBQIFIHDAILEACLCGETAIPVCEFAAAYFDMIRIDSQTNSSHLKDEFOFLN 1181
Qy 1200 SVTPRLQAEDCSIACLPRNHDKNRFDMDLPPDRCLPELITIDGSSNYINAAIMDSYRQP 1259
Db 1182 SVTPRLQAEDCSIACLPRNHDKNRFDMDLPPDRCLPELITIDGSSNYINAAIMDSYRQP 1241
Qy 1260 AAFITVQYPLNTVKDFWRLVYDYGCTSIUMLNEVDLSQCGPQWPEEGLRYGPIQVEK 1319
Db 1242 AAFITVQYPLNTVKDFWRLVYDYGCTSIUMLNEVDLSQCGPQWPEEGLRYGPIQVEK 1301
Qy 1320 MSCMDCDVNIRIPRI CNLNRPOBYLWMOQFOYLGWASHREVPGRSKFLKLTLOVEKW 1379
Db 1302 MSCMDCDVNIRIPRI CNLNRPOBYLWMOQFOYLGWASHREVPGRSKFLKLTLOVEKW 1361
Qy 1380 QEBCEBEGRTIIHCLNGGSGMFCAGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1439
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Db 1362 QEBCEBEGRTIIHCLNGGSGMFCAGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1421
Qy 1440 PEQYRFCYDVALEYLESS 1457
Db 1422 PEQYRFCYDVALEYLESS 1439
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RESULT 3

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US-09-887-669-2
; Sequence 2, Application US/09887669
; Publication No. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-669-2
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Query Match 97.0%; Score 7571; DB 9; Length 1439;

Best Local Similarity 97.3%; Pred. No. 0;

Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

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Qy 1 MD-VAAALPAFVALMLLYPWPILLGSAFGSAGGCTFDDGPGACDYHQDLYDDFEWVHV 59
Db 1 MDTTAAALPAFVALLLSLSPWLLGSAQGFAGGCTFDDGPGACDYHQDLYDDFEWVHV 60
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Qy 60 SAQEPHYLPPEMPOGSMVVDSSNHPGEGAKRLQPTMKENDTHCIDFSYLLSQKGLNP 119
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Qy 120 GTLNILVRNKGPLANPINNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESGGRSGYI 179
Db 121 GTLNILVRNKGPLANPINNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESGGRSGYI 180
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Qy 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKLMLORRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKLMLORRNGEDIPV 240
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Qy 240 AQTKNINHRFAASFRLOEVTKTDQDLYRCVTOSESGSVNFAQLIVRPPPIAPPOL 299
Db 241 AQTKNINHRFAASFRLOEVTKTDQDLYRCVTOSESGSVNFAQLIVRPPPIAPPOL 300
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Qy 300 LGVGPTVLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359
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Qy 360 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMTPTKTLIAEQARRIADWESLGYNITRC 419
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Db 541 AGPPTQVNLWNSTHHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNTISAPTLDYE 600
Qy 600 GVDASLNSTATITVLLRPAQAKGAPISAYQIVVEQLHPHETKREAGAMECVQVPVTYQN 659
Db 601 GVDASLNSTATITVLLRPAQAKGAPISAYQIVVEQLHPHETKREAGAMECVQVPVTYQN 660
Qy 660 ALSGAPYFAELPPGNLPPAPPTVGDNRITYGFNPPPLAPRKGYNIFYQAMSSVEKE 719
Db 661 AMSGAPYFAELPPGNLPPAPPTVGDNRITYGFNPPPLAPRKGYNIFYQAMSSVEKE 720
Qy 720 TKTCQVRIATKAATEBEVIPPDAKQTRDVVVKIAGISAGILVFILLVIVIVKSKL 779
Db 721 TKTCQVRIATK-AATEBEVIPPDAKQTRDVVVKIAGISAGILVFILLVIVIVKSKL 779
Qy 780 AKKRKDMGNTRQEMTHMVMNDRSYADOSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 839
Db 780 AKKRKDMGNTRQEMTHMVMNDRSYADOSTLHAEDPLSLTFMDQHNFSRY----- 831
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Db 842 ----ENHSATSSRLLDVPRYLCGTESPYQTLQHPAIRVADLLQHNLMKTSDSYGF 887
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Db 888 KEEYESFEGQSASWDVAKQONRAKRYGNIAYDHSRVILQPVEDDPSDDYINANYI- 946
Qy 960 IWLRYDGYORSHYIATQPVHETVYDFWRVMVQEOSACIWMVNTLVGVKVCYKWPD 1019
Db 947 ----DGYORSHYIATQPVHETVYDFWRVIMVQEOSACIWMVNTLVGVKVCYKWPD 1001
Qy 1020 DTEVYDGFQVTCVMEPLAEYVVRTFTLLRRGYNEIREVKQFHTGWDHGVPHATGLL 1079
Db 1002 DTEVYDGFQVTCVMEPLAEYVVRTFTLLRRGYNEIREVKQFHTGWDHGVPHATGLL 1061
Qy 1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIIVDMLDMAREGVVDIYNCVKALRSR 1139
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Db 1122 INMWQTEQYFIHDAIIEACLCGETAIPVCEFKAAAYFDMIRIDISQTNSSHLLKDBFQTLN 1181
Qy 1200 SVTPRLQAECDSCIACLRNHDKNRPMWMLPPDRCLPFLITIDGESSNTYINAAALMDSYRQ 1259
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Db 1302 MSCSMDCDVINRIFRICNLTRPQEGYLMVQOQYILGWASHREVPKSKFLILQVEKW 1361
Qy 1380 QBECEGEGRTIIHCLNGGSGMFCATGIVVEMVKRWVVDVHFAVKTLRNSKPNMVEA 1439
Db 1362 QBECEGEGRTIIHCLNGGSGMFCATGIVVEMVKRWVVDVHFAVKTLRNSKPNMVEA 1421
Qy 1440 PEQYRFCYDVALEYLESS 1457
Db 1422 PEQYRFCYDVALEYLESS 1439
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RESULT 4

US-09-887-669-8

; Sequence 8, Application US/09887669

; Publication No. US20020082397A1

; GENERAL INFORMATION:

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; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-669-8
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Query Match 62.0%; Score 4843.5; DB 9; Length 1452;
Best Local Similarity 61.9%; Pred. No. 0;
Matches 898; Conservative 206; Mismatches 318; Indels 29; Gaps 9;

Qy 22 LLGSAQCQFAGGCTTDDGACDHYQDLVDDFWVHVSAOEHPHYLPMPQGSVMVYDS 81
Db 14 LLTAAGETTSGGCLFDEPYSTCGYSQSEGGDFNWEQVNTLTKTPTSDPMWPSGSLMLVNA 73

Qy 82 SNHDPGEKARLQPLTMKENDTHCIDFSYLLYSQKGLNPGLTNILVRNVKGLANPIWNT 141
Db 74 SGRPEGORAHLLLPOLKENDTHCIDFHYFVSSKNSPPGLLVYKVNNGPLGNPINWIS 133

Qy 142 GFTGRDLRLAELAVSTWPNQYQVIFAEVSGGRSGYIAIDDIQVLSYPCDKSPHFLRLG 201
Db 134 GDPTRTWRAELALSTWPNFYQVIFEV-ITSGHQGYLAIDEVKVLGHPCRTTTHFLRIQ 192

Qy 202 DVEVNAQONATFOCIATGRDAVHNKMLQRRNGBDIPVAOPTKNINHRHFAASFLQEVTK 261
Db 193 NVEVNAQOFATFOCSAIGRTVAGDRLWLQGDIVDRDAPLKEIKVTSSRRFIASFNVVNTTK 252

Qy 262 TDQDLRYCVTQSESGSVSNFAQLIVREPPPIAPPQLLGVPYVLLIQLNANSIIGDGP 321
Db 253 RDAGKYRCMIRTEGGVGSINYAELVWKEPPVPIAPPQLASVGATVLTQLNANSINGDGP 312

Qy 322 IILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYEIRVLLTRPGEGGTGLPGPLIT 381
Db 313 IVAREVEYCTASGSWNRDQPVDSYSYKIGHLDPDTEYEISVLLTRPGEGGTGSPGALRT 372

Qy 382 RTKCAEPMRTPTKLKIAIQARRIAVDWESIGYINIRCHTFNVTICYHYFRGHNESRAD- 440
Db 373 RTKCADPMRGPRKLEVEVVKSRQITIRWEPFGYNVTRCHSYNLTVHYCYQVGQGVREE 432

Qy 441 -CLDMDPKAPOHVVNHLPPYTNVSLKMLTTPKESSEETIOTDEVDVGPVPVKSQ 499
Db 433 VSWDTENSHPOHTITNLSPYTNVSVKLLMMPKESQELTVQTDOLPGAVPTESIQ 492

Qy 500 TSFENKIFLNKKEPLENGIITQYEVSYSSIRSDPAVPVAGPPQTVSNLWNSTHHVFMH 559
Db 493 STFEKIFLOWREPTQYTVITLYEITYKAVSSDPDEIDLSNQSGRVSKLGNETHFLPFG 552

Qy 560 LHPGTYQFFIRASTVKGFGPATAINVTNTISAPSLPDYEGVDASLNSTATITVLLRPA 619
Db 553 LYPGTYSTIRASTAKGFGPPATNQFTTKISAFSPMPAYE-LETPLNQTNDNTVTVMLKPA 611

Qy 620 QAKGAPISAYQIVVEQLHPHETKREAGAMECVQVPVTYQNALSGGAPYFAELPPGNL 679
Db 612 QSRGAPSVYQIVVEEERPRETKTTEILKCYVPPIHFQNASLLNSQYFFAAEFPADSLQ 671

Qy 680 EPAPFTVGDNRITYKGFWNPPPLAPRKGYNIFYQAMSSVEKETKTCQVRIATKAATEBEV 739
```

Db 672 AAQPTTGDKNTYNGYNTPLLPYKSYRIYFQAASRANGETKIDCVQATKGAATPKP-- 729
Qy 740 IPDPAKQTRDVVYKIAGISAGILVIFILLVIVIVVVKSKLAKKRDAMGNTRQEMTHVN 799
Db 730 VPEPEKQTDHTVYKIAGIAGILVIFILLVIVIVVVKSKLAKKRDAMGNTRQEMTHVN 789
Qy 800 AMDSYADQSTLHAEDPLSLTMDQHNFSRLPNDP-----LYPTAVL-DENH 846
Db 790 SMDKSYAEQGTNCDE--AFSMDTHNLNGRSVSSPSTFMKTNTLSTSPNSYYPDETH 846
Qy 847 SATAESRLLDVPRY-LCEGTESPYQTQLHPAIRVADLLQHLINLMKTSYSGFKEYES 905
Db 847 TMSADTSSLVQSHYTKREPADVPYQTQLHPAIRVADLLQHLITOMKCAEGYFKEYES 906
Qy 906 FPEGQASWDVAKQONRAKNRYGNIITAYDHSRVILQVEDDPSSDYINAYIDIMLYRD 965
Db 907 FPEGQASWDVAKQONRAKNRYGNIITAYDHSRVILQVEDGTNSDYINGNYI-----D 960
Qy 966 GYQRPISHYATQGVHETVDFWRMVMQESACIIVMTNLVEGVRVKCYKWPDDTTEVYG 1025
Db 961 GYHRPNHYATQGMQETIYDFWRMVMWHENTASIMVTNLVEGVRKCCYKWPDDTTEYK 1020
Qy 1026 DFKVTCVEMEPLEAYVYRTTLLERGGYNEIREVKQFHTGWPDHGVPHYATGLLSFIRRY 1085
Db 1021 DIKVTLLIETELLAYVIRTAVERKGGIIEIREKQFHTGWPDHGVPHYATGLLGVRQV 1080
Qy 1086 KLSNPPSAGPIVHCSAGAGRTGCIYVIDIMLMAEREGVVVDIYNCVKALRSRRINNVO 1145
Db 1081 KKSPPSAGPLVHCSAGAGRTGCFIVIDIMLMAEREGVVVDIYNCVRELRSRRINNVO 1140
Qy 1146 EQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTNSSHLKDFOTLNSVTPRL 1205
Db 1141 EQYVFTIHDAILEACLCGETSVSPASQVRSLYDMNKLDPQTNSSQIKKEEFRTLMNVTPL 1200
Qy 1206 QAEDCSFACIIPRHNKRNRMWMLPPDRCLPLITIDGESNYINAAALMDSYVROPAFIVT 1265
Db 1201 RVSDCSFALLPRHNKRNRMWMLPPDRCLPLITIDGESNYINAAALMDSYKQPSAFIVT 1260
Qy 1266 QYPLNVTXKDFWRLVYDYGCTSIYMLNEVDLSQCPQYWPPEEGMLRYGPIQVECMSCMD 1325
Db 1261 QHPLNVTXKDFWRLVLDYHCTSVVMLNDVDPQALCPQYWPENGVRHGRGPQVEFVSADLE 1320
Qy 1326 CDVINRIFRINLTPRQGYLMVQOFOYLWASHREVPGRSKRFLKLILOVEKQWCEBEE 1385
Db 1321 EDIISRIFRINYAARPQDGYRMVQOFOFLGPMYRDTFVSKRFLKLIROVDKQWCEYNG 1380
Qy 1386 GEGRTIHLCLNGGGRGMPCAIGIVVEMVKRONVVDVFAVKTLLRNSKPNMVEAPEQYRF 1445
Db 1381 GEGPTVHCLNGGGRGRTFCAISIVCEMLRHQRTVDVFAVKTLLRNNKPNMVDLLDQYKF 1440
Qy 1446 CYDVALEYLES 1456
Db 1441 CYEVALEYLNS 1451

RESULT 5

US-10-408-765A-83
; Sequence 83, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 83

; LENGTH: 1452

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-83

Query Match

Best Local Similarity 61.1%; Score 4789.5; DB 16; Length 1452;

Matches 887; Conservative 211; Mismatches 324; Indels 29; Gaps 9;

Qy 22 LLGSALGQFSAGSAGCTPDDGPGACDYHQDLYDDPEWHVHSAQEHPHLPPEMQSGSYMVDS 81
Db 14 LLTAAGETFSGGCLFDEPYSTCGYSQSEGGDDFNWEQVNTLTKTPTSDPWPMPGSLMLVNA 73
Qy 82 SNHDPGEKARLQLPWKENDTHCIDFSLYLSQKGLNPGTLNLLVRVKNKPLANPINVNT 141
Db 74 SGPEQORAHLLPOLKENDTHCIDFHYFVSSKSNPPGLLVVKNVNGPLGNPINNIS 133
Qy 142 GFTGRDMLRAELAVSTFWPNEYQVIFEAESVGGSGRYAIDDIQVLSYPCDKGPHFLRLG 201
Db 134 GPTRTWRAELAISTFWPNFYQVIFEV-ITSGHQGYLAIDEVKVLGHPCTRTPHFLRIQ 192
Qy 202 DVEVNAQONATFOCIATGRDAVANKLWQRNGEDIPVAQTKNINHRFRFAASRLQEVTK 261
Db 193 NVEVNAQOFATFQCSAIGRTVAGDRLWLOGIDVRDAPLKEIKVTSSRRFIASFNVNTTK 252
Qy 262 TDQDLVRCVTOSESGSVSNFAOLIVREPPRTIAPPOLLGVGPTLLIQLNANSIIGDGP 321
Db 253 RDAGKTRCMIRTEGGVIGISNIAELVWKEPVPPIAPPOLASVGATYLIQLNANSINGDGP 312
Qy 322 IILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPTDEYRIVLLTRPGEGETGLPGPLIT 381
Db 313 IVAREVEYCTASGSWMDRQPDVSTSYKIGHLDPTDEYRIVLLTRPGEGETGLPGPALRT 372
Qy 382 RTKCAEPMRTPKLTKIABEQARIAVDWESLGNITRCHTFNTVITCYHFRGNESRAD- 440
Db 373 RTKCAEPMRGRKLEVEVKSQITIRWEPFGYVNRCHSYNLTVHYCYVGQGOEQVREE 432
Qy 441 -CLDMPKAPQHVNLHPVTVNLSKMLNPNRKRSEBETIQTDDSDVPGVPVKSLQ 499
Db 433 VSWDTEHSHPQHTITNLSPYTVNSVKILMNPGRKESQELIQTDDSDVPGVPVKSLQ 492
Qy 500 TSPENKIFLWKPELBPNGIITQYEVSYSSIRSFDPAPVPVAGPPQTVSNLWNSHTHFMH 559
Db 493 STEBKIFLQWREPTQTYGVTILYEITYKAVSSFDPEIDLSNQSGRVSKLGNETHPLFFG 552
Qy 560 LHPGTTYQFIRASTVKGFGPATAINVTNINSAPSLPDYEGVDASLNETATTTVLLRPA 619
Db 553 LYPGTTYFTIRASTAKFGPPATNQFTTKISAPMPAYE-LETPLNQTDNTVTVMUKPA 611
Qy 620 QAKGAPISAVQIVVEQLHPHRTKREAGMBCYQVPTVYNALSGGAPYFPAALPPGNLP 679
Db 612 HSRGAPVSVYQIVVEEERPRRTKKTTEILKCYVPIHFQNASLNSQYFPAALPPADSLQ 671
Qy 680 EPAPFTVGNRTYKGFNPPPLAPRKGNYIYFQAMSSVEKETKTCQVRIATKAAATEPEV 739
Db 672 AAQPTTGDKNTYNGYNTPLLPYKSYRIYFQAASRANGETKIDCVQATKGAATPKP-- 729
Qy 740 IPDPAKQTRDVVYKIAGISAGILVIFILLVIVIVVVKSKLAKKRDAMGNTRQEMTHVN 799
Db 730 VPEPEKQTDHTVYKIAGIAGILVIFILLVIVIVVVKSKLAKKRDAMGNTRQEMTHVN 789
Qy 800 AMDSYADQSTLHAEDPLSLTMDQHNFSRLPNDP-----LYPTAVL-DENH 846
Db 790 SMDKSYAEQGTNCDE--AFSMDTHNLNGRSVSSPSTFMKTNTLSTSPNSYYPDETH 846
Qy 847 SATAESRLLDVPRY-LCEGTESPYQTQLHPAIRVADLLQHLINLMKTSYSGFKEYES 905
Db 847 TMSADTSSLVQSHYTKREPADVPYQTQLHPAIRVADLLQHLITOMKCAEGYFKEYES 906
Qy 906 FPEGQASWDVAKQONRAKNRYGNIITAYDHSRVILQVEDDPSSDYINAYIDIMLYRD 965

Db 907 FFEQSAWDSAKKDNRMKNRYGNI IAYDHSRVLRTQIEGDTNSDYINGNYI-----D 960
Qy 966 GYORSHYIATQGPVHETVYDFWRMWQBSQACIWMVNLVEVGRVKYKWPDDTEYVG 1025
Db 961 GYHRENHYIATQGPQMETIYDFWRMWVHENTASIIIMVNLVEVGRVKCKYWPDDTEYK 1020
Qy 1026 DPKVTQVMEPLAEVYVTFELTERRGYNEIREVKGFHFTGHPDGHGVPVHATGLLSFIRRV 1085
Db 1021 DIKVTIETELLAEYVIRTFVKKGVHREIRIQFHTGPDHGVVHATGLLGFVRQV 1080
Qy 1086 KLSNPPSAGPIVHCHSAGAGRTGCVIIVIMLDMAREGVVDIYNCVKALRSRRINMVQT 1145
Db 1081 KSKSPSAGPLVHCHSAGAGRTGCVIIVIMLDMAREGVVDIYNCVRELSSRRVNVQT 1140
Qy 1146 BEQYFIHDAILEACLCGETAIPVCEFKAAFPDMIRIDSONSSHLDKDFOTLNSVTPRL 1205
Db 1141 BEQYFIHDAILEACLCGDTSPASQVRSYYDMNKLDPTQNSSQIKBEFRTLNMVPTL 1200
Qy 1206 QAEDCSIACLPRNHDKNRPMMLPPDRCLPFLITIDGSSNYINAALMDSYRQPAAFIVT 1265
Db 1201 RVEDCSIALPRNHEKNRMDLLPPDRCLPFLITIDGSSNYINAALMDSYKQPSAFIVT 1260
Qy 1266 QVPLENTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQYWPBEGMLRYGPIQVECMSCSMD 1325
Db 1261 QHPLENTVKDFWRLVLDYHCTSVMLNDVDPAQLCPQYWPENGVRHGHGPIQVEFVSADLE 1320
Qy 1326 CDVINRIFRICNLTLPQSGYLWQOXYLGNASHREVPGSKRSFKLILQVEKMQBEECE 1385
Db 1321 EDIISRIFRINYAARPDQHRMVQOQFLGWPMDYRDTVPKRSALLIRQVDKMQBEEYNG 1380
Qy 1386 GEGRTIICLNGGSGWFCAGIYVVMVKRQNVVDVHAKVTLNSKPNVVEAPEOYRF 1445
Db 1381 GEGRTVWHLNGGSGSGTFCALSIVCEMLRHQRTVDVHAKVTLNRNKNPMVDDLQYKF 1440
Qy 1446 CYDVALEYLES 1456
Db 1441 CYEVALEYLNS 1451

RESULT 6

US-10-205-219-15
; Sequence 15, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Receptor protein tyrosine phosphatase-lambda
US-10-205-219-15

Query Match 58.8%; Score 4591; DB 14; Length 1436;
Best Local Similarity 59.9%; Pred. No. 0;
Matches 859; Conservative 210; Mismatches 330; Indels 36; Gaps 12;

Qy 32 AGGCTFDDGFG---ACDYHQDLYDDFEWVHSAQEPHYLPPEPQGSYMWVDSNHPGE 88
Db 24 AAGCTFEASDFVWPCFESQAYDDFQWEOVRHPIQTRTFEDLPHGAYLMVNASQHTPGQ 83

Qy 89 KARLQLPTMKENDTHCIDFSYLLSQKGLNPGLTILNLRVNVKGPLANPIVNVGTGTGRDW 148
Db 84 RAHIIFOTLSENDTHCQFYSYFLSRDGHSPGLTGVYRVNGGPLGSVAVNMWTSHGROW 143
Qy 149 LRAELAVSTFWPNEYQVIFAEVSGSGSYTAIDDIQVLSYPCDKSPHFLRLGDEVEVNAQ 208
Db 144 HQAELAVSTFWPNEFQVLFALISPDHKGVIGLDDILLFSYPCAKAPHFSRLGDEVEVNAQ 203
Qy 209 QNATFOCIATGRDAVHKLWLRNGREDIIPVAQYKTNINHRPFAASFRLOEYTKTDDOYL 268
Db 204 QNASFOCWAAGRAAEHFFLQROSGVLVPAAGVRHIHSHRFLATFPPLASVGRSEQDYL 263
Qy 269 CVTOSERGSGVNSFAQLIVREPPPIAPPOLLGVGPTVLLIQLNANSIIGDGPILKEVE 328
Db 264 CVSQAPGAGVNSFAELIVKEPPIAPPOLLRAGPTVLLIQLNANSIIGDGPVIRKEIE 323
Qy 329 YRMTSGSWTETHAVNATPYKLMHLDPDTEYBIRVLLTRPGEGTGLPGPPLITRTKCAEP 388
Db 324 YRMARGPWAEVHVNLTQYKLMHLDPDTEYBISVLLTRPGDGTGRPGPPLISRTKCAEP 383
Qy 389 MRPKTILKIAIBIARRIADWESIGYMITRCHTFNVICHYHFRG--HNSRADCLMDP 446
Db 384 TRAPKGLAFABIQARQLTQWEPLGYNVTRCHTYAVSLCYRYTLGGSHNQITRECVKMR 443
Qy 447 KAPOHVNVHLLPPYTNVSLKMLLTNPEGRKSEETIIOTDEDPGVPVPVKSLOQTSFENKI 506
Db 444 GASRYTINKLLPFRNIHVRLLITNPEGRKEQKVTQDEDPVGGIAAESLTFPLEDMI 503
Qy 507 FLNWKPLENPNGIITQYEVSYSSIRSPDPAVPVAGPQTVSNLWNSTHVVHMLHPGTTY 566
Db 504 FLKWEEOQENGLITQYEVSYQSISSDPAVNVPGPRTISKLRNETVHVSNLHPGTTY 563
Qy 567 QPFRASTVKGFGPATVNTTINSAPSLPDYEGVDASLNETATITVLLPAPQAKGAPI 626
Db 564 LFSVARTSKFGQALTEITITNISAPSF-DYADMPSPLGSESENTITVLLRPAQGRGAPI 622
Qy 627 SAYQIVVEQLPHRTKREAGAMECVQVPVTVYONALSGGAPYVFAELPPGNLPEPAPT 686
Db 623 SVYQVVEEERPRRLRREPQACQCFVPLTTFETALARGLVHFGAELAAESLEAMPFTV 682
Qy 687 GDNRTYKGFWNPPPLAPRGYNIYFQAMSSVEKETKTCQVRIATKAAATEEPEVDPKAK 746
Db 683 GDNQTYRGFWNPPLPRKAYLIYFQAASHLKGELRNCIRIARAKAACKSRPL-EVSQR 741
Qy 747 TDRVVKIAGISA-GILVIFILLVVIIVIKSKLAKRKKDANGTRQENTHVMNDRSY 805
Db 742 SEEMGLILGICAGGLAVLILLGAIIVIRKGPVNMTK-ATVNYRQEKTHMMSAVDRSF 800
Qy 806 ADQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPTAVLDENHSATAESSRL-DVPRYLCE 864
Db 801 TDQSTLQSDERLGSFMDAPGYSPR-----GDQSGGVTEASLSLGGSPRRPG 849
Qy 865 GTESPYQTGQLHPAIRVADLLQHINLMKTSYSGFKEEYESFPEGQSASWDVAKKDQNR 924
Db 850 RKGSYPHTGQLHPAVRVADLLQHINQMKTASGYGFKQYESFPEG---WDATKKKDKLK 905
Qy 925 KRYGNIITADHSRVLQPVDEDDPSDDSYINANYIDILYRQGYQRPSPHYIATQGPVHETV 984
Db 906 GGRQEPVSAYDRHHVKLHPMLADPADYISANYI-----DGYHRSNFIATQGPKEMI 959
Qy 985 YDFWRMWQEOSACIWMVNLVEVGRVKYKWPDDTEYVGDYKVTCEMPELABYVVRT 1044
Db 960 YDFWRMWQEOSACIWMITKJLVEGRVKCSYWPEDSDNYGDIKITLVKTETLABYVVRT 1019
Qy 1045 FTLERRGYNEIREVKQHFHTGWPDHGVPHYATGLLSFIRRVKLSNPPSAGPIVHCHSAGA 1104
Db 1020 FALERRGYSARHEVRQHFHTAWPEHGVPHYATGLLAFIRRVKASTPDPAGPIVHCSAGT 1079
Qy 1105 GRTCYIIVDMLMAEREGVDIYNCVKALRSRRINNVQTEEQYIFHDAILEACLCGE 1164
Db 1080 GRTCYIIVDMLDMAECEGVVDIYNCVKTLCSRRVNMVQTEEQYIFHDAILEACLCGE 1139
Qy 1165 TAI PVCEPKAAVFDMIRIDSQTNSHLKDEFTLNSVTPRLQAEDCSIACLPRNHDKNRF 1224

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Db 1140 TTPVNFRTYREIMRIDPOSNSQRBEFQTUNSVTPPLDVEBCSIALPRNRDKRS 1199
Qy 1225 MDMLPPDRCLPFLITIDGESSNYNAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYG 1284
Db 1200 MDVLPDRCLPFLISSDGPNNYNAALTSYTSRAAFIVTLHLPLQSTTPDFWRLVYDYG 1259
Qy 1285 CTSIWMLEVDLSQ---CPQYWPBEGMLRYGPTQVCMSCMDCDVINRFRICNLTRP 1341
Db 1260 CTSIWMNLNQLNSAWPCLQYWPBEGMLRYGPTQVCMSCMDCDVINRFRICNLTRP 1319
Qy 1342 QEGYLMVQOFOYLGCWASHREVPKRSRFLKILQVEKWOBCBEGRTIIHCLNGGGRS 1401
Db 1320 QEGHLLVRHFQFLWSAYRTPDSKAFHLHLAEDVKWQ--AESGDGRTVVHCLNGGGRS 1377
Qy 1402 GMFCAIGVVMKRONQVVDVFAVKTLLRNSKPNMVEAPEQRYFCYDVALEYLES 1456
Db 1378 GTFCACATVLEMIRCHSLVDVFFAAKTLRNYKPNMVTMDQYHFCYDVALEYLEA 1432

RESULT 7
US-10-296-115-1283
; Sequence 1283, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1283
; LENGTH: 1499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1283

Query Match 58.68; Score 4577; DB 15; Length 1499;
Best Local Similarity 59.68; Pred. No. 0;
Matches 862; Conservative 206; Mismatches 331; Indels 48; Gaps 14;

Qy 34 GCTFDDGPG---ACDYHQDLYDDPFWVHVSQAQEPHYLPPPEMPOGSMVVDSSNHDGCEKA 90
Db 71 GCTFEESDPAVPCYEQAYDDPQWEQVRIHPGTRAPADLPHGSIYLMVNTSQAPQRA 130
Qy 91 RLQPLTMKENDTHCIDFSYLLYSQKGLNPGTLNILVRNKGPLANPIWNVTGTGRDWLR 150
Db 131 HVIFQSLSENDTHCVQFSYFLYSRDGHSPTGLGVYVRVNGGPLGSAVWMTGSHGRQWHQ 190
Qy 151 AELAVSTFWNEQVIFEAEEVSGRSYIAIDDIQVLSYPCDKSPHPLRLGDVEVNAQON 210
Db 191 AELAVSTFWNEQVIFEAEEVSGRSYIAIDDIQVLSYPCDKSPHPLRLGDVEVNAQON 250
Qy 211 ATPOCIATGDAVHKLWLORNGEDIPVAQTKNINHRFAASFLQEVTKDQDLYRCV 270
Db 251 ASFQCMAGRAAEAEFLRQSGALVPAAGVRHISHRRFLATPFLAAVSRABODLYRCV 310
Qy 271 TQSERGSGVS-NFAQLIVRPPRPPIAPPQLLGVGPTYLLIQLNANSIIGDGPILKEVEY 329
Db 311 SQAPRGRTSLNFAEFVKEPPTPIAPPQLLAGRTYLLIQLNTNSIIGDGPVIRKEIEY 370
Qy 330 RMTSGSWTEHAVNAPYKWLHLDPPDEYEIRVLLTRPGGGTGLPGPPLITRTKCAEPM 389
Db 371 RMARGPWAEBYHVASLQYKWLHLDPPDEYEIRVLLTRPGGGTGLPGPPLISRTKCAEPM 430
Qy 390 RTPKTKIAIOABRIADVESGLYNTTRCHTNVTICYHYFRG--HNESRADCLMDPK 447
Db 431 RAPKGLAFABIQARQLQWEPLGYNVTRCHTYVSLCYHYTLGSSHNQITRECVKTEQG 490
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Qy 448 APOHVVNHLPPYNNVSLKMLITNPEGRKESEETIIQTDDEVPGPVPVKSLQGTSEFNKIF 507
Db 491 VSRVTMKNLLPYRNVHVLVLTNPEGRKEGKEVTFQTDDEVPGIAAESLTFTPLEDMIF 550
Qy 508 LNKKEPLEPNGIITQVSEYSSRSRDPAPVAGPPTQVSNLWNSTHHVMHLPHTYQ 567
Db 551 LKWEPEQEPNGLITQYBISYQSISSDPANVPGRRTISKLNETTHVSNLHPGTYL 610
Qy 568 FFIRASTVKGFGPATANVTNISAPSLDPYEGVDASLNETATTITVLLRPAQAKGAPIS 627
Db 611 FSVRARTKGFGQAALTEITTNISAPSF-DYADWPSPLGESENITITVLLRPAQGRGAPIS 669
Qy 628 AYQIVVEQLH-PRHTKREACAMECYQVPTVYQNALSCGAPYFAAEPLPGNLPPEAPFTV 686
Db 670 VYQIVVEEQSGRLRREBPGQDCFPVPLTFEAALARGLDVDFGAEALAAASLPEAMPFTV 729
Qy 687 GDNRTYKGFNPPPLAPRKGYNIYFOAMSSVEKETKTCOVRATKAAATEBPEVDPDAKQ 746
Db 730 GDNKTYRGFNPPPLEPKAYLIYFOASHUKGETRLNCIRIARAKAKESKRPL-EVSQR 788
Qy 747 TDRVKIAGISA-GILVFIILLVVIIVVKSK-----LAKRKKDAMGNTRQ 792
Db 789 SEEMGLILGICAGGLAVLILLGAIIVIRKGRDHAYSYYPKPVNMTK---ATVNRQ 844
Qy 793 EMTMVNMDRSYADQSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTAVLDENHSATAES 852
Db 845 EKTHMSAVDRSFTDQSTLQEDERLGLSFMDTGYSTR-----GDQRSGGVTEA 893
Qy 853 SRL--DVPRVLCBGTSPYOTGOLHPAIRVADLLQHLNLMKTSDSYGFKEYESFFRGQS 911
Db 894 SSLGSGSPRRPCGRKSGPYHTGQHPAVRVADLLQHLNMQMTAGYGFKEYESFFRG-- 951
Qy 912 ASWDVAKQDNRAKRNIGNIIAYDHSRVILOPVEDDPSDDIYNANYIDILYLRDGYORPS 971
Db 952 --NDATKKDKVKSGRQEPMPAYDRHRVKLHPLMGDPENADYINANYIDIRINRGYHSN 1009
Qy 972 HYIATQGPVHETVYDFWRMVMWQSQSACIWMVNLVEVGRVKCYKWPDDTEVYGDPKVC 1031
Db 1010 HFATQGPKEVMYDFWRMVMWQHCSSIVMITKLVEVGRVKCSRYWPDESDTYGDIKIML 1069
Qy 1032 VEMEPLEAYVVRPTLERRGYNEIREVKOPHFQWPDHGVYPYHATGLLSFTRVKLSNPP 1091
Db 1070 VKTETLAAYVVRPTALERRGYNSARHEVRQPHFTAMPEHGVYPYHATGLLAFIRRVKASTPP 1129
Qy 1092 SAGPIVHVCSAGAGRTGCIYIDIMLDMABREGVVDIYNCVKALRSRRINNVOETEQYIF 1151
Db 1130 DAGPIVHCSAGTGRGCIYIVLDMLDMAECGVDIYNCVKLCSRVMNIQTEEQYIF 1189
Qy 1152 IHDAILLEACLCGETAIPVCEKAAAYFDMIRIDSQTNSSHLKDBFQTLNSVTPRLQABDCS 1211
Db 1190 IHDAILLEACLCGETTPVSEFKATYKEMIRIDPQSNSSQLREBFQTLNSVTPPLDVECS 1249
Qy 1212 IACLPRNHDKNRPMMLPPDRCLPPLITIDGESSNYNAALMDSYRQPAAFIVTQYPLN 1271
Db 1250 IALLPRNDRKNSMDLPPDRCLPFLISTDGSNNYNAALTSYTSRAAFIVTLHPLOS 1309
Qy 1272 TVKDFWRLVYDYGCTSIWMLENEVDLSQ---CPQYWPBEGMLRYGPTQVCMSCMDCDV 1328
Db 1310 TTPDFWRLVYDYGCTSIWMNLNQLNSAWPCLQYWPBEGPQYGLMEVFPMGSTADEDL 1369
Qy 1329 INRIFRICNLTRPOEGYLMVQOFOYLGCWASHREVPKRSRFLKILQVEKWOBCBEGEG 1388
Db 1370 VARVFRVQNTISRLQEGHLLVRHFQFLWSAYRTPDSKAFHLHLAEDGKWQ--AESGDG 1427
Qy 1389 RTIHCINGGGRSGMCAIGIVVMKRONQVVDVFAVKTLLRNSKPNMVEAPEQRYRCYD 1448
Db 1428 RTIVHCLNGGSGRTGCACATVLEMIRCHNLVDVFFAAKTLRNYKPNMVTMDQYHFCYD 1487
Qy 1449 VALEYLE 1455
Db 1488 VALEYLE 1494
```


;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
;; FILE REFERENCE: MRI-039
;; CURRENT APPLICATION NUMBER: US/10/176,847
;; CURRENT FILING DATE: 2002-06-21
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 22
;; LENGTH: 1463
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-10-176-847-22

Query Match 58.2%; Score 4542.5; DB 14; Length 1463;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 843; Conservative 242; Mismatches 341; Indels 61; Gaps 11;
3 VAAALPAFVALWLLYLPWLLGSLGQPSAGCTFDGPGACDHYQDL-YDDREWHVSA 61
4 LAALALLLRLQL-----PPLPGARASAPGCGCFDEHNSCGYSVALGTNGFTWEQINT 59
62 QEPHYLPPEPQGSVMVVDSSNHDPEGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGT 121
60 TERPMLDQAVPTGSGFMVNSGRASGQKALHLLFTLXENDTHCIDFHYFSSRRDSSPGA 119
122 LNILVRNKGGLANPIWNTGTRDMLRAELAVSTFWPNEYQVIFAEVSGGSGYIAI 181
120 LNVYKVGNGPQGNFVNVSVVTEGVWKAELAISTFWPHFYQVIFESVSLKHPGYIAV 179
182 DDLOVLSYPCDKSPHFLRGDVEVNAONATFOCIATGRDAVHNKMLQRNGEDIPVAQ 241
180 DEVRVLAHPCKRPHFLRLQNVNVCQNTATFOCIAGGKWSQHDKWLQOQWNGRDTALMV 239
242 TKINHRFRFAASFLRLQVTKTDQDLRYCVTQSERGSGVSNFAOLIVREPPRIAPPOLLG 301
240 TRVNHRRFATVSADTAQBSVSKYCVIRSDGSGSVNVAELIVKEPTPIAPPELLA 299
302 VGPTYLILQANANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMLDPTDEYR 361
300 VGATYLWKFNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMLDPTDEYR 359
362 VLTTRPEGCTGLPGPLITRTKCAEPMPRTKILAEIOARRTAVDWESLGNITRCHT 421
360 VLTTRPEGCTGLPGPLITRTKCAEPMPRTKILAEIOARRTAVDWESLGNITRCHT 421
422 FNTVICYHPRGHNESRADCLMDPKAPQVWVHLPYTVNLSKMLITNPEGRKSEETI 481
420 YNLTVQYQV--FNQOQYEAEBEVIQTSSTYTLRGLRPFMTIRLLLSNPEGRMESELV 477
482 IQTDEDVPGVPVKSLQGSTFENKIFLNWKEPLEPNGIITQYEVSYSSIRSFPDPAVPAG 541
478 VQTEEDVPGAVPLESIQGGPFEEKIYQWKPNETNGVITLYEINYKAVGSLDPSADLSS 537
542 PPQTVSNLWNSHTHVFMHLHPGITYQFPIRBASTVKGFGPDATAINTVNTNISAPSLDVEGV 601
538 QRGKVFKLNRNETHHFLVGLYGYTSYFTIKASTAKGFGPPVTTRIAKISAPSMPEYD-T 596
602 DASLNATATTITVLLRPAQAGAPISAYQIVVEQLHPHRTKBRAGAMECYQVPPVYONAL 661
597 DTPLNETDTTITVMLKPAQGRGAPSVYQIVVKEERLOKRRRAADIIECFSPVPSYRNAS 656
662 SGGAPYYFAAELPGLNLPAPFTVGNRTYKGFNPNPLAPRKGYNTIYFOAMSSEVKEIK 721
657 SLDSLHYFAAELKPNALPVQPTVGNKTYNGWNPPLPSKYSIYFOALSXANGETK 716
722 TQCVRIATKA-----AATEBEVIPPDAKQTDTRVVKIAGISAGILV 762
717 INCVRLATKAPMGSAQVTPGTPLCLLTGTASTQNSNTV-EPEKQVDNTVMKAGVIAGLLM 775
763 FILLLLVIVIVKK-----SKLAKKEDANGTRQEMTHVMNADERSYADOS 809
776 FIILLGVMLTIKRRRNAYSYSYLSQKRLAKKQKQTSQGAQREMGMPVSA-DKPTTKLS 834

Qy 810 TLHABDPLSTFTMDQHNFSRPLPNDPLVPTFAVLDENHSAETAESSRLLDVPRYLCEGTESP 869
Db 835 ASRNDGCFSSSQDVNGFTDGSRGELSQPTLTI-QTH-----PYRTCDPVEMS 881
Qy 870 YQTQLHPAJRVADLLQHINLMKTSDSYGPKKEEVESFEGOSASWDVAKKDONAKRYG 929
Db 882 YPRDQFOLAJRVADLLQHITQMKGGQYGFKEEYEALEPGQTASWDTAKEDENRKRYG 941
Qy 930 NIAYDHSRVILQPVEDDPSDIYANANYIDILYRDGYQRPESHYIATQGPVHETVYDFWR 989
Db 942 NIISYDHSRVLLVLDGDPHSDIYANANYI-----DCYHRPRHYIATQGPVHETVYDFWR 995
Qy 990 MWQEQSACIWMVNTNLVEGRCVKCYKYPDPDTEYVGFKTCVEMEPALAEVWTFILR 1049
Db 996 MIWQENSASIVMNTNLVEGRCVKCYKYPDPDTEYVGFKTCVEMEPALAEVWTFILR 1055
Qy 1050 RGYNEIRVQKQFTGMPDHGVPYHATGLLSFTRRVKLSNPPSAGPTVHHCASAGARTGC 1109
Db 1056 KGHEIRLRLDFTSWPDHGVPCYATGLLGFVQVFLNPPPEAGPIVHCSAGARTGC 1115
Qy 1110 YIVIDMLDMAEREGVVDIYNCVKALRRRINMVQTEEQYIFIHDAILEACLGETAIPV 1169
Db 1116 FIALDTMLDMAENEGVVDIFNCVRLRAQRVNLVQTEEQYVFDALILEACLGETAIPV 1175
Qy 1170 CEFKAAVFMIRIDTSQNSHLKDEPOTLNSVTPRLOAEDCSIACLPRNHDKNRFDMLP 1229
Db 1176 CEFRLSYINISRLDPQTNSSQIKDEPOTLNIIVTPRVPEDCSIGLLPRNHDKNRFDMLP 1235
Qy 1230 PDRCLPLITIDGESSNYINAAWMDSYRQAPAAFTVQYPLPNTVKDFWLVYDYGCTSI 1289
Db 1236 LDRCLPLISVDGESSNYINAAWMDSHKQAPAAFTVQYPLPNTVKDFWLVYDYGCTSI 1295
Qy 1290 MLNEVDLSQCCPQYWPBEGMLRYGPIQVECMSCMCDVINRIFRICNLRPQEGYLMVQ 1349
Db 1296 MLNEMDTAQFCMQWPEKTSKCGYPIQVEFVSADIDEDITHRIFRICNLMARPODGYR 1355
Qy 1350 QFOYLGWASHREVPKRSFLKILQVKEWQEBCEGEERTIHLNGGGRSGMFCFCAIGI 1409
Db 1356 HLQYIGWPAYRDTPPSKRSLLKVVRLKQWQEGYDQREGRTVVHCLNGGGRSGTFCFCA 1415
Qy 1410 VVMKVRQNVVDVPHAVKTLRNKSPKNMVEAPEQYRCYDVALEVLIES 1456
Db 1416 VCEMIQQNIIDVFHIVKTLRNKSNMNVETLEQYKFYVEVALEYLSS 1462

RESULT 10
US-10-205-823-343
; Sequence 343, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endegre, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25

QY 34 GCTFDDGPG---ACDYHODLYDDPFWHVHSAQBHYLPPPEMPOGSMYVDSNHDPOGEKA 90
Db 33 GCTFEEDGPAVPCBYEQYDDQFQMDPGS-----PADLPHGSLYLVNVTSHAPQORA 85
QY 91 RLQLPWTWKENDTHCIDFSYLLYSOKGLNPGTFLNLRVNGKGPLANPITVWVTGTGRDMLR 150
Db 86 HVIFQSLSENTHCVQFSYFLYSRDGHSPGTLGVYVRVNGPGLGSAVWMTGSHGROWHQ 145
QY 151 AELAVSTFWPNEYQVIFPEAVSGRSGYIAIDDIQVLSYPCDKSPHFLRLGLDVEVNAGON 210
Db 146 AELAVSTFWPNEYQVIFPEALISPDRCYMGDLDDICILSYPCAKAPHSRLGLDVEVNAGON 205
QY 211 ATQCTATGCRDAVHINKLWLRORNGEDIPVAQTKNINHRRAAASFRLOSVTKTDQDLYRCV 270
Db 206 ASFOCWAAGR-ABAEFLLQOGSALVPAAGVRHSHRSFLATFPFLAAVSRABQDLYRCV 264
QY 271 TQSERGSGVS-NEAQLIVRPPRPPIAPPOLLGVPTVLLQLNANSIIGDPTILKEVEY 329
Db 265 SQAPRGGTSINPAEFVWKEPPTPIAPPOLLRAGPTVLLIQLNANSIIGDPTIVRKEIEY 324
QY 330 RMTSGSWTETHAVNAPTYKLMHLDPDTEYERVLLTRPGEGGTLPGLPPLITRTKCAEPM 389
Db 325 RMARGPMAEVAHVSQTYKLMHLDPDTEYERISVLLTRPGGGTGRGLGPPFISRTKCAEPM 384
QY 390 RPTKTLKIAIOARRIADVHESLGYNITRCHTNVTICHYFRG--HN-----ESRAD 440
Db 385 RAPKGLAFABIOARQLTLOWEPLGYNVTTRCHTYVSLCYHYTLGSSHNQITPRVCEDDR 444
QY 441 CLDWDKAPQHVNVNHLPPYTNVSLKMLTNPBGRKESEETIIOITDDEVPVGPVKSLOGT 500
Db 445 CQPLHHEEPAAL-----SERREVVLTNPBGRKEGKEVTFQDDEVPVSGIAESLTFT 497
QY 501 SPENKILPNWKEPLEPNGIITQYEVSYSSIRSDPAVPVAGPPQTVSNLNSHTHVFMHL 560
Db 498 PLEDMIFLWKEEPOEPNGLITQYEVSYSSIESSDPAVNVQA-TSTISKLRNETVHVFSNL 556
QY 561 HPGTTVQFFIRASTVKGFGPATAINVTNINSASLDPYEGVDASLNETATITVILRPAQ 620
Db 557 HPGTTVLFVSFGARTGKFGQAALTEITTYISAFSL-DYADMPSPGSENNITVLLRPAQ 615
QY 621 AKGAPTSAYQIVVEOLH-PHRTKREAGAMECYOVPVTVQNALSGGAPYFAAELPCGNLP 679
Db 616 GRAPISVQVIVVEEGSRRLRREPCCGQCFVPLTFEALARGLVVDYFGAELASSLP 675
QY 680 EPAPFTVGDNRITYKGFNPPAPRKGNIIYFOAMSSVEKETKTCQVRIATKAATBEPEV 739
Db 676 EAMPFTVGDNKTYRGFWNPPLEPRKALYIYFOASHLKGTRLCNIRIARKAACKESKP 735
QY 740 IPDPKQTRVVKIAGISA-GILVFIILLVIVIVKSK-----LAKRKD 785
Db 736 L-EVSQRSEEMGLITGICAGGLAVLILLGAIIVIRKGRDHVAYSYYKPVNMVK-----790
QY 786 AMGNTRQETHMNVNDRSVADOSTLHAEDPLSITFMDQHNFSRPLNDPLVPTAVLDEN 845
Db 791 ATVNYRQEKTHMSAVDRSFTDOSTL---QPPGLSPMDTHGYSTR-----GEQ 835
QY 846 HS---ATAESSRLDVPRLYCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGFKEEY 903
Db 836 RSGGVTEASSLLGSPRCPGRKSPHYTQLHPAVERVADLLOHINOMKTAEGYGFKEEY 895
QY 904 ESFFEGSASWDVAKQDNRAKNYGNIIYDHSRVILQPVDDPSSDYINANYIDILWY 963
Db 896 ESFFEG----WDATKKDKVKGRQEPMPAYDRHRVKLHMLGDPNADYINANYI-----946
QY 964 RDGVORSHVIATGCPVHETVYDFWVMVQEQSACIVMTNLVEVGRVKCYKWPDDTEV 1023
Db 947 -DGYHRSNHPFIATQGPKEPVYDFWVMVQEQSSIVMTNLVEVAGCKSRYPWEDSDT 1005
QY 1024 YGDFKVTCEWELAEVYVVTFTLRRGYNEIREVKQFHTGWPDHGVPYHATGLLSFIR 1083
Db 1006 YGDIKIMLVKTEILAEVYVVTFTLRRGYNEIREVKQFHTGWPDHGVPYHATGLLSFIR 1065
QY 1084 RVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNVCVKALRSRRINMV 1143

Db 1066 RVKASTPPDAGPIVHCSAGTGTGCYIVLDVMDMAECSEGVVDIYNVCVTKLSCRCVNM 1125
QY 1144 QTEBQYIFHDALEACLEACGTAIPVCEPKAAAFDMIRIDSQTNSSHLKDEFOFOTLNSVTP 1203
Db 1126 QTEBQYIFHDALEACLEACGTTIPVSEPKATYKEMIRIDPQSNSSOLRREFOTLNSVTP 1185
QY 1204 RLQAECSACLPNRNHDKNRFDMLPPDRCLPPLITIDGESSNYINAAALMDSYRQPAFI 1263
Db 1186 PLDVEYSIALLPRNDRKNSMDVLPDRCLPPLISTDGSNNYINAAALTDSTYRSAFI 1245
QY 1264 VTQYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQG---CPOYWPBEGMLRYGPIQVECM 1320
Db 1246 VTUHLQSTTPDFWRLVYDYGCTSIYMLNQLNOSNSAWPCLQYWPBEGROQOYGLMEVEFM 1305
QY 1321 SCMSMCDVINRIFRICNLTRPQEGYLMVQOQYVGLWASHREVPKSRKSLKLLIQVEKWQ 1380
Db 1306 SGTADEDLVARVFRVQINISRLQEGHLLVRHFQFLRWSAYRDTPDSEKAFLLHLLAEVDKWQ 1365
QY 1381 ECEBEGEGRTIHLCLNGGRRSGMFCAGIIVEMVKQNVVDVFAVKTILRNSKPNMVPEAP 1440
Db 1366 --AESGDGRTIVHCLNGGRRGTSCALRTVLEMIRCHNLVDVSAKTLRNYKPNMVETM 1423
QY 1441 EOYRFCDYVALEYLES 1456
Db 1424 DQYHFCYDVALEYLEA 1439

RESULT 12
US-10-087-993-34
; Sequence 34, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Khaitonenkov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPI, CLK,
; AND SIRP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996

```
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-087-993-34

Query Match 55.4%; Score 4325; DB 13; Length 1430;
Beat Local Similarity 58.1%; Pred. No. 1.9e-313;
Matches 839; Conservative 197; Mismatches 345; Indels 64; Gaps 22;

QY 32 AGGCTFD--DGPACDYHQDLYDDFEWVHYSAQEPHYLPPPEMPOGSMYVVDSSNHDPE 88
DB 24 AAGCTFEASDPAVCEYSQAQYDDQWEQVRIHPTGTRAPADLPHGSYLMWNTSQHAPGQ 83
QY 89 KARLQLPKENDTHCIDPFSYLLYSQKGLNPOTLNLVNVKNGPLANPINVVTGTGRDW 148
DB 84 RAHVIFQSLSENDTHCVQFSYFLYSRDTG-GTLRVYRVNGGPLASAVNMTGSHGQW 142
QY 149 LRAELAVSTFWPNEVQVTFEAVSGRSGYTAIDDIQVLSYPCDKSPHFLRLGDVEVNAG 208
DB 143 HQAELAVSTFWPNEVQVTFEALISPDRRGYMGLDILLISYPCAKAPHSRLGDVEVNAG 202
QY 209 ONATFQCTATGRDAVHNKMLQRRNGEDI PVAQTNKINHRFAASFRLEQVTKTDOLYR 268
DB 203 QNASFQCMWAG-EPMRQRLQROQSALVP-AGAFGTATGATPLATFPPLAAVSRAEQDLYR 260
QY 269 CVTQSGRSGVSNFAQLVREPPRIAPPQLIGVGTPLLQNLNANSIIGDGPILLKEVE 328
DB 261 CVSQAPRG-GVSNFPELVKEPTPIAPPQLLRAGPTVLIQLNTNSIIGDGPVIRKEIE 319
QY 329 YNMTSGSWTETHAVNAPYKLMHLPDTEYETIRVLLTRPGEQGTG---LPGPLITRYKC 385
DB 320 YRMARGPMAEVHVASLQTYKLMHLPDTEYETIRVLLTRPGEQGTGWRATPHQ----- 372
QY 386 AEPMT---PKTKIAETQARRIADWESLGYNTTRCHTFNVTCYHYFERG--HNESRA 439
DB 373 -HQMRRAHEGPKGLAFAEIQAQRLTQWEPLGYNVTRCHTYVSLCYHYTLGSSHNQIR 431
QY 440 DCLDMDPKAPQHVNVHLPYTNVSLKMLITNPEGRKSEETIIQTDDEVPVGPVPSLQG 499
DB 432 ECVKTEQGVSRVYTKNLLPYRVNVHVLVTNPEGRKEGKEVTFQTDDEVPSGIAAESLTF 491
QY 500 TSFENKIFLNWKEPELPNGIITQYEVSYSSIRSPDPAPVAGPDPOTVSNLWNTSHVFMH 559
DB 492 TPLEDMIFLKWEPQPNGLITQYETISQSISSDPANVPVPRRTISKLRNETHYVFSN 551
QY 560 LHPGTYQFFIRASTVKGFPATAVNTNINISAPSLPYEGVDASINETATITVLLRPA 619
DB 552 LHPGTYLFSVARTKGFGQAALTEITTNISAPSF-DYADMPSPLGSENTITVLLRPA 610
QY 620 QAKGAPISQYQVWEQLPHRTKRBAGAMECYQVPVTVQNALSGGA----PYFFAAELPP 675
DB 611 QQRGAPISYQVIVEE---ERAGCGGTWTGLLPSAID--LRGGAGPRLVHYFGELAA 665
QY 676 GNLPEAPPTVGDNTYKGFVNPPDLAPRGYNYIFQAMSSVEKETKTQCVRIATKAATE 735
DB 666 SSLPEAMPPTVGDNTYKGFVNPPDLAPRGYNYIFQAMSSVEKETKTQCVRIATKAATE 725
QY 736 EPEVIPDPKQTDVVKVYGIAGISA-GILVFILLVVIIVIVKSKLAKKKDKAMGNTRQEM 794
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Db 726 SKRPL-EVSQRSEBGLILGICAGGLAVLILLGAILIIRKGPVNMWK-ATVNYRQEK 783
QY 795 THMVNMDRSYADOSTLHAEDPLSLTMDQHNFPRLPNDPLVPTAVLDENHSATASSR 854
Db 784 THMISAVDRSFTQSTLQEDERLGLSPMDTHGYSTR-----GDQRSGGVTEASS 832
QY 855 LL-DVPRYLCEGTESPYQTGOLHFAIRVADLLOHINLMKTSDSYGFKEEYESFPEGQSAS 913
Db 833 LLGSPRRPCRGKSPYHTGOLHFAIRVADLLOHINLMKTAEGYGFQKYESFPEG----- 888
QY 914 WDVAKQDNRAKNRYGNIIAVDHSRVILQPVEDDPSDDYINANYIDWLWYDGYQRPESHY 973
Db 889 WDATKKDKVKGSQEPMPAYDRHVKLHPMLGDPNADYINANYI-----DGYHRSNH 942
QY 974 IATQGPVHETVYDFWRMVWQESACIWMVNLVEVGRVKYKYPDDTDEVYDGFVKTQVE 1033
Db 943 IATQGPVHETVYDFWRMVWQESACIWMVNLVEVGRVKYKYPDDTDEVYDGFVKTQVE 1002
QY 1034 MEPLAEVVRFTLEREGYNEIREVKQFHTGWDHGVPHVHATGLLSFIRVKLSNPPSA 1093
Db 1003 TETLAEVVRFTLEREGYNEIREVKQFHTGWDHGVPHVHATGLLSFIRVKLSNPPSA 1062
QY 1094 GPIVHCSAGAGRTGCVIVIDIMLDMAREBGVVDIYNCVKALRRRRINMVQTEQYIFIH 1153
Db 1063 GPIVHCSAGAGRTGCVIVIDIMLDMAREBGVVDIYNCVKALRRRRINMVQTEQYIFIH 1122
QY 1154 DAILEACLCGETAIPVCEFAKAYFDMIRIDSQTNSSHLKDBFQTLNSVTPRLQAECSIA 1213
Db 1123 DAILEACLCGETTIPVSEFAKAYFDMIRIDSQTNSSHLKDBFQTLNSVTPRLQAECSIA 1182
QY 1214 CLPNHDKNRFMDMLPDRCLPFLITIDGSSNYINAAALMDSYRQPAFIVTQYPLPNTV 1273
Db 1183 LLPNRDNKNSMDVLPDRCLPFLITIDGSSNYINAAALMDSYRQPAFIVTQYPLPNTV 1242
QY 1274 KDFWRLVYDGYCTSIYMLNEVDLSQG---CPQYWPEEGMLRYGPIQVECMSCMDCDVIN 1330
Db 1243 PDFWRLVYDGYCTSIYMLNEVDLSQG---CPQYWPEEGMLRYGPIQVECMSCMDCDVIN 1302
QY 1331 RIFRCLNTRPQEGYLMVQOQYLYGWASHREVPGSKSFLKLILOVEKQWECBEGRT 1390
Db 1303 RVFRVQNISRLQEGDLLVRHFQFLRWASAYRDTDPDSKKAFLHLLAEVDKWKQ--AESGDGRT 1360
QY 1391 ITHCLNGGSRGSMFCATGIWVWVKRONVDVFAVXTLRNSKNMVEAPEQYRFCYDVA 1450
Db 1361 IVHCLNGGSRGSMFCATGIWVWVKRONVDVFAVXTLRNSKNMVEAPEQYRFCYDVA 1420
QY 1451 LEYLE 1455
Db 1421 LEYLE 1425

RESULT 13
US-10-296-115-1190
; Sequence 1190, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1130
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1190
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Query Match	31.6%;	Score 2471.5;	DB 15;	Length 623;
Best Local Similarity	72.3%;	Pred. No. 1.7e-175;		
Matches 451;	Conservative 74;	Mismatches 86;	Indels 13;	Gaps 3;
Qy	834	DPLVPTAVLDENISATAESSRLLDVPRY-LCEGTESPQTGQLHPALRVADLLQHLNLMK	892	
Db	11	DPRVRT-----HTMASDTSLSVQSHYTKREPADVPYTGQLHPALRVADLLQHLITQMK	64	
Qy	893	TPDSYGFKEBYESFEGQSASWDVAKKDONRAKNRYGNIILAYDHSRVILOPVEDDDPSSDY	952	
Db	65	CAEGYGFKEEYESFEGQSAPWDSAKDENRMKNRYGNIILAYDHSRVRLQTIEGDTNSDY	124	
Qy	953	INANYIDILWYRGYQBPISHYIATQGPVHETVTDVFRWVWQEOSACIUMVTNLVVEGRVK	1012	
Db	125	INGNYI-----DGYHRPNHYIATQGPMEQETIYDFWRNVWHENTASIIIMVTNLVVEGRVK	178	
Qy	1013	CYKYWPDDEVYGDVKYTCVEMEPLAEYVVRTFTLBERGYNEIREVKQPHFTGMPDHGVP	1072	
Db	179	CKKYWPDDEVYKDIKVTLIETELLAEYVIRTFAVEKRGVHEIREIRQPHFTGMPDHGVP	238	
Qy	1073	YHATGLLSFRFRVKLSNPPSAGPIVWHCSAGAGRTGCYIVIDIMLMAEREGVVDIYNCV	1132	
Db	239	YHATGLLGFVRVQVKSPPSAGPLVWHCSAGAGRTGCFIVIDIMLMAEREGVVDIYNCV	298	
Qy	1133	KALRSRRINMVQTEEQYIFIHDAILEACLGETAIPVCEPKAAFYDMIRIDSTQTNSSLK	1192	
Db	299	RELRSRRVNMVQTEEQYVFIHDAILEACLCGDTSVPASQVRSLYYDMNKLDPQTNSSQIK	358	
Qy	1193	DEFOQLNSVTPRLQAEPCSIACIUPRNHDKNRFMDMLPPDRCLPFLITIDGESSNYNAAL	1252	
Db	359	EEFRTLNMVTPTLRVEDPCSTALLPRNHEKNRKMIDILPPDRCLPFLITIDGESSNYNAAL	418	
Qy	1253	MDSVROPAAFIVQYPLNTPVKDFWRLVVDYDGCTSIUMLNEVDLSQCPQYMWEEGMLRY	1312	
Db	419	MDSYQSPSAFIVTQHPNLNTPVKDFWRLVLVDYHCTSVVMLNDVDPQAQICPQYMWEEGVHRH	478	
Qy	1313	GP1QVECMSCMDCDVINRIFRCNLTRPOEGYLMWQOFOYLGWASHREVPGSKRFLKL	1372	
Db	479	GP1QVEFVSADLREDIISRLFRINYAARPQDGYFWVQOFOFLGWPMTDTPVSKRFLKL	538	
Qy	1373	ILQVEKMQEBCGEGETIITHCLNGGGRSGMFCAGIIVWMVKRONVVDVVFHAVKTLRNS	1432	
Db	539	IRQVDKMQEEYNGEGRTVVHCLNGGGRSGTFFCAISIVCEMLRHQRTVDVVFHAVKTLRNN	598	
Qy	1433	KPNMVEAPQYRCYDVALBYLS 1456		
Db	599	KPNMVDLLDQYKFCYEVALBYLS 622		

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RESULT 14
US-10-296-115-1390
; Sequence 1390, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1390
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1390

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Query Match	28.4%;	Score 2216;	DB 15;	Length 815;
Best Local Similarity	54.0%;	Pred. No. 3.1e-156;		
Matches 409;	Conservative 126;	Mismatches 216;	Indels 6;	Gaps 4;

Qy	22	LLGSALGQPSAGCGTDFDGPACDYHQDLVDDPEWHVVSQAQBHYHLPPEMPQGSYMWVDS	81
Db	14	LLLLTAAGETESGGLFDEPYSTCGYSQSEGDENWEQVNTLTKPTSDPMWPSGFLMVA	73
Qy	82	SNHDPEKARLQLPWKENDTHCIDFSYLLYSOKGLNPGTLNLIVRVNKGPLANPINVVT	141
Db	74	SGRPEGORALLLPOLKENDTHCIDPHYFVSSKSNPPGLLNVYVKNVNGPLGNPINNIS	133
Qy	142	GFTGRDWLRAELAVSTFWPNEXYQVIFEAEVSGRSGYIAIDDIQVLSYPCDKSPHFURLG	201
Db	134	GDPTTWNRAELAISTFWPNFYQVIFEV-ITSGHQGYLAIDEVKVLGHPCTRTPHFLRIQ	192
Qy	202	DVEVNAQONATFOCIATGRDAVHNKWLQRNGEDI PVAQTKNINHRRFAASFRLOEVTK	261
Db	193	NVEVNAQOFATFQCSAIGRTVAGRDAPLQGIQDVRDAPLKEIKVTSRRRFTASFNVVNTK	252
Qy	262	TDQDLRCVTCQSRGSGVNSFAOLI VREPPRIAPQLLGVGPTYLLIQLNANSIIGDGP	321
Db	253	RDAGKYRCMIRTSGGVGISNYAELVNEKPPVPIAPPQLASVGATYLIWQLNANSINGDP	312
Qy	322	IILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYIEIRVLLTRPEGGTGLPGPLIT	381
Db	313	IVAREVEYCTASGSMDNRQPDVSTYSKIGHLDPDTEYIEISVLLTRPEGGTGSPGPAIRT	372
Qy	382	RTKCAEPMRTPKTLKTAETQARIADVWESLGYNI TRCTFTFNVTICYHYPRGHNESRAD-	440
Db	373	RTKCADPMRGPRLKEVVEVKSQITIRWEPFGYNNVTRCHSYNLTIVHYCYQVGQEQVREE	432
Qy	441	-CLDMDPKAPQHVNVHLPPVTNYSKMLTNPGRKESBETIIQTDEDPGVPVVKSLQG	499
Db	433	VSWDENTSHPOHITWLSPTNVSVKLLMNPGRKESQELI VQTDEDLPCAVPTSGIQ	492
Qy	500	TSPENKIFLNMKBLPENGII TOEYVSYSIRSDFPAVPVAGPQPTVSNLWNSTHHVFMH	559
Db	493	STPEEKIFLQWRBPTQTYGVTILYEITYKAVSFDPEIDLSNQSGRVSKLGNETHFLPFG	552
Qy	560	LHPGTYQFFIRASTVKGCPATAINVTNNI SAPSLPDYEGVDASLNETAATTITVLLRPA	619
Db	553	LYFGTTYSFYIRASTAKFGFPATNQFTTKISAPSMPAYE-LETPLNQTDNTVTVMLKPA	611
Qy	620	QAKGAPISAYQIVVEOLHPRHTRKEAGMBCYQVPVTVYQNALSGGAPYYPAAELPGCNLP	679
Db	612	HSRGAPVSVQIVVEERPRTKTTEILKCYVPVTHFQNASLLNSQYYPAAEFPADSLQ	671
Qy	680	EPAPFTVGDNRITYKGFWNPP LAPRKGYNIIYFOAMSSVEKETKTQCVRIATAKAAATEPEV	739
Db	672	AAQPFITGDNKTYNGYWNTEPLLPKYSYRIYFOAASRANGETKIDCQVATKGAATPKP--	729
Qy	740	IPDPAQOTDRVVKIAGISAGILVFILLLLLVIVIVVK	776
Db	730	VPBPEKQOTDHTVKIAGVIGAILLVFVIFGLVGLVMKK	766

RESULT 15
US-09-808-602-54
Sequence 54, Application US/09808602
Patent No. US20020155115A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishnu
APPLICANT: Mezes, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05

Db 1 MDVAAALPAFVALWLLYPWPLLGSAALQGFAGGCTFDDGPGACDYHQDLYDDFEWVHVS 60
Qy 61 AQEHPYLPPEMPOGSGYVMVDSNNHDPGKARLQLPTMKENDTHCIDFSYLLYSOKGLNPG 120
Db 61 AQEHPYLPPEMPOGSGYVMVDSNNHDPGKARLQLPTMKENDTHCIDFSYLLYSOKGLNPG 120
Qy 121 TLNLIIVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGSGYIA 180
Db 121 TLNLIIVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGSGYIA 180
Qy 181 IDDIQVLSYPCDKSPHFLRLGDVEVNAQONATFOCIATGRDAVNKLWLQRRNGEDIPVA 240
Db 181 IDDIQVLSYPCDKSPHFLRLGDVEVNAQONATFOCIATGRDAVNKLWLQRRNGEDIPVA 240
Qy 241 QTKNINHRRFAASFRLOEVTKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOLL 300
Db 241 QTKNINHRRFAASFRLOEVTKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOLL 300
Qy 301 VGVPYLLIOLNANSIIGDGPILILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPDTEYEI 360
Db 301 VGVPYLLIOLNANSIIGDGPILILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPDTEYEI 360
Qy 361 RVLLTRPCEGGTGLPGPLITRTKCAEPMWRTPKTLKIAEIQARRIAVDWESLGYNITRCH 420
Db 361 RVLLTRPCEGGTGLPGPLITRTKCAEPMWRTPKTLKIAEIQARRIAVDWESLGYNITRCH 420
Qy 421 TFNVTICVHYFRGHNESRADCLMDPKAPQHVNVNHPPTVNVSLKWLILTNPEGRKESBET 480
Db 421 TFNVTICVHYFRGHNESRADCLMDPKAPQHVNVNHPPTVNVSLKWLILTNPEGRKESBET 480
Qy 481 LIQDTEDEVPVVKVLSQGTSPENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVPA 540
Db 481 LIQDTEDEVPVVKVLSQGTSPENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVPA 540
Qy 541 GPQTVSNLWNSHTHVFHMLHPGTTYPFFIRASTVKFGPATAINVTNTNISAPSLPDYEG 600
Db 541 GPQTVSNLWNSHTHVFHMLHPGTTYPFFIRASTVKFGPATAINVTNTNISAPSLPDYEG 600
Qy 601 VDASLNATATTITVLLRPAQAGAPISAYQIIVVEQLHPHRTKREAGAMECYQVPVYQNA 660
Db 601 VDASLNATATTITVLLRPAQAGAPISAYQIIVVEQLHPHRTKREAGAMECYQVPVYQNA 660
Qy 661 LSGGAPYFAAELPCGNLPEAPFTVGNRTYKGFNPNPLAPRKGYNIYFQAMSSVEKET 720
Db 661 LSGGAPYFAAELPCGNLPEAPFTVGNRTYKGFNPNPLAPRKGYNIYFQAMSSVEKET 720
Qy 721 KTQCVRIATKAAATEBEPEVIPPAPKQTDVRVKIAGISAGILVFILLLLVIVIVKSKLA 780
Db 721 KTQCVRIATKAAATEBEPEVIPPAPKQTDVRVKIAGISAGILVFILLLLVIVIVKSKLA 780
Qy 781 KKRKDMGNTRQEMTHVMNADRSYADQSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTA 840
Db 781 KKRKDMGNTRQEMTHVMNADRSYADQSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTA 840
Qy 841 VLDEHNSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADLILOHINLMKTSYSGFK 900
Db 841 VLDEHNSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADLILOHINLMKTSYSGFK 900
Qy 901 BEYESFFEQSGASWDVAKKQDNKRNRYGNI IAYDHSRVILQPVDEDDPSSDYINANYIDI 960
Db 901 BEYESFFEQSGASWDVAKKQDNKRNRYGNI IAYDHSRVILQPVDEDDPSSDYINANYIDI 960
Qy 961 WLRYDGYQRP SHYIATQGPVHETVDFWRVMWQESACIWMVTNLVEGRVKCYKYWPD 1020
Db 961 WLRYDGYQRP SHYIATQGPVHETVDFWRVMWQESACIWMVTNLVEGRVKCYKYWPD 1020
Qy 1021 TEVYGDVKVTCVMEPELAEYVYRTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLLS 1080
Db 1021 TEVYGDVKVTCVMEPELAEYVYRTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLLS 1080
Qy 1081 FIRRVKLSNPPSAGPTVHVCHSAGAGRTGCIYVIDIMLMAEREGVVDYINCVALRSRRI 1140
Db 1081 FIRRVKLSNPPSAGPTVHVCHSAGAGRTGCIYVIDIMLMAEREGVVDYINCVALRSRRI 1140

Qy 1141 NMVQTEBOYFIHDAIILEACLCGETAIPVCEPKAAYFDMIRIDTSQTNSSHLKDBFOTLNS 1200
Db 1141 NMVQTEBOYFIHDAIILEACLCGETAIPVCEPKAAYFDMIRIDTSQTNSSHLKDBFOTLNS 1200
Qy 1201 VTPRLOAEDCSIACLPRNHDKNRMFMDLPDPRCLPFLITIDGESSNYINAALMDSYRQPA 1260
Db 1201 VTPRLOAEDCSIACLPRNHDKNRMFMDLPDPRCLPFLITIDGESSNYINAALMDSYRQPA 1260
Qy 1261 AFIVTQVPLPNTVKDFWRLVVDYDCTSIVMNLNEVDLSQGCPCQYWPPEGMRLRYGPQVECM 1320
Db 1261 AFIVTQVPLPNTVKDFWRLVVDYDCTSIVMNLNEVDLSQGCPCQYWPPEGMRLRYGPQVECM 1320
Qy 1321 SCSMDCDVINRI FRI CNLTRPOEGYLMVQOYQYLGWASHREVPGSKSFLKLILOVEKWQ 1380
Db 1321 SCSMDCDVINRI FRI CNLTRPOEGYLMVQOYQYLGWASHREVPGSKSFLKLILOVEKWQ 1380
Qy 1381 EECBEGEGRTI IHCNLCGGRSGMFCAGIIVVMVKRQNVVDVFAVKTLRNKNMVEAP 1440
Db 1381 EECBEGEGRTI IHCNLCGGRSGMFCAGIIVVMVKRQNVVDVFAVKTLRNKNMVEAP 1440
Qy 1441 EQYRFICYDVALEYLESS 1457
Db 1441 EQYRFICYDVALEYLESS 1457

RESULT 2
JC6312
protein-tyrosine-phosphatase (EC 3.1.1.3.48) receptor-type - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C:Accession: JC6312
R:Yang, Y.; Gil, M.C.; Choi, E.Y.; Park, S.H.; Pyun, K.H.; Ha, H.
Gene 186, 77-82, 1997
A:Title: Molecular cloning and chromosomal localization of a human gene homologous to th
A:Reference number: JC6312; MUID:97199372; PMID:9047348
A:Accession: JC6312
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1440 <YAN>
A:Cross-references: GB:L77886
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe
-tyrosine-phosphatase homology
C:Keywords: phosphoric monoester hydrolase
F:31-194/Domain: NAM homology <NAM>
F:209-272/Domain: immunoglobulin homology <IMM>
F:294-372/Domain: fibronectin type III repeat homology <3FR>
F:911-1131/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 96.1%; Score 7506.5; DB 2; Length 1440;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1404; Conservative 19; Mismatches 16; Indels 19; Gaps 3;

Qy 1 MD-VAAALPAFVALWLLYPWPLLGSAALQGFAGGCTFDDGPGACDYHQDLYDDFEWVHV 59
Db 1 MD-TTAAAVPAFVALLLSLPWPLLGSAQGFAGGCTFDDGPGACDYHQDLYDDFEWVHV 60
Qy 60 SAQEPHYLPPEMPOGSGYVMVDSNNHDPGKARLQLPTMKENDTHCIDFSYLLYSOKGLNP 119
Db 61 SAQEPHYLPPEMPOGSGYVMVDSNNHDPGKARLQLPTMKENDTHCIDFSYLLYSOKGLNP 120
Qy 120 GTLNLIVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGSGYI 179
Db 121 GTLNLIVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGSGYI 180
Qy 180 AIDDIQVLSYPCDKSPHFLRLGDVEVNAQONATFOCIATGRDAVNKLWLQRRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAQONATFOCIATGRDAVNKLWLQRRNGEDIPV 240
Qy 240 AQTKNINHRRFAASFRLOEVTKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOL 299
Db 241 AQTKNINHRRFAASFRLOEVTKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOL 300

300 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE 359
Db LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE 360
360 IRVLLTRPGECCGTGLPGPPLITRTKCAEPMTPTKTLKIAEQARRIADVWESLYNITRC 419
Db IRVLLTRPGECCGTGLPGPPLITRTKCAEPMTPTKTLKIAEQARRIADVWESLYNITRC 420
420 HTFNVTICYHYFRGHNSRADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESBE 479
Db HSFNVITICYHYFRGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESBE 480
480 TIIOTDEDPGVPVKSLQGTSPFNKIFLWKEPLENGIITQYEVSYIRSIRSDPAVPV 539
Db TIIOTDEDPGVPVKSLQGTSPFNKIFLWKEPLENGIITQYEVSYIRSIRSDPAVPV 540
540 AGPPQTVSNLWNSHHVFMHLPGTQYOFFIRASTVKGFPGPATVNTVNTNISAPSLPDYE 599
Db AGPPQTVSNLWNSHHVFMHLPGTQYOFFIRASTVKGFPGPATVNTVNTNISAPSLPDYE 600
600 GVDASLNETAFTITVLLRPAQAAGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVTYQN 659
Db GVDASLNETAFTITVLLRPAQAAGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVTYQN 660
660 ALSGAPYYFAAELPPGNLPEPAPFTVGDNRITYKGFNWPPLAPRGNIYFQAMSSVEKE 719
Db AMSGAPYYFACRTPPGLPEPAPFTVGDNRITYKGFNWPPLAPRGNIYFQAMTSVEKE 720
720 TKTCQVRIATKAAATEPEVLPDPAKQTDVVKIAGISAGILVFILALLVIVIVKSKL 779
Db TKTCQVRIATKAAATEPEVLPDPAKQTDVVKIAGISAGILVFILALLVIVIVKSKL 780
780 AKKRKDMANGTROEMTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPT 839
Db AKKRKDMANGTROEMTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFSRY ----- 832
840 AVLDENHSATBSRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHINLMKTSDSYGF 899
Db -----ENHSATBSRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHINLMKTSDSYGF 888
900 KEEVESFEGQSASWDVAKKQDNKRNRYGHIITAYDHSRVILQPVEDDPSSDYINANYID 959
Db KEEVESFEGQSASWDVAKKQDNKRNRYGHIITAYDHSRVILQPVEDDPSSDYINANYI - 947
960 IWLRYDGYQRPISHYIATQGPVHETVYDFWVMVWQEQSACIVMTNLVEGRVKCYKWPD 1019
Db -----DGYQRPISHYIATQGPVHETVYDFWMIWQEQSACIVMTNLVEGRVKCYKWPD 1002
1020 DTEVYDGFVKTCVEMEPALBYVVRTFTLRRGYNEIREVKQFHTGMPDHGVPVHATGLL 1079
Db DTEVYDGFVKTCVEMEPALBYVVRTFTLRRGYNEIREVKQFHTGMPDHGVPVHATGLL 1062
1080 SFIRRVKLSNPPSAGPIVHCHSAGAGTCYIVIDIMLDAEREGVVDIYNCVKALBSRR 1139
Db SFIRAVKLSNPPSAGPIVHCHSAGAGTCYIVIDIMLDAEREGVVDIYNCVKALBSRR 1122
1140 INMVQTEEQYIFIHDAILEACLGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFOTLN 1199
Db INMVQTEEQYIFIHDAILEACLGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFOTLN 1182
1200 SVTPRLQAECDSCIACLPRNHDKNRFDMLPPDRCLPLIITIDGESSNYINAAALMDSYRQP 1259
Db SVTPRLQAECDSCIACLPRNHDKNRFDMLPPDRCLPLIITIDGESSNYINAAALMDSYRQP 1242
1260 AAFIVTQYPLNVTVKDFWRLVYDGYCTSIYMLNEVDLSQCPQWPWPEGLMRGPIQVEK 1319
Db AAFIVTQYPLNVTVKDFWRLVYDGYCTSIYMLNEVDLSQCPQWPWPEGLMRGPIQVEK 1302
1320 MSCMDCDVNIRIFRINLNRPOBYLWVQFOYVLGWASHREVPGRSKSLKILQVEKW 1379
Db MSCMDCDVNIRIFRINLNRPOBYLWVQFOYVLGWASHREVPGRSKSLKILQVEKW 1362
1380 QBECEBEGEGRITIIHCLNGGSGMFCAGIIVWEMVKRQNVVDVFAVKTLLRNSKPNMVEA 1439

Db 1363 QBECEBEGEGRITIIHCLNGGSGMFCAGIIVWEMVKRQNVVDVFAVKTLLRNSKPNMVEA 1422
QY 1440 PEQVRFYCDVALEYLESS 1457
Db 1423 PEQVRFYCDVALEYLESS 1440
RESULT 3
S17669
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type mu precursor - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: S17669
R:Gibbank, M.P.B.G.; van Btten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.;
FEBS Lett. 290, 123-130, 1991
A:Title: Cloning, expression and chromosomal localization of a new putative receptor-like
A:Reference number: S17669; MUID:92008644; PMID:1655529
A:Accession: S17669
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1452 <GEB>
A:Cross-references: UNIPROT:P28827; EMBL:X58288; NID:g32455; PIDN:CAA41226.1; PID:g32456
A:Note: the authors translated the codon TAT for residue 1340 as His, TTC for residue 13.
C:Genetics:
A:Gene: GDB:PTPRM; PTPRL1
A:Cross-references: GDB:1128093; OMIM:176888
A:Map position: 18p11.2-18p11.2
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe
-tyrosine-phosphatase homology
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1452/Product: protein-tyrosine-phosphatase, receptor type mu #status predicted <MAT
F;21-745/Domain: extracellular #status predicted <EXT>
F;22-184/Domain: MAM homology <MAM>
F;139-262/Domain: immunoglobulin homology <IMM>
F;284-364/Domain: fibronectin type III repeat homology #status atypical <FN3A>
F;379-470/Domain: fibronectin type III repeat homology <FN3B>
F;482-574/Domain: fibronectin type III repeat homology <FN3C>
F;586-674/Domain: fibronectin type III repeat homology <FN3D>
F;746-762/Domain: transmembrane #status predicted <TM>
F;763-1452/Domain: intracellular #status predicted <INT>
F;842-1452/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;923-1143/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1213-1437/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;72, 92, 131, 249, 406, 414, 448, 454, 534, 544, 598, 651, 681/Binding site: carbohydrate (Asn) (co
F;206-260/Diulfide bonds: #status predicted
F;1095/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1101/Binding site: substrate phosphate (Arg) #status predicted
F;1389/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1395/Binding site: substrate phosphate (Arg) #status predicted
Query Match 61.6%; Score 4812.5; DB 1; Length 1452;
Best Local Similarity 61.4%; Pred. No. 7.4e-316;
Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;
QY 22 LLGSALQGSAGACTGDDGGACDYHQDLYDDFEWVHVSQAEPHYLPPEMPOGSMYVVD 81
Db 14 LLTATAGTFSGGCLDEPYSTCGYQSGEGDDFNWQVNTLTXTSDPWPSSSLMLVNA 73
QY 82 SNHDPGEKARLQPTWKENDTHCIDFSYLLYQKLNPGTGLNLRVKNKPLANPINVT 141
Db 74 SGRPEGORAHLLPOLKENDTHCIDFHYFVSSKSNPPGLLVVVKVNGPLGNPINNIS 133
QY 142 GFTGRDWLRAELAVSWFNPNEYQVIEAEVSGRSGYIADDDIQVLSYPCDKSPHFLRLG 201
Db 134 GDFTRNTRAEALAISTFWPNFYQVIEFV-ITSGHQGYLAIDEVKVLGHPCRTPHFLRIQ 192
QY 202 DVVNAGQONATFOCIATGRDAVNKLWLRNGEDIPVAOTKNNHRRFAASPRLOQVTK 261
Db 193 NVEVNAQGFATFOCSAIGRTVAGRLWQGLQIDVRDAPLKEIKVTSRRFASFNVNVTTK 252
QY 262 TDQDLRYCVCVTSRGRSGVSNFAQLIVREPPRIAPPQLLGVGPTYLLIQLNANSIIGDGP 321

Db 253 RDAGKYRCWIRTEGGVGISYAEVLVVEPPVPIAPQLASVGATYMLQLNANSINGDP 312
Qy 322 IILKEVEYRMTSGSWETHAVNAPYKLUWHLDPDTEYEIRVLLTRPGEGGTGLPGPLIIT 381
Db 313 IVAREVEYCTASGWNDRQPDVSTSYKICHLDPDTEYEISVLLTRPGEGGTGSPGALRT 372
Qy 382 RTKCAEPNRTPTKLAIEIOARRIADVWESLGYNTIRCHTFENVITCYHYFFGHNESRAD- 440
Db 373 RTKCADPWRGGRKLEVVVKRQITIRWEPFGYNVTRCHSNLTVHYCYQGGQEQVREE 432
Qy 441 -CLDMDPKAPQHVNVNHLPPYTNVLSKMLITNPEGRKESEETIIOTDEDVPGVPVKSLOQ 499
Db 433 VSMDETENSHPOHTITNLSPYTNVSVKLIILMNPGRKESQELIVOTDEDLPGAVTESIQ 492
Qy 500 TSFENKIFLNKKEPLNEPNIITQYEVSYSTRSPDPVAVPGPQTVGNLNNSTHHVPMH 559
Db 493 STFEKIEFLQWREPQTQYGVITLYEITYKAVSSFPDEIDLNSQSRVSKLGNETHFLPFG 552
Qy 560 LHPGTTYOFFTRASTVKGFGATAINVTNITSAPSLPDYEGVDASLNSTATITVLLRPA 619
Db 553 LYPGTYFTIRASTAKFGPGPATNQFTTKISAPSNPAYE-LETPLNQTDNTVTVMKLRPA 611
Qy 620 QAKGAPISAYQIVVQQLPHRHTKREAGAMECYQVPVTYQNALSGGAPYFFAAELPPGNLP 679
Db 612 HSRGAPSVYQIVVEERPRRTKTEILKCYVPPIHFQNASLLNSQYFFAAELPPADSLO 671
Qy 680 EPAPTVGDNRTYKGFWMNPLAPRKGYNIFYOAMSSVEKETQCVRIATKAAATEPEEV 739
Db 672 AAQPTIGDNKTYNGYMNTPLLPYKSYRIYFOAASRANGETKIDCVQVATKGAATPKD-- 729
Qy 740 TPDPAKQTRVVUKIAGISAGILVFTLLLVIVIVKSKLAKRKADMGNTROEMTHVN 799
Db 730 VPEPEKQTDHTVKIAGVLAGILFLVIFLGVLVNMKKRKLAKRKETWSSTRQEMTMVN 789
Qy 800 ANDRYADQSTLHARDPLSLTFMDQHNSPRLNDP-----LVPTAVL-DSNH 846
Db 790 SMDKSYAEQGTNCDE---AFSPMDTHNLGRSVSPSSFTKMTNTLSVSPNSYYPDETH 846
Qy 847 SATAESRLLDVPRY-LCEGTESPYQTQLHPAIRVADLLQHINLMKTSYSGFKEEYES 905
Db 847 TWASDTSSLVQSHTYKKREPADVPYQTQLHPAIRVADLLQHIITQMKCAEGYGFKEYES 906
Qy 906 FPEGQASWDVAKDONAKRNYGNI IAYDHSRVILQPVEDDPSDYINANYIDILWYRD 965
Db 907 FPEGQASAPWSAKDONAKRNYGNI IAYDHSRVRLQITGDTNSDYINGNYI-----D 960
Qy 966 GYORPSHYIATQGPVHETVYDFWRVMWQEOSACIVVMVNLVEGVKVCYKWPDPDTEVYG 1025
Db 961 GYHRPNHYIATQGPVHETVYDFWRVMWVHENTASIIIMVNLVEGVKCKYWPDPDTEIYK 1020
Qy 1026 DPKVTCVMEPIAEYVYVFTTLERRGYNEIREVKQFHFTGMPDHGVYPYHATGLLSFIRRV 1085
Db 1021 DIKVTLIETELLAEYVIRTFAVEKRGVHEIRIQFHFHTGMPDHGVYPYHATGLLGIVRQV 1080
Qy 1086 KLSNPSAGPIVHCSAGRGTCYVIDIMLDMAREGVGVDIYNCVKALRSRRNMVQT 1145
Db 1081 KSKSPSAGPLVHCSAGRGTCYVIDIMLDMAREGVGVDIYNCVKALRSRRNMVQT 1140
Qy 1146 BEQYFIHDAILEACLCGBTAPVCEFKAAYPDMIRIDSQTNSSHLKDBEFQTLNSVTPRL 1205
Db 1141 BEQYFIHDAILEACLCGDTSPASQVRSRYLYDMKNLDPQTNSSQIKEFRILANVTPL 1200
Qy 1206 QAEDCSIACLPRNHNKRMFMDLPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT 1265
Db 1201 RVEDCSIALPRNHNKRMFMDLPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT 1260
Qy 1266 QYPLNTWKDFWRLVYDYCTSIYMLNEVDLSQGCQYQWPEEGMLRYGPIQVECHSCSND 1325
Db 1261 QHPLNTWKDFWRLVYDYCTSIYMLNEVDLSQGCQYQWPEEGMLRYGPIQVECHSCSND 1320
Qy 1326 CDVINRIFRICMLTRPOEGYLMVQFOYILGWASHREVPGSKSFLKLIILQVEKWBECBE 1385

Db 1321 EDIISIRIFRIYNAARPQDGYRMVWQOQFQLGMPMYRDTPVSKRSFLKLIRQVDKMQEETNG 1380
Qy 1386 GEGBTIIHCLNGGGRSGMFCAGIIVWVKRQNVVDVFAVKTLRNSKPNMVAPEQVRF 1445
Db 1381 GEGBTIVHCLNGGGRSGTFCAGIISVCEMLRHQRTVDVFAVKTLRNNKPNMVDLLDQYKF 1440
Qy 1446 CYDVALEYLES 1456
Db 1441 CYEVALBYLNS 1451
RESULT 4
S17670
Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type mu precursor [validated] - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: S17670
R:Gebblink, M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.;
FEBS Lett. 290, 123-130, 1991
A:Title: Cloning, expression and chromosomal localization of a new putative receptor-like
A:Reference number: S17669; MUID:92008644; PMID:1655529
A:Accession: S17670
A:Molecule type: mRNA
A:Residues: 1-1452 <GEB>
A:Cross-references: UNIPROT:P28828; EMBL:X58287; NID:G53234; PIDN:CAA41225.1; PID:G53235
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe
C:tyrosine-phosphatase homology
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; trar
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-1452/Product: protein-tyrosine-phosphatase, receptor type mu #status predicted <MAI
F:21-745/Domain: extracellular #status predicted <EXT>
F:22-184/Domain: MAM homology <MAM>
F:193-262/Domain: immunoglobulin homology <IMM>
F:284-362/Domain: fibronectin type III repeat homology <FN3A>
F:379-470/Domain: fibronectin type III repeat homology <FN3B>
F:482-574/Domain: fibronectin type III repeat homology <FN3C>
F:586-674/Domain: fibronectin type III repeat homology <FN3D>
F:746-762/Domain: transmembrane #status predicted <TMN>
F:763-1452/Domain: intracellular #status predicted <INT>
F:842-1452/Domain: leukocyte common antigen cytosolic domain homology <IAC>
F:923-1143/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1213-1437/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:72_92_131_249_406_414_448_454_534_544_598_651_681/Binding site: carbohydrate (Asn) (co
F:206-260/Disulfide bonds: #status predicted
F:1095/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1101/Binding site: substrate phosphate (Arg) #status predicted
F:1389/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1395/Binding site: substrate phosphate (Arg) #status predicted
Query Match 61.4%; Score 4793.5; DB 1; Length 1452;
Best Local Similarity 61.3%; Pred. No. 1.4e-314; Indels 29; Gaps 9;
Matches 889; Conservative 208; Mismatches 325;
Qy 22 ILGSAFGSAGGCTFDDGPGACDHYQDLYDDFEWVHVYSAQEPHYLPPEMPOGSMVYVDS 81
Db 14 LLLTAAGETPFGGCLFDEPYSTCGYSQADEDDFNWEQVNTLTKTSDPMPGSGFMLVNT 73
Qy 82 SNHDPGEKARLOPTMKENDTHCIDFSVLLYSQKGLNFGTLLILVRVKNGLPLANINWVT 141
Db 74 SGKPEGQRAHLLPOLKENDTHCIDFHYFVSSKSNAPGLLNVYKVVNNGPLGNPIMNIS 133
Qy 142 GFTGRDWLRALAVSTFWPNEYQVITFEAEVSGRSGYTAIDDIQVLSYPCDKSPHFLRLG 201
Db 134 GDPTRTHRAELALISTFWPNFYQVIFEV-VTSGHGYLALIDEVKVLGHPCRTKPHFLRIQ 192
Qy 202 DVEVNAGQATFQCIATGRDAVHNKMLQRRNGEDIPIVAQTKNINHRPFAASFRLOQEVTK 261
Db 193 NVEVNAGQATFQCSAIGRTVAGDRLWLQGDVDRDAPLKEIKVTSRRFIASFNVNVTTK 252
Qy 262 TDQDLRYCVTOSERGSGVSNFAQLIVRPPRPPIAPPQLLGVGPTVLLIQLNANSIIGDP 321
Db 253 RDAGKYRCWIRTEGGVGISYAEVLVVEPPVPIAPQLASVGATYMLQLNANSINGDP 312

Qy 322 ILLKEVEYRMTSGSWTETHAVNARTYKLVHLDPDTEYEIRVLLTRPGEGGTGLPGPLIT 381
Db 313 IVAREVYCTASGWNDRQPVDSYSYKIGHLDPDTEYEISVLLTRPGEGGTGSPGPAIR 372
Qy 382 RTKCAEMPTPKTLKIAEIOARRIADVWESLGYNITRCHTFNVITCYHYRGNHESRAD- 440
Db 373 RTKCADPMRGPRKLEVEVSKRQITIRWEPGYNVTRCHSNLVVHYQYVGQGEQVREE 432
Qy 441 -CLDMDPKAPQHVNVHLPYTNVSKMLITNPEGRKSEETIIQTDEDVPGVPVKSLQG 499
Db 433 VSWDTDNHPQHTITNLSPYTNVSKLILNPEGRKESQELTVQTDLDLPGAVPTEIQG 492
Qy 500 TSPENKIFLWKEPLENGIITQYEVSYSSRSRDPVAVGAPPTQTVSNLWNSHHVPMH 559
Db 493 SAFEKIFLOWREPTQYVITLTYEITYKAVSSDPEDIDLSNQSGRVSFKLGNETHFLPFG 552
Qy 560 LHPGTTQFFIRASTVKGFGFATAVNTVNTNISAPSLDPYEGVDASLNATETIIVLLRPA 619
Db 553 LYFGTYSFIRASTAKGFGPPATNQFTKLISAFSMPAYE-FETPLNQTDNTVIVMLKPA 611
Qy 620 QAKGAPISAYOIVVEQLHPHRTKREAGAMECYQVPVTVYQNALSGGAPYFAAELPPGNLP 679
Db 612 QSRGAPSVYQIVVEERPRRTKTTBILKCYVPVIFHQNASILNSQYFAAEPFADSLQ 671
Qy 680 EPAPFTVGNRTYKGFNPPDLAPRKGNIYFQAMSSVEKETQCVRIATKAAATEBPEV 739
Db 672 AAQPFITGDNKTYNGYNTLPHKSYRIYQAASTRANGETKIDCVRVATKGAVTPKP-- 729
Qy 740 IPDPAKOTDRVVKTAGISAGILVPIILLVIVLVKSKLAKKEDAMGNTROBMTMVN 799
Db 730 VPEPEKQDHTVKIAGVIAGLLEFVILPLGVVLVKKRKLAKKRTWSSRQBMVTMVN 789
Qy 800 AMRSYADQSTLHAEDPLSLTFMDQHNPSRLNDP-----LVPTAVL-DENH 846
Db 790 SMDKSYAEQTCNDE---AFSEFMGTHNLGSRVSSPSSFTKNTLTSTVPSNYYPDETH 846
Qy 847 SATABSRLLDVPRY-ICEGTESYQTCQLHPAIRVADLQHLINLMKTSOSYGFKEYES 905
Db 847 TMASTDSLAQPHYTKKREADVQTCQLHPAIRVADLQHLITQMKCAEGYGFKEYES 906
Qy 906 FFEQASWDAVAKDONKRNRYNIITAYDHSRVLQPVDEDDPSDDYINANYIDILYRD 965
Db 907 FFEQASWDAVAKDONKRNRYNIITAYDHSRVLQPVDEDDPSDDYINANYIDILYRD 960
Qy 966 GYORPSHYIATQGPVHETVDFWNVWVQEOSACIVMTNLVEGRVACIKYKWPDDTEVYG 1025
Db 961 GYHRPNHYIATQGPVHETVDFWNVWVQEOSACIVMTNLVEGRVACIKYKWPDDTEVYG 1020
Qy 1026 DFKVTCEMPELARYVTRFTLRRGYNEIREVKQFHTGMPDHGVPHATGLLSFTRV 1085
Db 1021 DIKVTLLDTELLAEYVIRTEAVEKRGITHEIREIQFHTGMPDHGVPHATGLLSFTRV 1080
Qy 1086 KLSNPPSAGPIVHCSAGAGTCGYVIDIMLMDAREGVVDIYNCVKALRSRINNVQT 1145
Db 1081 KSKSPNAGPLVHCSAGAGTCGYVIDIMLMDAREGVVDIYNCVKALRSRINNVQT 1140
Qy 1146 EEOYIFTHDALEACLGCTAI PVECFKAAVFDIMRIDSQTNSSHLKDEFOTLNSVTPRL 1205
Db 1141 EEOYIFTHDALEACLGCTAI PVECFKAAVFDIMRIDSQTNSSHLKDEFOTLNSVTPRL 1200
Qy 1206 QAEDCSIACLRNRHDKRFDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVT 1265
Db 1201 RVEDCSIALPRNHEKRCMDILPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVT 1260
Qy 1266 QYPLPNTVKQFWRVLVYDYGCTSIYVNLNEVLSQCQPVWBEGLMYRGPQVECMSCMD 1325
Db 1261 QHPLPNTVKQFWRVLVYDYGCTSIYVNLNEVLSQCQPVWBEGLMYRGPQVECMSCMD 1320
Qy 1326 CDVNIIRFICNLTRPOEGLYLVQOQFVYLGWASHREVPVGRSFLKILLOVEKWOEECEE 1385
Db 1321 EDIISIRFIRIYNARPODGHMVOQFQFLGMPFMTDTPVSKRSFLKILROVDKWOEEYNG 1380
Qy 1386 GEGRTIIHCLNGGGRSGMFCAGIVVEMVRQNVVDVFAVKTLRNKNPNVFAEQRYR 1445

Db 1381 GEGPTVHCLNGGGRSGMFCAGISIVCEMLRHQRVDFHVAVKTLRNNKPNVMDLLDQYKF 1440
Qy 1446 CYDVALEYLES 1456
Db 1441 CYEVALEYLNS 1451
RESULT 5
JC5290
protein-tyrosine-phosphatase (EC 3.1.3.48) - human
N;Alternate names: Phosphotyrosine phosphatase
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC5290
R;Wang, B.; Kishihara, K.; Zhang, D.; Hara, H.; Nomoto, K.
Biochem. Biophys. Res. Commun. 231, 77-81, 1997
A;Title: Molecular cloning and characterization of a novel human receptor protein tyrosi-
ma cells.
A;Reference number: JC5290; MUID:97223402; PMID:9070223
A;Accession: JC5290
A;Molecule type: mRNA
A;Residues: 1-1436 <MAN>
A;Cross-references: UNIPROT:O00197; GB:U73727; NID:g19233222; PIDN:AA851343.1; PID:g192332
C;Comment: This enzyme belongs to type II receptor protein tyrosine phosphatase which me-
and an immunoglobulin-like domains.
C;Genetics:
A;Gene: hptp-J
C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe-
-tyrosine-phosphatase homology
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;22-188/Domain: MAM homology <MAN>
F;203-266/Domain: immunoglobulin homology <IMM>
F;288-366/Domain: fibronectin type III repeat homology <3PR>
F;826-1436/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;903-1123/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1193-1418/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1075/Active site: Cys (phosphocysteine intermediate) #status Predicted
F;1081/Binding site: substrate phosphate (Arg) #status Predicted
F;1370/Active site: Cys (phosphocysteine intermediate) #status Predicted
F;1376/Binding site: substrate phosphate (Arg) #status Predicted
Query Match 59.1%; Score 4619; DB 2; Length 1436;
Best Local Similarity 60.4%; Pred. No. 8.2e-303;
Matches 866; Conservative 203; Mismatches 329; Indels 36; Gaps 12;
Qy 32 AGCTPD--DGGACDYHQDLVDDDEWVHVSAQEHPVLPPEMPQGSVMVVDSSNHPGE 88
Db 24 AAGCTFEASDPAVPCESYQAQYDDDFQWQVRIHPGTRAPADLPHGSLYVMTVSQHPAQ 83
Qy 89 KARLQLPMKENTHCDIFSYLLYSOKGLNPGTINILVRVKNGLANPIVNVGTGTRDW 148
Db 84 RAHVIFQSLSENTHCVQFSYFLYSRDCHSPGLTGVTVRVNGGPLGSVAVNMTGSHQROW 143
Qy 149 LRAELAVSTFWPNEYQVIFPEARVSGRSGYAIADDDIOVLSPCDKSPHFLRLGDEVNAG 208
Db 144 HQAELAVSTFWPNEYQVIFPEALISPDRRGYMGLDDILLVSPCAKAPHFSLRGDEVNAG 203
Qy 209 QNATFQCIATGRDAVKNLWLRNGEDIPVATQKNINHRFAASFLQEVTKTDQDLR 268
Db 204 QNASFQCAAGRAAEAEERFLQCSGALVPAAGVRRHISHRRFLATFTFLAAVSRAEQDLR 263
Qy 269 CVTQSERGSGVNSPAQLIVREPRTAPPOLLGVGPTYLILQNLANSIIGDGPILKEVE 328
Db 264 CVSQPRGAGVNSPAELIVKEPPTTAPPOLLRAGPFLIILQNTNSIIGDGPILRKEIE 323
Qy 329 YRMTSGSWTETHAVNARTYKLVHLDPDTEYEIRVLLTRPGEGGTGLPGPLITRTKCAEP 388
Db 324 YRMARGPMAEVHVSQTYKLVHLDPDTEYEISVLLTRPGEGGTGTRGPPLISRTKCAEP 383
Qy 389 MRPKTLKIAEIOARRIADVWESLGYNITRCHTFNVITCYHYRGNHESRADCLMDP 446
Db 384 MRAPKGLAPAEIOARRIADVWESLGYNITRCHTFNVITCYHYRGNHESRADCLMDP 443

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QY 447 KAPQHVNVHLPPYTNVSLKMLITNPEGRKESEETIIQTDDEVPQVPVKSLQTSFENKI 506
Db 444 GVSRTIIKNLPIYRNVHVLVLTNPEGRKEGKVTFTQDDEVPQVIAAESITFTPLEDMI 503
QY 507 FLNWKPELEPGLIITQYEVSYSSIRSPDPVAVPAGPQTQVSNLWNSTHHVFMHLPGTTY 566
Db 504 FLKWEPEQENGLIITQYELISYQSISSDPVAVNVPGRPTISKLRNETYHVFSNLHPGTTY 563
QY 567 QFFIRASTVKGCPATAINVTNINISAPSLPDYEGVDASLNETAATITVLLRPAQAGAPI 626
Db 564 LFSVRARTCKGFGQAALTEITNISAPSF-DYADMPSPLGESSENTITVLLRPAQGRGAPI 622
QY 627 SAYQIVVQLHPHRTKRAGAMECVQVPTVYNALSGGAPYVEAAELPPGNLPEPAPTV 686
Db 623 SVYQIVVEERARRURRPPGGQDCFPVLTTEAALARGLVHYFGAELAAASDPAMPPTV 682
QY 687 GDNRTYKGFNPLPRGYNIIYFQAMSGSVKETKTQCVRITAKAAATEEPEVDPDAKQ 746
Db 683 GDNQYRGFNPPLEPRKAYLIYFOAASHLKGDTLNCIRIARKAACKESKRPL-EVSQR 741
QY 747 TRRVKIIAGISA-GILVFILLLVIVIVVKSUKAKRKDAMGNTRQEWTHMVMNDRSY 805
Db 742 SEEMGLILGICAGGLAVLILGAIIVIRKGPVNMTK-ATVNVYRQEKTHMMSAVDRSF 800
QY 806 ADOSTLHAEDPLSLTFMDQHNFSPLPNDPLVPTAVLDENHSATAESRLI-DVPRYLCE 864
Db 801 TDQSTLQDBERLGLTFMDTHGYSTR-----GDQRSGVTEASLLGGSPRRPCG 849
QY 865 GPESPYQTQGLHPALRVADLQHILMKTSYSGFKEEYGFQESASWDVAKKDQNR 924
Db 850 RKGSPYHTQGLHPARVADLQHINQMTAEGYGFQEYESFEFEG----WDATKKDKVK 905
QY 925 KNRYGNIITAYDHSRVLQVEDDPSDYINANVYIDWLVRGYQRPSPHYIATQGVPHETV 984
Db 906 GSRQPMFAYDRHRVVKLHPMLGDPNADYINANYI-----DGYHRSNHFIIATQGPKEMV 959
QY 985 YDFPWFVQEQSACIVMTNLVEYGRVKYKWPDDTEVYGFQKTCVEMEPLEAVYVVT 1044
Db 960 YDFWRVWQEHGCSIVMTIKLVEYGRVKCSRYWPEDSDTYGDIKMLVKTTETLABYVVT 1019
QY 1045 FTLERRGYNEIREVKQFHTGPDHGVPHATGLLSFTRRVKLSNPPSAGPIVHVCSAGA 1104
Db 1020 FALERGYSARHEVQFHTAPEHGVPHATGLLAFIRRVKASTPPDAGPIVHCSAGT 1079
QY 1105 GRTGCVIVIDMLDAERGVVDIYNCVKALRSRINMVQTEBEQYIFIHDAILEACLCGE 1164
Db 1080 GRTGCVIVLDMDAECEGVVDIYNCVKTLCSRRVNMITQTEBEQYIFIHDAILEACLCGE 1139
QY 1165 TAIPECFKAAYFDMIRIDSONSSHLKDEFOITLNSVTPRLOAEDCSIACLRNDKRRF 1224
Db 1140 TTIPESEFKATYKEMIRIDPQNSQLREEFQITLNSVTPPLDVEBCSIALPRNDRKRS 1199
QY 1225 MDMLPPDRCLPLIITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYG 1284
Db 1200 MDVLPDRCLPLISTDGSNNYINAAALDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYG 1259
QY 1285 CTSIVMLNEVDLSQG---CPQWPEGMRLRYGP1QVECMSCSMOCDVINRIPRINLTRP 1341
Db 1260 CTSIVMLNQLNQSNAWPCQWPEGRQYQYGLMEVEPMGTAEDLVARVFRVQNISSL 1319
QY 1342 QEGYLMVQOFOYLGNASHREVPGSKESFLKLLOVEKQWEECEEGERTIHCINGGERS 1401
Db 1320 QEGHLLVRRHFQRLRSAYRDTDPDSKAFHLHLAEVDKQW--AESGDGRTIVHCLNGGERS 1377
QY 1402 GMFCAIGIVVEMKRONVVDVFAVKTILNSKPNMVEAPEQYRVCYDVALEYL 1455
Db 1378 GTFCACATVLEMIRCHNLVDVFAAKTLRYKPNVETWDQYHFCYDVALEYL 1431
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RESULT 6
S72441

protein-tyrosine-phosphatase (EC 3.1.3.48) pi - human

N:Alternate names: FMI protein; receptor-like protein tyrosine phosphatase pi
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S72441
R:Crossland, S.; Smith, P.D.; Crompton, M.R.
Biochem. J. 319, 249-254, 1996
A:Title: Molecular cloning and characterization of PTP-psi, a novel receptor-like protein-tyrosine-phosphatase
A:Reference number: S72441; MUID:97024447; PMID:8870675
A:Accession: S72441
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1442 <CRO>
A:Cross-references: UNIPROT:Q92735; EMBL:X95712; NID:g166422; PIDN:CAA65016.1; PID:g1616
A:Experimental source: mammary; cell line MCF-7
C:Genetics:
A:Gene: fmi
C:Function:
A:Description: regulates cellular function by dephosphorylating phosphotyrosine residues
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat-tyrosine-phosphatase homology
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:29-188/Domain: NAM homology <NAM>
F:288-366/Domain: fibronectin type III repeat homology <3FR>
F:910-1130/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 55.8%; Score 4359; DB 2; Length 1442;
Best Local Similarity 58.0%; Pred. No. 2.8e-285;
Matches 845; Conservative 196; Mismatches 333; Indels 82; Gaps 21;

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QY 34 GCTDDGPG---ACDYHQDLYDDEFWVHVSQAQEPHYLPPEMPQGSYMVVDSSNHDPGSKA 90
Db 33 GCTFEESDPAVPCYEQSQAYDDFQWDPGS-----PADLPHGSLYLMVNTSQHAPGQRA 85
QY 91 RLQPLTKKENDTCHIDPSYLLYSQKGLNPGTLNLTILVRVKNKPLANPIWNTVGTGRDWLR 150
Db 86 HVI FQSLSENTHCVQFSYFLYSRDSHPGLTGVYVRVNGGPGLSAVNMWMTSGHGRQWHQ 145
QY 151 AELAVSTFWPNEYOVIFEAESVGGSGSVIATDDTQVLSYPCDKSPHFRLRLGDVEVNAGQN 210
Db 146 AELAVSTFWPNEYQVLFALISLPPRRGVMGDDICILSYCAKAFHFRSLRGDVEVNAGQN 205
QY 211 ATFCIATGRDAVHNKMLQRRNGEDIPVAOTKKNINHRFAASFLQELQVTKTDQDLYRCV 270
Db 206 ASFQCMAGR-AEAEFLQRCQSGALVPAAGVRHISHESFLATPPLAAVSAEQDLYRCV 264
QY 271 TQSRGSGVS-NPAQLIVREPPRIAPPQLLGVGPTYLLIQLNANSIIDGPIILKEVEY 329
Db 265 SQAPRGRTSLNFAEFMVVKEPPTPIAPPQLLRAGPTYLLIQLNTNSIIGDGPVIRKBEY 324
QY 330 RMTSGSTETHAVNAPTYKWLHLDPTDEYETRLVLTTRPGEGTGUPGPPLITRTKCAEPM 389
Db 325 RMAGPMAEVHVAVALQTYKWLHLDPTDEYETRLVLTTRPGEGTGUPGPPLISRTKCAEPM 384
QY 390 RTPKTLKIAETQARRIAVDWESLGYNITRCHTFNVITCYHYPRG--HN-----ESRAD 440
Db 385 RAPGLAPAEIQAQRLTIQWEPLGVNVTCHTYTVSLCYHYTGLGSHNQTIIPRVCEDRAR 444
QY 441 CLDMDPKAPQHVNVHLPPYTNVSLKMLITNPEGRKESEETIIQTDDEVPQVPVKSLQGT 500
Db 445 CQPLHHEBPAAL-----SERSREVLTNPEGRKEGKVTFTQDDEVPQVIAAESLFT 497
QY 501 SFENKI FLNWKPELEPGLIITQYEVSYSSIRSPDPVAVPAGPQTQVSNLWNSTHHVFMHL 560
Db 498 FLEMIFLWKBEPOENGLIITQYELISYQSISSDPVAVNVA--TSTISKLRNETYHVFSNL 556
QY 561 HPGTTYQFFIRASTVKGCPATAINVTNINISAPSLPDYEGVDASLNETAATITVLLRPAQ 620
Db 557 HPGTTYLFSVGARTCKGFGQAALTEITTYISAPSL-DYADMPSPLGESSENTITVLLRPAQ 615
QY 621 AKGAPISAYQIVVEQLH--PHRTKREAGAMECVQVPTVYNALSGGAPYVEAAELPPGNL 679
Db 616 GRGAPISYQIVVEEEOGSRRLRREPRGGQDCFPVLTTEAALARGLVHYFGAELAAASLP 675
```

Qy	680	EPAPFTVGDNRTYKGFWNPPPLAPRKGYNIYFOAMSSVEKETKTQCVRIATKAAATBPVEV	7339
Db	676	EAMPFTVGDNRTYRGFNPPLEPRKAVLIYFOAAASHLKGETRLNCIRIARKAACKESKRP	735
Qy	740	IPDPAKOTDRVVKTAGISA-CILYFIILLVIVIVVKS-----LAKRKD	785
Db	736	L-EVSGSEEMGLIGICAGGLAVLILGLGAILVIIRKGRDHYAYSYPKVPNMWK-----	790
Qy	786	AMGNTRQEMTHVMAMDRSADQSTLHAEDPLSLTFMDQHNFSRPLENDPLVPTAVLDEN	845
Db	791	ATVNVREQETHMMSAVDRSFTDQSTL---QPPLSFMDTHGYSTR-----GEQ	835
Qy	846	HS--ATAESSLLDVPRLCEGTESPQTGOLHFAIRVADILLOHINLMKTSDSGPKEEY	903
Db	836	RSGGVTRASSLUGSPRRPCGRKSGPYHTVQLHFAVRVADILLOHINQMKTAEYGFGKQEY	895
Qy	904	ESFFEGOSASMDVAKQDNRAKRYGNIAYDHRSVILQPVEDDPSSDIYANVIDIWLY	963
Db	896	ESFFEG---WDATKKXKVKGSQEPMPADVHRVKVLHPLMGPNADYINANVY-----	946
Qy	964	RDGYORPESHYIATQGPVHETVYDFWRVMWQBSQACIYVMVNLVVEGRVKCYKYPDDTVE	1023
Db	947	DGYHRSNHFATQGPKEPMYDFWRVMWQBSQSIYMITKLVEVAGCKSRYPEDSDT	1005
Qy	1024	YGDFFKVTCEMEPIAEYVVRFTFLERRGYNEIREVKQFHFTGWDHGVPHYHATGLLSFR	1083
Db	1006	YGDIFKIMLVKTETLAEYVVRFTFLERRGYSARYEVRFHFWPEHGVPHYHTTGLLAPFR	1065
Qy	1084	RVKLSNPPSAGPIVHVHCSAGAGRTGCYIVIDIMLDMAREGVDIYNCVKALRSRRINMV	1143
Db	1066	RVKASTPPDAGPIVHCSAGTGRGTCYIVLDVMDMAECEGVVDIYNCVKTLCSRCVNI	1125
Qy	1144	QTEQYQYFIHDAIIEACLGBETAI PVCEFFKAAYPDMIRISQTSNSHLKQBFQTLNSVTP	1203
Db	1126	QTEQYQYFIHDAIIEACLGBETTIPVSEFKATYKEMIRIDPQSNSSQLRBEFQTLNSVTP	1185
Qy	1204	RLQAECDSCIACLPRNHKNRPMDMPLPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFI	1263
Db	1186	PLDVEEYSIALLPNRDKNSMDVLPDRCLPFLISTDGSNNYINAAALTDSYTRSAAFI	1245
Qy	1264	VTQYPLNTVKDFWRLVYDYGCTSIYVMLNEVDLSQG---CPQYWPBEGMLRYGPIQVECM	1320
Db	1246	VTLHPLQSTTPDFWRLVYDYGCTSIYVMLNLNQSNASWPCLYQWPBEGRQYGLMEVEFM	1305
Qy	1321	SCSMDCDVINRIIFRICMLTRPOEGYLMVQOBYLQWASHREVPQSKSFLKLILOVEKWQ	1380
Db	1306	SGTADEDLVARVFRVQNISRLQEGHLLVRRHFQFLRWGSAYRDTDPSEKAFHLHLAEVDKWQ	1365
Qy	1381	EECEBEGGRITIHCLNGGGRSGMFCATGIVVEMVKRQNVVDVHFHVAKTLRNSKPNMVEAP	1440
Db	1366	--AESGDGRTIVHCLNGGGRGRTSCARTVLEMRCHNLVDVSPFAKTLRNYKPNMVEYTM	1423
Qy	1441	EQYRFCYDVALEYLES	1456
Db	1424	DOYHFCYDVALEYLEA	1439

RESULT 7
I58148
protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58148; S46218
R:Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
Neuron 11, 387-400, 1993
A:Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
A:Reference number: I58148; MUID:93357030; PMID:8352946
A:Accession: I58148
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1501 <NAL>
A:Cross-references: UNIPROT:Q64605; GB:L199333; NID:q310242; PIDN:AAA42309.1; PID:q310243

A;Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus norvegicus.
B;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
C;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase from rat liver.
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Accession: S46218
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-1501 <ZHA>
A;Cross-references: EMBL:L12329; NID:G294573; PIDN:AAC37657.1; PID:G294574
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; cyg
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosinase
F;47-109/Domain: immunoglobulin homology <IMM1>
F;149-209/Domain: immunoglobulin homology <IMM2>
F;246-300/Domain: immunoglobulin homology <IMM3>
F;413-506/Domain: fibronectin type III repeat homology <3PR>
F;862-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1358-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status Predicted
F;1148/Binding site: substrate phosphate (Arg) #link PTP1 #status Predicted
F;1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status Predicted
F;1439/Binding site: substrate phosphate (Arg) #link PTP2 #status Predicted

Query Match	Score	DB 1	DB 2	Length
Best Local Similarity	19.4%	1516.5	1501	
Matches 420	29.8%	Pred. No. 1.6e-93		
Conservative	205	Mismatches	471	
Indels	315	Gaps	46	

Qy	204	EVNAGQATFOCIATGRDAVHNKLWRNG-----EDIPVACTKNINHRRFAASFRLOBV	259
Db	242	EIMPGNNVITCVAVGSPMPYVK-WMOGAEDLTPEDDMPVG--RVV-----LELT	288
Qy	260	TKTDQDLYRCVTQSERGSGVSNFAQLIUREPBPRIAPPOLLGVGPTYLLIQLNANSIIGD	319
Db	289	DVKDSANYTCVAMSSLGV-IEAVAQITVKSJUPKAPGTPVTVENTATSIITVWDSGN---P	344
Qy	320	GPIILKEVEYRMTS--GSWTETHAVNAPTYKLMHLDPOTEYIEIRVLLTRPGEGGTGLPGF	377
Db	345	DPVSYYVIEYKSKSDQGPYQIKEDITTRYSIGGLSPNSEYEIYW--SAVNSIGQGPPE	402
Qy	378	PLITRTKCAEBMRPTKLTABEIOARRIADVWES-----LGNITRCHTFNTVICYH	429
Db	403	SVVTRTEQAPASAPRNVQARMLSATMIQVMBEPVEPNGLIRGV-------449	
Qy	430	YFRGHNESADCLDMDPKAPOHVNVNHLPPYTNVSLKMLITNPGRKESSEETIIQT---	484
Db	450	YY-----TMEPEHPGVNQKH-NVD-DSLTTVVGSLLEDETYTVRVLAFTS	493
Qy	485	--DEBVPGPVPVKSLOG-----TSPENKIFLNWKSPLEPNGIITOVEVSYSS--	529
Db	494	VGDGPLSDPIQVKTQOGVPGQPMNLRAEAKSETSIGLSWSAPROBS--VIKYEFLFREGD	551
Qy	530	-----ISEPAPVAVGPPQTVSNLWNSTHHVFMHLHGTTYQCFIRASTVKVGFQGPATAI	584
Db	552	RGREVGRTFPD-----TTAFVDEDLKENTBYAFKLAARSPOGLGAFTAV	595
Qy	585	NVTNISAPS-----LPD-----YEGVDASLN-ETATTIT	613
Db	596	VCORTLQAISPKNFVKVMIMKTSVLLSWEPFDNYSPTPYKIYNGLTLDVDRGTTKKLI	655
Qy	614	VLLRP-----AQAKGAPISAYQIVVEQLHPHTKREA-----GAME	649
Db	656	THLKPHTFYNFLNRGSSLGGLQOTV-----TARTAFNMLSGKSPVAPKPDNDGSIV	708
Qy	650	CY-----QVPVTVQNALSGGAPYFAAELP-----PGNLP-----	679
Db	709	VYLPDQSPVTQN-----YFVVMVPLRKSQGGQFPILLGSPEDMDLBELIQDLSRL	760
Qy	680	-----EPAPFTVGDNRITYKGFVWNPPLAPRKGNVNYFOAMSS	715
Db	761	QRSLRHSROLEVRPPYIAARFSLPVAFFHPGNOKQYGGFNNRGLPEGHRYVFLVAV---	818


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QY 749 RVKIAGISAGILVFIILLLVV-VIVKSKLAKKRGKDMGNTROETHMVMNMDRSYAD 807
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
847 GEEGLIWIGVSLVLAFTICVIAILLYKNKPKSKRDS-----885
QY 808 QSTLHAEDPLSLTMDQHPSPNDPLVPTAVLDENHSATASSRLLDVPRVLCBGT 867
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
886 -----EPRTKLLNNAETPHHPKDPV-----ENRRI-----912
QY 868 SPYOT-GOL-HPAIRVADLLQHLNMTKTSYSGKEEYESFEQGSASWDVAKKQDNRAK 925
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
913 -NFQTPGMLSHPPVPSLAETHLKANDNLKLSQEVESIDPQQPTWEHNSLVNPKP 971
QY 926 NRYGNITAYDHSRVLQVEDDPSDYINAYIIDWLYRDGYQRPSHYATQGPVHETVY 985
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
972 NRYANVAYDHSRVLPIEGIVGSDYINAYI-----DGYRKQNAVYATQGPLPETFG 1025
QY 986 DFRWVWQESQACVMTNLNVEGRVKCYKMPD-DTEVYGDVFKVTCVEMEPLAEVVRT 1044
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1026 DFRWVWQESRATVMMTKLEKSRKICQDQWPGRGDITYGMIQVLLDTIELATFCVRT 1085
QY 1045 FTLERRGYNEIREVKQHFHTGWDPHGVPHYATGLLSFRRVKLGNSPPSAGPIVVCSCAGA 1104
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1086 FSLHKGSSSEKREVRQFTAMPDGHVPEYPTPLAFRLRRVKTCPNPDAGPIVVCSSAGV 1145
QY 1105 GRTGCVIVIDMLMAEREGVVDIYNCVKALRSRRINNVQTEQYIFIHDAILEACLCGE 1164
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1146 GRTGCFIVIDAMLERIKHEKTVDIYGHVTLMRSQRNVQTEQDQYSFIHDALLEAVACGN 1205
QY 1165 TAIPVCEFAAYPMIRIDSTNSHLKDEPOTLNSVTPRLQAECDSCIAPRHNDKQRF 1224
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1206 TEVPARNLYTYIQKLAQIEGVEHVTGMELEFKRL--ANSKAHTSRFTSANLPCNKKFNRL 1263
QY 1225 MDMLPPDRCLPFLITIDG-BSSNVYNAALMDSYRQPAAFIVTQVPLNTVKDFWRLVVDY 1283
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1264 VNIMPYETTRVCLQPIRGVEGSDYINASFIDYQKAYATATQGLAETTFDFWRLWEN 1323
QY 1284 GCTSIVMLNEVDL--SQGCPQYWEPEGLRYGPIQVECMSCMDCVINRIFRNICLTRP 1341
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1324 NSTIVMLTKLREMGKCHQYPAERSARYQYFVVDPMVA--EYNNPQVILREFKVTDA 1380
QY 1342 QEGY-LMVQFOYLGWASHREVPGSKSFLKLILQVEKWQECBEGGRITIIHCLNGGR 1400
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1381 RDGQSRVTRQFQFDW-PQGVKPSGEGFDIFQGVHKTKEFQD-DGPISVHCSSAGVR 1438
QY 1401 SGNFCAIGIVEMVKRQNVVDVHAVKTLRNSKNMVEAPEQYRCYDVALEYLES 1456
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1439 TGVFITLSIVLERMYEGVVDIFQTVKMLR-TQPMVQTEDEYQFCYQAALEYLGS 1493

RESULT 9
S46216
leukocyte antigen-related protein precursor - rat
N;Alternate names: leukocyte common antigen homolog
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S46216; S23252; A41032; A33154
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Accession: S46216
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1898 <ZHA>
R;Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
Biochem. J. 284, 569-576, 1992
A;Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three
A;Reference number: S23252; MUID:92287069; PMID:1599438
A;Accession: S23252
A;Status: nucleic acid sequence not shown
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A;Molecule type: mRNA
A;Residues: 1361-1604;1649-1898 <HAS>
R;Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
J. Biol. Chem. 266, 19688-19696, 1991
A;Title: Cloning bacterial expression, purification, and characterization of the cytoplasmic
A;Reference number: A41032; MUID:92011772; PMID:1918076
A;Accession: A41032
A;Molecule type: mRNA
A;Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
A;Cross-references: GB:M60103; NID:G205130; PID:AAA41510.1; PID:G205131
R;Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
submitted to the Protein Sequence Database, December 1990
A;Reference number: A33154
A;Accession: A33154
A;Molecule type: mRNA
A;Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>
C;Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
cgy
C;Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; t
F;1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>
F;28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT>
F;28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>
F;47-109/Domain: immunoglobulin homology <IMM1>
F;149-209/Domain: immunoglobulin homology <IMM2>
F;246-300/Domain: immunoglobulin homology <IMM3>
F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-593/Domain: fibronectin type III repeat homology <FN3C>
F;606-695/Domain: fibronectin type III repeat homology <FN3D>
F;708-799/Domain: fibronectin type III repeat homology <FN3E>
F;811-895/Domain: fibronectin type III repeat homology <FN3F>
F;906-990/Domain: fibronectin type III repeat homology <FN3G>
F;1002-1079/Domain: fibronectin type III repeat homology <FN3H>
F;1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TMM>
F;1276-1898/Domain: intracellular #status predicted <INT>
F;1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;54-107,156-207,253-298/Disulfide bonds: #status predicted
F;117,250,295,721,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1539/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1545/Binding site: substrate phosphate (Arg) #status predicted
F;1830/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1836/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.1%; Score 1494; DB 2; Length 1898;
Best Local Similarity 28.2%; Pred. No. 7.6e-92;
Matches 462; Conservative 214; Mismatches 534; Indels 426; Gaps 56;

QY 68 PPEMPOG-----SYMVVDSSNHDPGEKARLQLPTMKENDTHC-----IDFS- 108
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
436 PPEPGLVGRVRYVTPDS-----RRPLSAMHKGNTDAGLLTTVGSLLPGIYSL 486
QY 109 -YLLYSOKGLNPGTLNILVRNKGPLANPIVNTVGTGROWLRAELAVSTFW---PNE-- 162
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
487 RVLAFTAVGDPSPPIQVKTQGVPAQP---ADFOAK--AESDTIQLSWLLPPQERI 540
QY 163 --YQVIFEARVSGRSGYIAIDIQVLSYPC-DKSP-----HFLRLGVDFVWAG-----Q 209
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
541 IKYELVWAAEDRGQHKVTFDPTS--SYTLEDKPDLYHFQLAARSDLGVGVTPTVE 598
QY 210 NATFO-----CIATGRDAVNKLWL-----QRRN-----GEDIPVA 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
599 ACTAQSTPSAPPKVTCTVSTGTTVRVS-WVPPPSAPSRNGIITQYSVAVSVDGEDRKRH 657
QY 241 QTKNINHRFAASFRLEQVTKTDQDLYRCVTCQSGRSGVSNFAQLIVREPPRPIAPQLL 300
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
658 VVDGIS--REHSDWLLGLEKTEYRVWVRAHTDVGGPSSPVLVTRTDEVDVSGPFRKV 715
QY 301 GVGP-----TYLLI---QLNANSIIGDGPITILKEVEYR 330
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
716 EVEPLNSTAVHVSWKLVPVKNQGRQIRGYQTVVRLENGPRGQPIQD--VMLAEAQET 773
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QY 331 MTSGSWTETHAVNAPTYKWLHLDPTTEYIEIRV-LLTRPGEGETGLPGPLIRTKCAEPM 389
Db 774 TISG-----LTPETYSITVAAYTTKGDG-----SKPKVVTITGAVPG 813
QY 390 RTPKTKLIAEIOARRIAVDW-----ESLGYNITRCHTFENVITCYHYFPGHESRADC 441
Db 814 R--PTMVSTTAMHTALLQWHPKLPGLGELGYRL-----QYRADEARNT 858
QY 442 LMDPKAPQHVNVHLPPTVNVSLKMLNPNPKRKESEETIIQTDEDPGVPV-----VKSL 497
Db 859 IDFGKDDQHTVTVGLHGKATVIFRLAAKNRAGPGSEFEKEITTPEDAPSGFPQNLRTVGL 918
QY 498 QGTSPENKIFLNWKEPL--EPNGIITQVEYSYSSIRSPDPAVPVAGPQTQVSNLWNSTHH 555
Db 919 TTSTTE-----LAWDPFVLAERNGRITNTVTVYRDINS-----QHELQNVTDGVHL 964
QY 556 VFMLHPGTGYOFFTRASTVKGFGP-----ATAINVTTNISAPS 594
Db 965 TLLGLKPDITTDIKVRAHTSKAGPLSPSIQSRTPMEQVFAKPRVAAAMKTSVLLSWE 1024
QY 595 LPD-----YEGVDASLN-----ETATTITVLLRPAQAKG-----623
Db 1025 VPDYSKSAVPFKILYNGQSEVGDGHSRMRKLIADLPNTSEYFVLNMRGTSAGGLQHLVSI 1084
QY 624 -----APISA-----YQIVV-----633
Db 1085 RTAPDLLPKQLPASAFIEDGRFSLSPQVOPSLVRWFYIVVPIIDRVGNNLAPRWST 1144
QY 634 -EQLH-----PHRTKEAGAMECYQVPVTVQNALSGGAPYFAAELPPGNL 678
Db 1145 PEELELLELEAIEGEBEKQRRRRQAERLK-----PYVAAQV--DEL 1185
QY 679 PEPAPFTVGDNRITYKGFNPPPLAPRKNYIYFQAMSSVEKETK-----TQCVRATK 730
Db 1186 PE--TFTLGDKNYRGFYNRPLSPDLSYQCFVLASLKEPMDQKRYASSPYSDIIVVQVTP 1243
QY 731 AAATEPEVIDPAKQTRVRVKIAGISAGILVFILLLLVIVVVKSLAKRKRDMGMT 790
Db 1244 AQQQEPEML-----WVTGFLAVILILIVIAI-----LLFKK-----1278
QY 791 RQEMTHVMNAMDR---SYAQDQLTHAEDPLSLTFMDQHNFSRPLPNDPLVPTAVLDENHS 847
Db 1279 ---RTHSPSSKDEQSIGLKDSLLAHSDDPVEMRNL-----1311
QY 848 ATAESSRLLDVPRYLCEGTESPYQTQL--HPAIRVADLLOHINLMKTSDSYGFKEEYES 905
Db 1312 -----YQTPGMRDHPPIPIITDLADNIELRKANDGLKFSQEYES 1349
QY 906 FPEGQASWDVAKQDONRAKNRYGNIAYDHSRVILQPVEDDDPSDDYINANYIDILWYRD 965
Db 1350 IDPGQOFTWENSNSVNFKNRYANVIAVDHSRVLLTSIDGVPGSDYINANYI-----D 1403
QY 966 GYORPSHVIATQGPVHETVDFWRMVWQEOSACIWMVNLVEGRVKCYKWP--DDTEVY 1024
Db 1404 GYRKQNAVIATQGPIDETMGDFWRMVWQRIATVVMTRLEKSRVKCDQWPARGTETY 1463
QY 1025 GDFKVTCEVMEPLABYVVRITFLRRGYNEIREVKQFHFTGPDHGVPHYATGLLSPIRR 1084
Db 1464 GLIQVTLVDVTVELATYTMRTFALHKSQSGSEKELAQFQFMAWPDHGVPEYPTPIILAFLR 1523
QY 1085 VKLSNPPSAGPIVWCHSAGAGTGCYIVIDIMLMAEREGVVDIYVNCVKALRSRRINMVQ 1144
Db 1524 VKACNPLDAGPMVWCHSAGVGTGCFIVIDAMLERMKHEKTVDIYGHVTCRMSQRNVMVQ 1583
QY 1145 TEEQYIFTHDALEACLCGETAI PVCEFKAAFYDMIRIDISQTSNSHLKDEFOTLNSVTPR 1204
Db 1584 TEDQVTFHEALEALEAMCHTEBVLARNLYAHTQKLGQVPPGESVTAMELEFKLL--AGSK 1641
QY 1205 LOAEDCSIACLRNDKRNFMDDPPDRCLPLFITIDG--ESSNYINAAALMDSYRQPAAFI 1263
Db 1642 ARASRFISANLPCNKFKNRLNVMIPVELTRVCLQIRGVGEGSDYINASFLDGYRQOKAVI 1701

QY 1264 VTQYPLNTVKDFWRLVYDYDCTSIIVMLNEVDL--SQSCPOYWPBEGMLRYGPIQVECMS 1321
Db 1702 ATQGLPAASTEDFWRLMWEHNSTIIIVMLTKUREMGREKCHOYWPAERSARIQYFVVDPM 1761
QY 1322 CSMDCDVINRIFCNILNTRPOEGY-LMVQOQYQYLWASHREVPGSKRSLKLIQLVEKWK 1380
Db 1762 --EYNNPQYILREFKVTDAARDGOSRTIROQFTDM-PEQGVPKTGEFIDFIGQVHKTK 1817
QY 1381 BECEGEGERTIIHCLNGGSGRSMFCAGIIVVEMVKRQNVVDVFAVKTILRNSKPNVPEAP 1440
Db 1818 EQFGQ-DGPIIVHCSAGVGRGVFTILSVILRMRVYEGVDMFQTVKTLRTQRPANVQTE 1876
QY 1441 EYRRCFYDVVALEYLES 1456
Db 1877 DQYQLCYRAALEYLG 1892
RESULT 10
TDHULK
leukocyte antigen-related protein precursor - human
N:Alternate names: leukocyte common antigen homolog
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S03841; J00051
R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 168, 1523-1530, 1988
A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ho
A:Reference number: J00051; MUID:89035978; PMID:2972792
A:Accession: S03841
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1897 <STR>
A:Cross-references: UNIPROT:P10586; EMBL:Y00815; NID:g34266; PIDN:CAA68754.1; PID:g34267
C:Genetics:
A:Gene: GDB:PTPRF; LAR
A:Cross-references: GDB:120138; OMIM:179590
A:Map position: lp34-lp34
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
og
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
P:1-16/Domain: signal sequence #status predicted <SIG>
P:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>
P:17-1250/Domain: extracellular #status predicted <EXT>
P:37-99/Domain: immunoglobulin homology <IMM1>
P:139-199/Domain: immunoglobulin homology <IMM2>
P:236-230/Domain: immunoglobulin homology <IMM3>
P:308-330/Domain: fibronectin type III repeat homology <FN3A>
P:403-489/Domain: fibronectin type III repeat homology <FN3B>
P:501-583/Domain: fibronectin type III repeat homology <FN3C>
P:596-685/Domain: fibronectin type III repeat homology <FN3D>
P:698-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>
P:810-893/Domain: fibronectin type III repeat homology <FN3F>
P:905-989/Domain: fibronectin type III repeat homology <FN3G>
P:1001-1078/Domain: fibronectin type III repeat homology <FN3H>
P:1251-1274/Domain: transmembrane #status predicted <TM>
P:1251-1897/Domain: intracellular #status predicted <INT>
P:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
P:1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>
P:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
P:444-97,146-197,243-288/disulfide bonds: #status predicted
P:107,240,285,711,956/Binding site: carbohydrate (Asn) (covalent) #status predicted
P:1538/Active site: Cys (phosphocysteine intermediate) #status predicted
P:1544/Binding site: substrate phosphate (Arg) #status predicted
P:1829/Active site: Cys (phosphocysteine intermediate) #status predicted
P:1835/Binding site: substrate phosphate (Arg) #status predicted
Query Match 19.1%; Score 1492.5; DB 1; Length 1897;
Best Local Similarity 28.9%; Pred. No. 9.6e-92;
Matches 469; Conservative 211; Mismatches 551; Indels 393; Gaps 59;
QY 68 PPMPQ-----SYMVDS-----SHNDPGEKARLQPTMKENDTHCIDFS--YL 110

Db 426 PPEPGLVGRYRVYTPDSRRPPNWKHNTDAG-----LLTVGSLLPQIITYSLVL 479
Qy 111 LYSQGLNPGFLNLRVNVKGPLANPIWNVGTGDRWLRAELAVSTFW-----PNE-----Y 163
Db 480 AFTAVGDPSPPTIQVTKQGVPAQP-----ADFOAE--VESDTRIQLSWLLPPQERIMY 533
Qy 164 QVIFEAEVSGSGSVIAIDDIQVLSYPC-DKSPHFL-----RLG-----DVEVNA 207
Db 534 ELVTWAAEDEDQHKVTFDPTS--SYTLEDLKPOTLYRFQLAARSDMGVGVFTTIEART 591
Qy 208 GQNA-----TFQCIATGRDAVHNKML-----QRRNGEDIPVACTKININRRFAASFLQ 257
Db 592 AQSTPSAPPQKVMCSMGSTTVRVS-WVPPADSRNG-----VITQYSAHEAVDGEDGR 646
Qy 258 EVT-----KTDQDL-----YRCVTQ--SERGSGVSNPAQLIVREPPRPPIAPQLLG 301
Db 647 HVDGIGREHSSWDLVGLKTEYRVVRAHTDVGPGPESPVLVRTDEDVSPGPPKVE 706
Qy 302 VGP-----TYLLIQLNAN-----SIIGDGPILLKEVEYR 330
Db 707 VEPLNSTAVHYKLPVPSKOHGQIRGVQVTVYRLE-NGEPRGLPIIQD--VMLAEAQWR 763
Qy 331 MTSGSWTETHAVNAPTVKLWHLDPDTEYRIV-LLTRPGEGLTGLPGPPLITRTKCAEPM 389
Db 764 PEESEDYET-----TISGLTPEITYSVTVAAAYTKGDGAR--SKPKLVITTVGAVPG 812
Qy 390 RTPKTLXIAEQARRIAVDM-----ESLGYNITRCHTNFNVITICYHYFRGHNESRAD 441
Db 813 R--PTWMTISTAMNTALLQWHPKPELGLGYRLQYRA-----DEARPNT 857
Qy 442 LDMDPKAPQHVNHLPYTNVSLKMLITNPEGKRESEETIOTDEDVGPVP-----VKS 497
Db 858 IDFGKDDQHFVTVGLHKGTTYIFPLAANKRAGLGEFEKEIRTPEDLPSPQPQLHVTGL 917
Qy 498 QGTSFENKIFLNWKEPL--BENGIIITOYEVSYSSIRSFDPAPVPAGPQTVSNLWNSTH 555
Db 918 TTSTTE-----LANDPPVLAENGRIISYTVVFRDINS-----QOELQNTTDTFR 963
Qy 556 VFMLHPGTYQFFIRASTVKFGP-----ATAINVTNIGAPS 594
Db 964 TLTLGLKDDTYDIKVRATWSKSGPLSPISQSRTPVEQVFAKNFRVAAAKTSLVLSWE 1023
Qy 595 LPD-----YEGVDASLN-----ETATTIVLLRPAQAKG-----623
Db 1024 VPDSYKSAVPFKILYNGQSVEDGHSRKLADIQNPTEYSFVLNMRSGSAGGLQHLVSI 1083
Qy 624 -----APISAY-----OIVVEQLHPHRTKEAGAM-- 648
Db 1084 RTAPDLLPHKPLPASAVIEDGRFPLSMHVQDPSLVRFWFIYVVPV-----DRVGSMLT 1138
Qy 649 -----ECYQVPVITYQNALSGGAPY-----YFAAELPPGNLPEPAPPTVGDNR 690
Db 1139 PRWSTPELELDELLEALEOGGEBQRRRRQAERLKPVAQLDVL--LPE--FTFLGDKX 1194
Qy 691 TYKGFNPPPLAPRGYNIYFOAMSSVKEKY-----TQCVRATKAAATEBEPEVPD 742
Db 1195 NYRGFYNRPLSPDLSYQCFVLASLKEPMDQKRYASSPYSDEIVVQVTPAQOQEBEPL-- 1252
Qy 743 PAKQTDVVKIAGISAGILVFILLVIVIVKSKLAKRKDKAMGNTRQEMTHVNMAD 802
Db 1253 -----WVGVPVAVILLIIVIAI-----LLFKRK-----RTHSPSSKD 1286
Qy 803 R---SYAQDQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPTAVLDENHSATAESSRLDVP 859
Db 1287 EQSIGLKSLLAHSSDPVEMRLN-----1310
Qy 860 RYLCEGTESYQTQL--HPAIRVADLLQHINLMKTSYGFKEEYESFFEGOSASWDVA 917
Db 1311 -----YQTPGMRDHPPIPTDLADNLERLKANDGLKFSQYESIDPGQOFTWENS 1360
Qy 918 KQDNRAKNYGNIIAYDSRVLQPVEDDPSDDYINANVIDIWLRYDGRQORSHYIATQ 977
Db 1361 NLEVNFKNRYANVIAYDHSRVLITSDIGVPGSDYINANYI-----DGYRKONAYIATQ 1414

Qy 978 GPVHETVYDFRMVWVWQESACIVMVTNLVEGRVKCYKYP-DDTEVYDGFKVCVEMEP 1036
Db 1415 GLPETMGDFRMVWMEQRTATVVMTRLEEKSRVKCQYWPARGTETCGLIQVLLDIVE 1474
Qy 1037 LAEYVVTFTLERGYNEIREVKQFHETGHPDHGVPYHATGLLSFIRVKLSNPSAGPI 1096
Db 1475 LATYVTRFALHKSSEKRELQFQFMAMPDGHGVPYPTPILAFLLRRVKACNPLDAGPM 1534
Qy 1097 VVHCSAGRTGTCYIVIDIMDMAEREGVVDIYVNCVKALASRRINMVQTEQYIFIHDAI 1156
Db 1535 VVHCSAGRTGTCFVIDAMLERMKHEKTVDIYGHVTCMRSORNYMVQTEQYVFIHEAL 1594
Qy 1157 LEACLCBETAIPVCEFAKAYFDMIRIDSQNSSHLKDDEFQTLNSVTRPRLQABDCSACL 1216
Db 1595 LEAATCGHTVPARNLYAHIQKLGQVPPGESVTAAMELEFKLLAS--SKAHTSRFISANLP 1652
Qy 1217 RNDHKNRPMDLDPDRCLPELITIDG--ESSNYINAAALMDSYROPAAFTVQYPLNPTVKD 1275
Db 1653 CNFKNRLVNMIPVELTRVCLQPIRGVSGSDYNASFLDGYRQOKAYIATQGLAEATED 1712
Qy 1276 FRLVLDYDGTSTVMLNEVDL--SOGCPQYWPEEGMLRYGPIQVECMSCSMDCDVINRIF 1333
Db 1713 FWRMLMEHNSIIVMLTKREMGEKCHQYWPASRSARYQYFVVDPA--EYNNPOYIL 1769
Qy 1334 RICNLTRPOEGY-LMVQOQFQYLGWASHREVPGSKRSFLKILQVEKWQEBCEGEGRIT 1392
Db 1770 REFKVTARDQGSRTIRQFQTDW-PEQGVKTEGEGFIDFQVHKTEQFGQ-DGPITV 1827
Qy 1393 HCLNGGSRGSMFCAIGIVEMVRQNVVDVFAVKTLNRSKPNMVEAPEQYRFCDVALE 1452
Db 1828 HCSAGVGRGVFTTILSIVLERMYEGVVDVFQTVKTLRTQRPAMVQTEQYQLCYRALE 1887
Qy 1453 YLES 1456
Db 1888 YLGS 1891

RESULT 11

A56178

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
N;Alternate names: protein-tyrosine-phosphatase BPTP-2

C;Species: Homo sapiens (man)

C;Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004

C;Accession: A56178; S12052; B44929

R;Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.

J. Biol. Chem. 270, 6722-6728, 1995

A;Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.

A;Reference number: A56178; MUID:95204468; PMID:7896816

A;Accession: A56178

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1912 <PUL>

A;Cross-references: UNIPROT:P23468; GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653

R;Krueger, N.X.; Streuli, M.; Saito, H.

EMBO J. 9, 3241-3252, 1990

A;Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase delta isoforms.

A;Reference number: S12049; MUID:9106018; PMID:2170109

A;Accession: S12052

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 390-1912 <KRU>

A;Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790

A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T. R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yachi, Y.

Cancer Res. 52, 737-740, 1992

A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.

A;Reference number: A44929; MUID:92119637; PMID:1370651

A;Accession: B44929

A;Molecule type: mRNA

A;Residues: 1756-1804, 'C', 1806-1845 <ADA>

A;Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546

A;Experimental source: pre-B cell NALM-6
A;Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBIP:78087)
A;Note: the authors did not report the entire codon for residue 90
C;Genetics:

Query Match	19.0%; Score 1482.5; DB 2; Length 1912;
Best Local Similarity	27.2%; Pred. No. 4.6e-91;
Matches	464; Conservative 222; Mismatches 534; Indels 487; Gaps 57;
Qy	51 YDFEWM-----VHVSAGPHYLP-----BEMPO 73
Db	386 YSDYEFRRVAVNNTGRGPPPEVLTQSEQAPSDRDVQARMLSSTIILVQWKEPEPN 445
Qy	74 GS-----YMWVDSNHPGEEKARLQPTWKEN--DTHCIDFSYLL-----YSOKGLNPGT 121
Db	446 GQIQGRVYVYTMDFQHVNN-----WMKHNVADSQITIGNLVPQKTSYVKVL-----493
Qy	122 LNILVRNKKGLPANIWNVGTGRDMLRAELAVSTFWPNEYQVIFRAEYSGGRSGYIAI 181
Db	494 --AFTSGDGLSSDI-----QVITQTGVG-----517
Qy	182 DDIQVLSYPCD--KSPHFLRLGDVEVNAQONATFOCIATGRDAVHNKMLQRRNGEDIPVA 240
Db	518 ---QPLNFKAPESETSILLSWTTPRSDTIANYSELVY--XGGEH-----GEE-----559
Qy	241 QTKMINHRRFAASFRLOEVBTKTDQDLVRCVQTQSERGSGVSNFAQLIVRE--PPRIAPPOL 299
Db	560 QRIETEP---CTSVYRLOGLKNSLYYFLAARSQGLGAST--AEISARTWQSKESAPQD 615
Qy	300 LGV---GPTYLLIQNANSIIGDGPILK--EVEYRMTSGSWETHAV-----NAPTYKLM 350
Db	616 ISCTSPSSTSLVSWQPPPEVKEQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYVLE 675
Qy	351 HLDPTVEIIRVLTRPEGGTLPGPPLIIRTKCAEPMRTPKTLKAEIQARRIADWE 410
Db	676 QLEKWTEY--RITVTAHTDVGGPESUSVLIRTNEDVPSGPPRKEVEAVNASTSVKVSWR 733
Qy	411 S-----LGVNITRCHTFNVTICVHYPRGN-----435
Db	734 SPVPNKQHQRIGVQV-----HYVRMENGEPKQPMLKDVMADAOQWEPDDTT 781
Qy	436 -----ESRADCLMDPK-----APQHVNHLPPYTNVS 463
Db	782 EHDMIISGLQPEYSYSLTVATYTKGDGARKPKLVSTGTGAVGPKRLVINH-----TQMN 837
Qy	464 LKMILTNPE-----GRK-----ESEFIITQD-----485
Db	838 TALIQWHPPVDTFGPLYRILKFGRKDEMEPLTLTFESEKEDHFTATDIHKGASYVFRLSA 897
Qy	486 -----EDVPGVPVKSLOQTSFENKIFLNWKBPL--EPNGIITQYEVS 526
Db	898 RNKVGFGEMWKEISIPREVPTGFPQNLHSGTSTSVQLSWQPPVLAERNGIITKYTL 957
Qy	527 YSSIRSFDPAPVPVAG---PPQTVSNLMNSTHHVFMHLHPGTTYOFFIRASTVKFGFP---580
Db	958 YRDINI---PLIPMEOLIVPADTMTLTG-----LKPDTTYDVKKVRAHSTKSGPGVSP 1007

RESULT 12
A48758
protein-t-
C;Species

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48758
R;Pan, M.G.; Kim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.
J. Biol. Chem. 268, 19284-19291, 1993
A;Title: Cloning and expression of two structurally distinct receptor-linked protein-tyr
A;Reference number: A48758; MUID:93374907; PMID:836131
A;Accession: A48758
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1496 <PAN>
A;Cross-references: GB:L19180
A;Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as Gl
as Phe
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; trans
F;149-209/Domain: immunoglobulin homology <IMM1>
F;246-300/Domain: immunoglobulin homology <IMM2>
F;318-405/Domain: fibronectin type III repeat homology <FN3A>
F;411-504/Domain: fibronectin type III repeat homology <FN3B>
F;509-599/Domain: fibronectin type III repeat homology <FN3C>
F;600-684/Domain: fibronectin type III repeat homology <FN3H>
F;880-1496/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1256-1477/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1140/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1146/Binding site: substrate phosphate (Arg) #status predicted
F;1429/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1435/Binding site: substrate phosphate (Arg) #status predicted
Query Match 18.98; Score 1475.5; DB 1; Length 1496;
Best Local Similarity 29.54; Pred. No. 9.3e-973; Indels 315; Gaps 46;
Matches 415; Conservative 202; Mismatches 471;
QY 204 EVANQGNATFOCIATGRDAVHNKWLQRRNG----EDIPVAQTQKINHRFAAFLQEV 259
DB 242 EIMPGGNVITCVAGSPMPYVK-WMOGAEDLPEDDMPVG--RNV-----LELT 288
QY 260 TKTDQDLRYCVTOSERGSVNFQAQLIVREPPRIAPQLLQGLVGYPTLLQLNANSIIGD 319
DB 289 DVKDSANPCVAMSSLG-V-IEAVADITVKSIPKAGFPVVTENTATSIITWTDAGNDPV 347
QY 320 GPIILKEVRYMTSGSWTETHAVNAPYKLVHLDPDTEYRIV-LLRPGEGGTGLPGPP 378
DB 348 SYVLSIIKARM--GRIRSKTSTTTTYSIGSLSPNSEYIHWVSNVSIQGA-----PSES 401
QY 379 LITRTKCAEMRPKTLKIAEIOARRIADVWES-----LGVNITRCHTFNVTCYHY 430
DB 402 VVTRGEQAPASAPRNVOARMLGATTMIVQWEPEPENGILRGYV-----Y 448
QY 431 FRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKSEETIIQT-----484
DB 449 Y-----TWPEHPVGNQKH-NVD-DSLLTTVGSILEDTYTVRVLAFTSV 492
QY 485 -DEDVPGVPVKSLQ-----TSPENKIFLNKSPLENGIITQYEVSYSS---529
DB 493 GDGPLSDPIQVKTQQGVGQPMNLRAEAKSETSIGLSWAPROES--VIKYELLFREGDR 550
QY 530 ----IRSFDPVAVPAGPPQTVSNLWNSHTVFMHLPGTTPYQFFIRASTVKGPGPATAIN 585
DB 551 GREVGRTFDP-----TTAFVVEDLKENTSYAFRLAARSPOGIGAFATV 594
QY 586 VTNISAPS-----LPD-----YEGVDASLN-ETATTITV 614
DB 595 RQRTLQAISPKNPKVVKMIMKTSVLLSWFEFDNYSPTPKIQVNGLTLDVDRGTTKLIT 654
QY 615 LLRP-----AQAKGAPISAYQIVVEQLPHRTKREA-----GAMEC 650
DB 655 HLKPHPTFNFVLTNRGSSIGLQTV-----TARTAFNMLSKGSPVAKPDNDGSIV 707
QY 651 Y-----QVPTVYQNALSGAPYYFAELP-----PGNLP-----680
DB 708 YLPDGGSPVTVQN-----YFIVMVPLKSRGGQFPILLPSPEMDLBELIQLSRLQ 759

QY 681 -----PAPFTVGDNRTYKGFNWPPLAPRKGNYIVPQAMSSV 716
DB 760 RRSIRHSRQLVEPRPYIAARFSILPAVHPGNGKQYGGFNDRGLEPGHRYVFLAV--L 817
QY 717 EKETKTQCVRIATKAAATEBEVI--PDPAKQTDVVKIAGISAGILVFIILLVVI-VI 773
DB 818 QKNEPT-----FAAGPFSDFOLDNPDQPIVDGEEGLIWWIGPVLAIVFIICIVTAIL 871
QY 774 VKSKLAKKAKDAMGNTRQEMTHVMAMDRSYAQDSTLHAEDPLSLTFMPOHNSPRLPN 833
DB 872 LYXNKPSKEKDS-----EPRTKLLNADLAPHPK 903
QY 834 DPLVPTAVLDENHSATAESRLLDVPYLCGTESTPYQT-GQL-HPAIRVADLLQHNLM 891
DB 904 DPV-----EMRRI-----NFQTPGMLSHPPITIDMAEHERL 936
QY 892 KTSDSYGFKEEYESPFEGQSASNDVAKQONRAKNRYGNIIAYDHSRVILQVEDDSSD 951
DB 937 KANDSLKLSQEYESIDPGQQTWEHNSLEANKPNRYANVIAYDHSRVILQVEGIMGSD 996
QY 952 YINANTIDILWYRDGYQRPISHYIATQGVHETVYDFWRVWVWQBSACIVMVTNLVEGVR 1011
DB 997 YINANYV-----DGYRRQNAVYATQGPLPETGDFWRVWVWQBSATVMMTRLEESRV 1050
QY 1012 KCVKYPD-DTEVYGFVKVTCVEMPLAEYVVTFTLLRRGYNEIREVKQFHFTGWPDHG 1070
DB 1051 KCDQYWPNRGTETGYFTVLTLLDMELATFCVATFSLHKNSSSEKREVRHFQFTAMPDHG 1110
QY 1071 VPYHATGLLSFIRVKLSNPPSAGPIVHCHSAGAGTCYIVIDIMLDMAREGVVDIYN 1130
DB 1111 VPSYPTPFLAFLRRVKTCPNPPDAGPVVHCHSAGVGTGCFIVIDAMLERIRTEKTVDVYG 1170
QY 1131 CVKALASRRINMVQTEBQYIFIHDAILEACLCCETAIPVCFEKAAYEDMIRISQTSNSH 1190
DB 1171 HVTLMRSQRYMVQTEBQYIFIHDAILEACLCCETAIPVCFEKAAYEDMIRISQTSNSH 1230
QY 1191 LKDFOTLNSVTPRLQAECSIACLPRNHDKNRPMMLPPDRCLPFIITDG-ESSNYIN 1249
DB 1231 MELEFKRL--AAPRHLTRDSFTASLPCNKFKNLNLVILPYESSRVCVLPQIRGVEGSDYIN 1288
QY 1250 AALMDSYRQPAARIVTQYPLPNTVKDFWRLVYDYGCTSIYMLNEVDL--SQGCPQYWPEE 1307
DB 1289 ASPIDGYRQOKAVIATQGLAETTEDFWRALWENNSTIVVMLTKLRMGREKCHQYWPAAE 1348
QY 1308 GMLRYGPIQVCEMSCMDCDVINRIFRICNLTRPOEGLYLVQOFOYLGWASHREVPGSKR 1367
DB 1349 RSARYQYFVVDPA--EYNNPEYILREFKVTARDGQSRTVR-QFTDM-PEQAPKSGE 1403
QY 1368 SFLKLILQVEKMOECEBEGEGRTHIHLNGGGSGMFCAGIVVMVKRQNVVDVFAVK 1427
DB 1404 GFIDFIGVHKTKEQFGQ-DGPISVHCSAGVGRGTGVFTLSIVLERMRVYEGVDFQTVK 1462
QY 1428 TLNSKPNMVEAPEQYRFDVDALE 1452
DB 1463 VLRTQRPAMVQTEDEYQFCQAALE 1487

RESULT 13

S46217

protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
N;Alternate names: leukocyte common antigen-related phosphatase
C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S46217; S51174; A49104

R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phos

A;Reference number: S46216; MUID:94347119; PMID:8068021

A;Accession: S46217

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1863 <ZHA>

A;Cross-references: UNIPROT:Q64605; EMBL:L11587


```

Qy 1437 VEAEQYRFCYDVAALEYLS 1456
Db 1838 VQTEDEYQFCFQALEYLGS 1857

RESULT 14
D54689
Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precursor
N:Alternate names: MTP delta type D
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form A
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: D54689; A54689
R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A:Title: MTP delta, a putative murine homolog of HTP delta, is expressed in specialized
A:Reference number: A54689; MUID:93360986; PMID:8355697
A:Accession: D54689
A:Status: preliminary
A:Molecule type: mRNA
A:Experimental source: brain
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIPI:136537)
A:Accession: A54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-398, 799-1691 <MI2>
A:Experimental source: brain
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBIPI:136524)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogly
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F;42-95/Domain: immunoglobulin homology <IM3>
F;114-196/Domain: fibronectin type III repeat homology <FN3A>
F;1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1449-1671/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1333/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1339/Binding site: substrate phosphate (Arg) #status predicted
F;1623/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1629/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.6%; Score 1452.5; DB 1; Length 1691;
Best Local Similarity 28.7%; Pred. No. 4e-89;
Matches 414; Conservative 205; Mismatches 466; Indels 359; Gaps 42;

Qy 253 SFRLQEVTKDQLYRCVTSQSGVSNPAQIIVREPPRIAPPQLGV---GPTYLLI 309
Db 361 SYRLQGLKPNLSYVFLRSATSPQGLGAST-AEISARTMQKPSAPPDICTSPSSSILV 419
Qy 310 QLNANSIIGDPIILK-EVEYRMTSGSWETHAV-----NAPTYKLWHLDPDTEYRVL 363
Db 420 SWQPPVPEKQNGIITEYSLKYAVDGEDYKPHIEIGNSDITKYLEQLEKWTVEY--RIT 477
Qy 364 LTRPGEGCTGLPGPPLITRTKCAEPMTPTKLIAETQARRIADWES-----LG 413
Db 478 VTAHTDVGPNPESLSVLIRTDDEVPSPKKEVEAVNATAVKVSWRSVPVNKQHQIRG 537
Qy 414 YNITRCHTFNVITCYHYFRGHNS-----RADCLDM----- 444
Db 538 YQV-----HYVKMGEPEKSAMKLKVDLADAQDMILISGLQPEYSYSLTVTAYT 585
Qy 445 -----DPKAPQVNVNHLPPYTNVSLKMLTNPE-----G 473
Db 586 TKGDGARKPKLVSTGTSVFGKPLVINH---TOMNTALIOWHPVDVTFGLQGYRLKEG 641
Qy 474 RK-----ESEETIIQTD-----EDVPGPV 492
Db 642 RKMEPLTTLFSEKEDHFTATDIHKGASVFFLSARNKVGFGEEVMKEISVPEEIP 701
Qy 493 PVKSLQSTSPENKIFLNWKEPL---EPNGIITQYEVSYSSIRSPDPVPPVAG---PPQTIVS 547

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Db	702	PQNLSHSEGTSTSTSVLSQSWQPPVLAERNGVITKTYTLLYRDINV--PULPMHLLVPA DTSM	759
Qy	548	NLANNSTHHVFMHLHPGTYOFFIRASIVKFGGATALNVTTNISAPSLPDYEGVDASL--	605
Db	760	TLTG-----LKSDTYDVKRAHTSKRGSP-----YSPSVQFRTLP-----VDOSMFA	802
Qy	606	-----NETATTITVLLR---PAQAKGAPISAYOI-----VVEQIHLPHRTKR-----EAGAMEC	650
Db	803	KNPHVKAVMKTSVLLSWEI PENYNPAILSKFFMMMDGKMVEEDGRATOKLI VNLKPEKS	862
Qy	651	YQPVPTVQNALSGAPYFAAEI PPG-----NLPE-----	680
Db	863	YSFVLITNRGNSAGGLQHRVTAKTAPDLVLRTPAFIGKTNLDGMITVQLPDVPANENIKGY	922
Qy	681	-----	681
Db	923	YIILVPLKSRGKFIKPWESPDEWELDELKEISRKRIRSYRGREVELKPYIAAHFDVLP	982
Qy	682	APFTVGDNRTYKGFWMPPPLAPRGYNIYFOAMSVEKETKTQCVRITAKAAATEEPEVIP	741
Db	983	TEFTLGDGHYGFNTKQLSGQOEY-VFFVLA VMDHAESK----MYATSPSPDPVVSMDL	1037
Qy	742	DPAKQDTRVVKIAGISAGIL--VFIIILLVIVIVKSKL-AKKRKDAMGNTRQEMTHMV	798
Db	1038	DPQIPITDEEGLIWWGVPVLAUVFIIICIVAILLYKRAESRSKSLPSNKEVPSH--	1095
Qy	799	NAMDRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTAVLDENHSATAESSRLDDV	858
Db	1096	-----HPTDPVELRLN-----	1107
Qy	859	PRYLCEGTSPYQTGOL--HPAIRVADLLQHINLMKTSDSYGFKEEYSEFFEGQSASWDV	916
Db	1108	-----FQTPGWA SHPPILLELADHIERLXANDLNKESQYESIDPQOQTWEH	1156
Qy	917	AKKQDNRAKRYGNIIAYDHSRVILQVEDPSSDYINANYIDIMLYRGYORQPSHYIAT	976
Db	1157	SNLEVNKPKRYANVAYDHSRVLLSAIEGIPGSDYVNANYI-----DGYRKQNIAYIAT	1210
Qy	977	QGPVHETVDFWEMVWQESACIWMVTNIVEVGRVKCYKYWPD-DPEVVGDFKVCVTVEME	1035
Db	1211	QGSLPETFGDFWMIW--EQEATVMMTKLEERSRVKCDQYWPSPRGTFHGLVQVTLDDTV	1269
Qy	1036	PLAYYVVRTPLERRGYNEIREVKQPHFTGWPDHGVPHYATGLLSPIRWKLSNPPSAGP	1095
Db	1270	ELT-YCVRFALYNGSSEKKVKRQOFTANPDHGVPEHPTFLAFLRRVKTCNPPDAGP	1328
Qy	1096	IVVHCSAGAGRTGCTYVIDIMLDMAREGVDIYNCVKALRRRRINMVQTESQYIFIHDA	1155
Db	1329	MVHCSAGVGTGCFIVIDAMLERIKHEKTVDIYGHVTLMAQRNVWQTEQYIFIHDA	1388
Qy	1156	ILEACILGGETAIPVCEFKAAYPDMIRIDSQTSSHLKDFQFNLNSTVPRLOAEDCSIACL	1215
Db	1389	LLEAVTCGNTEVPARNLYAIQKLTQIETGENVTGMELEFKRLAS--SKAHTSRFTISANL	1446
Qy	1216	PRNHDKNRFMDLPPDRCLPFLITIDG-BSSYNVINAALMDSYRQPAFTVTOYPLPNTVK	1274
Db	1447	PCNKFNRLVNIIMPESGRVCLQPIRGVSGDYINASFUDGVRQKXAYIATQGLPAETTE	1506
Qy	1275	DFWRLVVDYGCTSI VMLNEVDL--SGQCQYWPMEGLMRYGPIQVECMSCSDCDVINRI	1332
Db	1507	DFWRMLWEHNSTIVVMLTKLREMGREKCHQYPAERSARYQYFVVDPMW--EYNNPQYI	1563
Qy	1333	FRICNLTRQEBGYLMVQOQYQYLGWASHREVPQSKRSFLKLIQVEKNQWCECEGEGRITII	1392
Db	1564	LREPKVTDARDOSRTVRQFQTDW-PEQGVPKSGEGFIDFIGVHKHTKEQFOG-DGPISV	1621
Qy	1393	HCLNGGGRSMFCAIGIVVEMVKRONVDVFEHAVKTLRNSKNMVEAPEQYRQYFCYDVALE	1452
Db	1622	HCSAGVGRGVFTLISILERMRYEGVMDIFQTVKMLRTQRPAWQTEQYQFCYTRAALE	1681
Qy	1453	YLES	1456

Db 1682 YLGS 1685

RESULT 15

CS4689

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor

N:Alternate names: MPTP delta type B/C

N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C

C:Species: Mus musculus (house mouse)

C:Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004

C:Accession: CS4689; B54689

R:MiZuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.

Mol. Cell. Biol. 13, 5513-5523, 1993

A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized

A:Reference number: A54689; MUID:93360986; PMID:8355697

A:Accession: CS4689

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1894 <MIZ>

A:Cross-references: UNIPROT:Q64487

A:Experimental source: brain; splice form B

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:137487)

A:Accession: B54689

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-352,'H',354-535,'S',537-601,1002-1894 <MIZ>

A:Experimental source: brain; splice form C

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBI:136530)

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ocy

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F:45-107/Domain: immunoglobulin homology <IMM1>

F:245-299/Domain: immunoglobulin homology <IMM2>

F:317-399/Domain: fibronectin type III repeat homology <FN3A>

F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1542/Binding site: substrate phosphate (Arg) #status predicted

F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.6%; Score 1452.5; DB 2; Length 1894;

Best Local Similarity 28.7%; Pred. No. 4.8e-89;

Matches 414; Conservative 205; Mismatches 466; Indels 359; Gaps 42;

Qy 253 SPRLQEVTKDQDLVRCVTSQSRGSGVNFQAOLIVREPPRTAPQLLGV---GPTYLLI 309

Db 564 STRLOGLPNSLYYFRLSATSPQGLGAST-ABISARTWQKSPAPQDISCSPSSTSLIV 622

Qy 310 QLNANSIIGDGPILIK-EVEYRMTSGSWTETHAV-----NAPTYKLMHLPDPTYEIRVL 363

Db 623 SQWPPPEVKQNGIITEYSLKYAAVDGEDYKPEHIGNSSDITTKYLLEQLEKWEY--RIT 680

Qy 364 LTRPQGGTGLPGLPIITTKCAEPWPTKTKIAIOARRIANDWES-----LG 413

Db 681 VTAHTDVGFWPESLSVLINTDVPSPKVEVEAVNATAVKVSWRSVPVNKHQGIIRG 740

Qy 414 YNITRCHTFNVITCVHYFRGHNES-----RADCLDM----- 444

Db 741 YQV-----HYVMKNGEPKSAMLKDVMLADAQDMIIISGLQPETSYSLTVTAIVT 788

Qy 445 -----DPKAPQVWVHLPPYTVTVSLKMLTNPE-----G 473

Db 789 TKGDGARKPKLVSTTGSVPKPRLVINH-----TQNTALIQWHPVDTFGLQGYRLKEG 844

Qy 474 RK-----ESETTIQTD-----EDVPGPV 492

Db 845 RXDMEPLTTLEPSEKEDHPTATDTHKGASYVFRLSARNKVGFGGEEMVKREISVPETGPF 904

Qy 493 PVKSLQGTSFENKIFLNWKEPL--EPNGIITQYEVSYSSIRSFDDPAVPVAG---PPQTVS 547

Db 905 PQLHSGTSTSTSVQLSQPPVLAERNGVITKTYLLYRDINV--PLLPMHLLVPAADTSM 962

Qy 548 NLWNSTHHVFMHLHPGTYOFFIRASTVKGFGPATAINVTNINISAPSLPDYEGVDASL-- 605

Db 963 TLTG-----LKSDDTTYDVVKRAHTSKRGP-----YSPSVQFRTLP-----VDQSMFA 1005

Qy 606 ----NETATTITVLLR-----PAQAKGAPISAYQI-----VVEOLHPHRTKR-----EAGAMEC 650

Db 1006 KNFHVKAAMKTSVLLSWEIENYNPALSKFFMMMDGMVEVDGRATQKLVNKLPEKS 1065

Qy 651 YQVPTVYNALSGGAPYFAELPPG-----NLPE----- 680

Db 1066 YSFVLITNRGNSAGGLQHRVTAKTAPDVLRTKPAFIGTKNLDGMTVQLPDVPAENIKGY 1125

Qy 681 -----P 681

Db 1126 YIIIVPLKSRGKFIKPWESPDEMDLDELKKEISKRKRSIRYGREVELKPYIAAHFDVLP 1185

Qy 682 APFTVGDNRITYKGFNPPLAPRGYNIYFQAMSVSEKETKTQCVRIATKAAATEPEVIP 741

Db 1186 TEFTLGDDKHGGTNNKQLSQGQY-VFFVLAVMDHAESK-----MYATSPYSDPVMMDL 1240

Qy 742 DPAKQTDREVVKIAGISAGIL--VEILLVIVIVIKSKL-AKKRKDAMGNTROEMTHV 798

Db 1241 DPQPIITDDEGLIWMVGPVLAVFIIICIVIAILLYKKRAESKSLPNSKEVPSH-- 1298

Qy 799 NAMDRSYADOSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTAVLDENHSATAESRLLDV 858

Db 1299 -----HPTDPVELRLN----- 1310

Qy 859 PRYLCEGTSPYQYQGL--HPAIRVADLLHINLMKTSDSYGPKEEYESFPEGOSASWDV 916

Db 1311 -----FQPPGMAHPPPILELADHIEELKANDNLKFSQVEISIDPGQOFTWEH 1359

Qy 917 AKQDNRAKNRYGNI IAYDHSRVILQPVEDDPSSDIYINANYIDIWLRYDGYQRPESHYAT 976

Db 1360 SNLEVNPKRYANVIAVDHSRVLLSALIEGIPGSDYVNAVY-----DGYRKQNAVYAT 1413

Qy 977 QGPVHETYPFWRMVMQEQSACIWMVNLVEVGRVKYKVPD-DTEVYGFQKFTCVEME 1035

Db 1414 QGSLPETFGDFWRIM-EQEAETVMVMTKLEERSVKCDQYWPSPRGTTGHLVQVTLDTV 1472

Qy 1036 PLAENVVVTFTLERRGYNEIREVKQHFHTGHPDHPVHAATGLLSFTRRVKLSPPPSAGP 1095

Db 1473 ELT-YCVRTFALYNGSSEKRVKQFOFTAMPDGHGVPEHPPTFLAFLRLRVKTCNPPDAGP 1531

Qy 1096 IVVHCSAGAGTCGYIVIDIMDMAEREGVVVDIYNCVKALRSRRINMVQTEEQYIFIHDA 1155

Db 1532 MVVHCSAGVGRGTGCFIVIDAMLERIKHEKTVDIYGHVTLMAQRNVMVQTEDQYIFIHDA 1591

Qy 1156 ILEACLCGETAI PVCEPKAAFYDMIRDSQNSSHLKDQFOTLNSVTPRLQAEDCSIACL 1215

Db 1592 LLEAVTCGTEVPARNLYAYIQKLTQIETGENTGMELEFKRLAS--SKAHTSRFISANL 1649

Qy 1216 PRNHDKSRFMDLPPDRCLPELITIDG-ESSNYIINAALMDSVROPAAFIYQYPLPNTVK 1274

Db 1650 PCNFKRNLNIMPYESGRVCLQPIRGVEGSDYNASLDGYRQOKAVIATQGPAAETTE 1709

Qy 1275 DFWRLLVDYDGTSTVMLNEVDL--SQGCPQYWPBEGMLRYGPIQVCMSCMDCDVINRI 1332

Db 1710 DFWRMLHEHNSTIVMLTKLEMGREKCHQWPAERSARYQYFVVDPA-----EYNMPOVI 1766

Qy 1333 FRI CNLTRPQSGYLMVQOFOYLGWASHREVPGSKRSFLKLQLQVEKWECEBEGERTII 1392

Db 1767 LRPEKVTDARDQSRVTRQFTDW-PEQGVPKSGEGFIDFICQVHKTEQEQ-DEPISV 1824

Qy 1393 HCLNGGSGSMFCALIGIVEMVKQNVVDVPHAVKTLNSKPNMVEAPEQVFCYDVALE 1452

Db 1825 HCSAGVGTGFTILSIVLERMRVEGVVDIFQTVKQLRTQRPAMVQTEDQYFCYRAALE 1884

Qy 1453 YLES 1456

Db 1885 YLGS 1888

Search completed: June 1, 2005, 13:56:28
Job time : 51.7393 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:32:43 ; Search time 169.044 Seconds
(without alignments)
4413.635 Million cell updates/sec

Title: US-09-887-669-1
Perfect score: 7809
Sequence: 1 MDVAAAALPAFVALWLLYPW.....EAPQYRFCVDVALEYLESS 1457

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7809	100.0	1457	1	PTPK_MOUSE	P35822 mus musculus
2	7592.5	97.2	1440	2	Q6W6J2	Q86WJ2 homo sapien
3	7589.5	97.2	1440	2	Q68D78	Q86dt8 homo sapien
4	7582	97.1	1439	1	PTPK_HUMAN	Q15262 homo sapien
5	4822.5	61.8	1486	2	Q68FW4	Q86fm4 mus musculus
6	4812.5	61.6	1452	1	PTPM_HUMAN	P28827 homo sapien
7	4793.5	61.4	1452	1	PTPM_MOUSE	P28828 mus musculus
8	4732.5	60.6	1390	2	Q86V60	Q86v60 homo sapien
9	4675	59.9	1434	2	Q6YI48	Q6Yi48 gallus gall
10	4619	59.1	1436	2	Q00197	Q00197 homo sapien
11	4610	59.0	1436	2	Q2850	Q2850 homo sapien
12	4602.5	58.9	1439	2	P78399	P78399 homo sapien
13	4597	58.8	1436	2	Q35564	Q35564 mus musculus
14	4591	58.8	1436	2	P70125	P70125 mus musculus
15	4579	58.6	1454	1	PTPT_MOUSE	Q99m80 mus musculus
16	4542.5	58.2	1463	1	PTPT_HUMAN	O14522 homo sapien
17	4497.5	57.6	1434	2	Q6E5N7	Q6E5n7 brachydanio
18	4426	56.7	844	2	Q8C462	Q8c462 mus musculus
19	4359	55.8	1442	2	Q22735	Q22735 homo sapien
20	4339	55.6	1430	1	PTPU_HUMAN	Q92729 homo sapien
21	3482.5	44.6	1195	2	Q9PUX2	Q9pum2 xenopus lae
22	2665	34.1	492	2	Q8IV94	Q8iv94 homo sapien
23	2630.5	33.7	990	2	Q6PDN0	Q6pdn0 mus musculus
24	2534	32.4	502	2	Q8WUL3	Q8wul3 rattus norv
25	2270	29.1	465	2	Q3IB99	Q3ib99 potamotrygo
26	1918	24.6	617	2	Q66JY9	Q66jy9 mus musculus
27	1699.5	21.6	542	2	P70643	P70643 rattus norv
28	1527.5	19.6	1788	2	Q9IA70	Q9iaj0 xenopus lae
29	1526	19.5	1502	2	Q9UM81	Q9um81 homo sapien
30	1514.5	19.4	1501	2	Q9QW00	Q9qw00 rattus sp.
31	1511.5	19.4	1501	2	Q7T117	Q7t117 mus musculus

32	1508	19.3	1529	2	Q6PG86	Q6pg86 mus musculus
33	1506.5	19.3	1887	2	Q9QW67	Q9qw67 rattus sp.
34	1500	19.2	278	2	Q8C819	Q8c819 mus musculus
35	1495	19.1	1499	2	Q90815	Q90815 gallus gall
36	1495	19.1	1898	2	Q9EQ17	Q9eq17 mus musculus
37	1494	19.1	1898	2	Q84604	Q84604 r protein-t
38	1492.5	19.1	1897	1	PTPF_HUMAN	P10586 homo sapien
39	1487.5	19.0	1948	1	PTNS_HUMAN	Q13332 homo sapien
40	1485.5	19.0	1254	2	Q8VBV0	Q8vbv0 mus musculus
41	1482.5	19.0	1912	1	PTPD_HUMAN	P23468 homo sapien
42	1480	19.0	1898	2	Q86W50	Q86ws0 homo sapien
43	1477	18.9	273	2	Q99KV5	Q99kv5 mus musculus
44	1477	18.9	1191	2	Q7Z3X4	Q7z3x4 homo sapien
45	1461	18.7	1889	2	Q7Q0X2	Q7q0x2 anopheles g

ALIGNMENTS

RESULT 1

ID	PTPK_MOUSE	STANDARD;	PRT;	1457 AA.
AC	P35822;			
DT	01-JUN-1994	(Rel. 29, Created)		
DT	01-JUN-1994	(Rel. 29, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DB	Receptor-type protein-tyrosine phosphatase kappa precursor			
DB	(EC 3.1.3.48) (R-PTP-kappa).			
GN	Name=Ptprk; Synonyms=Ptprk;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=RI; TISSUE=Brain;			
RX	MEDLINE=93233655; PubMed=8474452;			
RA	Jiang Y.P., Wang H., D'Eustachio P., Musacchio J.M., Schlessinger J.,			
RA	Sap J.;			
RT	"Cloning and characterization of R-PTP-kappa, a new member of the			
RT	receptor protein tyrosine phosphatase family with a proteolytically			
RL	cleaved cellular adhesion molecule-like extracellular region.";			
RL	Mol. Cell. Biol. 13:2942-2951(1993).			
CC	-I- FUNCTION: Regulation of processes involving cell contact and			
CC	adhesion such as growth control, tumor invasion, and metastasis.			
CC	Forms complexes with beta-catenin and gamma-catenin/plakoglobin.			
CC	Beta-catenin may be a substrate for the catalytic activity of PTP-			
CC	kappa.			
CC	-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-I- TISSUE SPECIFICITY: High levels in liver and kidney. Lower levels			
CC	in lung, brain and heart. Not seen in spleen and testis.			
CC	-I- DEVELOPMENTAL STAGE: Developmentally regulated with highest			
CC	expression found in developing areas or in areas capable of			
CC	developmental plasticity.			
CC	-I- PFM: This protein undergoes proteolytic processing.			
CC	-I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
CC	Receptor class 2B subfamily.			
CC	-I- SIMILARITY: Contains 4 fibronectin type III domains.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.			
CC	-I- SIMILARITY: Contains 1 MAM domain.			
CC	-I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; L10106; AAA40021.1; --			
DR				

QY 1201 VTPRLQEDCSIACLPRNHDKRNFMMLPPDRCLPFLITIDGSSNTYNAALMDSYRQPA 1260
 Db 1201 VTPRLQEDCSIACLPRNHDKRNFMMLPPDRCLPFLITIDGSSNTYNAALMDSYRQPA 1260
 QY 1261 AFIVTQPLPNTVKDFWRLVVDYDCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECM 1320
 Db 1261 AFIVTQPLPNTVKDFWRLVVDYDCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECM 1320
 QY 1321 SCSMDCDVINRIFRICNLTRPQGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKQW 1380
 Db 1321 SCSMDCDVINRIFRICNLTRPQGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKQW 1380
 QY 1381 ECEBEGGRTIHCNGGSGSGMFCAGIIVVMKRNQVVDVFAVKTILRNSKNVVEAP 1440
 Db 1381 ECEBEGGRTIHCNGGSGSGMFCAGIIVVMKRNQVVDVFAVKTILRNSKNVVEAP 1440
 QY 1441 EQYRFCYDVALEYLESS 1457
 Db 1441 EQYRFCYDVALEYLESS 1457

RESULT 2
 ID Q86WJ2 PRELIMINARY; PRT: 1440 AA.
 AC Q86WJ2
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mutant receptor type protein tyrosine phosphatase K (EC
 DE 3.1.3.48)
 DE Name=PTRPK;
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE=22679345; PubMed=12794170;
 RA Novellino L., Renkvist N., Rini P., Mazzocchi A., Rivoltini L.,
 RA Greco A., Deho P., Squarcina P., Robbins P.F., Parmiani G.,
 RA Castelli C.;
 RT "Identification of a mutated receptor-like protein tyrosine
 RT phosphatase kappa as a novel, class II HLA-restricted melanoma
 RT antigen.";
 RL J. Immunol. 170:6363-6370(2003).
 DR EMBL; AF533875; AAC49502.1; -;
 DR HSP; P28827; IRPM.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN.III.
 DR InterPro; IPR000387; Tyr_PP.
 DR InterPro; IPR008957; Gal_bind_like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000998; MAM.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00629; MAM; 1.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR PRINTS; PR00700; PRTPHPTASE.
 DR SMART; SM00060; FN3; 3.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00137; MAM; 1.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS50853; FN3; 3.
 DR PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS0060; MAM_2; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
 KW Glycoprotein; Hydrolase; Receptor.
 SQ SEQUENCE 1440 AA; 162271 MW; B140BC621878586A CRC64;

Query Match 97.2%; Score 7592.5; DB 2; Length 1440;
 Best Local Similarity 97.5%; Pred. No. 0;
 Matches 1421; Conservative 12; Mismatches 6; Indels 19; Gaps 3;

QY 1 MD-VAAALPAFAVALMILLYPWPILGSLGQSPAGGCTFDDGPGACDTHODLYDDPFWHV 59
 Db 1 MDTAAALPAFAVALLLSPWLLLSAQGGFSAGGCTFDDGPGACDTHODLYDDPFWHV 60
 QY 60 SAOBPHYLPPMPQGSVMVVDSSNHDGPKARLQPTMKENDTHCIDFSYLLYSQKGLNP 119
 Db 61 SAOBPHYLPPMPQGSYMIVDSDHDGPKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120
 QY 120 GTLNILVRNKGPLANIMNVGTGTRDMLRAELAVSTFWPNSYQVIFEAESGSGSYI 179
 Db 121 GTLNILVRNKGPLANIMNVGTGTRDMLRAELAVSTFWPNSYQVIFEAESGSGSYI 180
 QY 180 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQATFQCIATGRDAVHNKLMLORRNGEDIPV 239
 Db 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQATFQCIATGRDAVHNKLMLORRNGEDIPV 240
 QY 240 AQTNNHRRFAASFRLOEVTKTDOLYRCVTOSESGSGVSNFAQLIVRPPRIAPQL 299
 Db 241 AQTNNHRRFAASFRLOEVTKTDOLYRCVTOSESGSGVSNFAQLIVRPPRIAPQL 300
 QY 300 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYTKLMLHLPDTEYE 359
 Db 301 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYTKLMLHLPDTEYE 360
 QY 360 IRVLLTRPGEGLPGPPLITRTKCAEPMTPTKTKIAIBIQARRIAVDWESLYNTRC 419
 Db 361 IRVLLTRPGEGLPGPPLITRTKCAEPMTPTKTKIAIBIQARRIAVDWESLYNTRC 420
 QY 420 HTFNVTICVHYFRGHNESRADCLMDPKAPQHVNVHLPYTNVSLKMLTNPEGRKSEE 479
 Db 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVNVHLPYTNVSLKMLTNPEGRKSEE 480
 QY 480 TIIQTDEDVPGVPVKSLOQTSFENKIFLNWKEPLENGIITQYEVSYSSIRSDPAVPV 539
 Db 481 TIIQTDEDVPGVPVKSLOQTSFENKIFLNWKEPLENGIITQYEVSYSSIRSDPAVPV 540
 QY 540 AGPPQTVSNLWNSTHVFHMLHFGTTPYFFIRASTVKGFGPATINVTNISAPSLDYE 599
 Db 541 AGPPQTVSNLWNSTHVFHMLHFGTTPYFFIRASTVKGFGPATINVTNISAPSLDYE 600
 QY 600 GVDASINETAATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTYQN 659
 Db 601 GVDASINETAATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTYQN 660
 QY 660 ALSCGAPYFAAELPPGNLPEPAPFTVGDNRKTYGFWNPPLAPRKGNINIFQAMSSVEKE 719
 Db 661 AMSGAPYFAAELPPGNLPEPAPFTVGDNRKTYGFWNPPLAPRKGNINIFQAMSSVEKE 720
 QY 720 TKTCQVRIATKAAATEEPIPPAKQTDVVKVIAGISAGILVPIILLVIVIVKSKL 779
 Db 721 TKTCQVRIATKAAATEEPIPPAKQTDVVKVIAGISAGILVPIILLVIVIVKSKL 780
 QY 780 AKRKDAMGNTRQEMTHMVMNDRSADQSTLHAEDPLSLTFMDQHNFSRLPNDPLVPT 839
 Db 781 AKRKDAMGNTRQEMTHMVMNDRSADQSTLHAEDPLSLTFMDQHNFSRLPNDPLVPT 832
 QY 840 AVLDEHNSATAESSRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHINLMKTSDSYGF 899
 Db 833 -----ENHSATAESSRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHINLMKTSDSYGF 888
 QY 900 KEEYSPFEGQSASWDVAKKQDNRAKNRYGNIITAYDHSRVILQPVEDDPSDDYINANYID 959

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Db 889 KEEESFEFGSASWDVAKQNRKAKRYGNIIAYDHSRVILQPVEDDPSSDIYANII- 947
QY 960 IWLXYDGRQPSHYIATQPVHETVYDFWRMVMWQSQSACIVMVTNLVVEVGRVKCYKWPD 1019
Db 948 -----DGQRPSHYIATQPVHETVYDFWRMVMWQSQSACIVMVTNLVVEVGRVKCYKWPD 1002
QY 1020 DTEVYDGRQPSHYIATQPVHETVYDFWRMVMWQSQSACIVMVTNLVVEVGRVKCYKWPD 1079
Db 1003 DTEVYDGRQPSHYIATQPVHETVYDFWRMVMWQSQSACIVMVTNLVVEVGRVKCYKWPD 1062
QY 1080 SPIRVKLSNPPSAGPIVHCSAGAGRTGCTIVIMLDMAREGVVDIYNCVKALRSRR 1139
Db 1063 SPIRVKLSNPPSAGPIVHCSAGAGRTGCTIVIMLDMAREGVVDIYNCVKALRSRR 1122
QY 1140 INNVQTEBQYIFIHDAILEACLCGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDBEFQTLN 1199
Db 1123 INNVQTEBQYIFIHDAILEACLCGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDBEFQTLN 1182
QY 1200 SVTPRLQEDCSIACLPRNHDKNRMMDLPPDRCLPFLITIDGESSNVIINAALMDSYRQP 1259
Db 1183 SVTPRLQEDCSIACLPRNHDKNRMMDLPPDRCLPFLITIDGESSNVIINAALMDSYRQP 1242
QY 1260 AAFIVTQYPLNTVDFWRLVVDYDCTSVMLNEVDLSQGCPOQYWPESGMLRYGPIQVEK 1319
Db 1243 AAFIVTQYPLNTVDFWRLVVDYDCTSVMLNEVDLSQGCPOQYWPESGMLRYGPIQVEK 1302
QY 1320 MSCSMDCDVINRIFRICNLTRPOEGLVMVQFOYLGWASHREVPGSKSFKLILQVEKW 1379
Db 1303 MSCSMDCDVINRIFRICNLTRPOEGLVMVQFOYLGWASHREVPGSKSFKLILQVEKW 1362
QY 1380 QBECEGEGRTIIHCLNGGSGMFCAGIVVEMVKRQNVVDVHFAVTKLRNSKPNMVEA 1439
Db 1363 QBECEGEGRTIIHCLNGGSGMFCAGIVVEMVKRQNVVDVHFAVTKLRNSKPNMVEA 1422
QY 1440 PEYRFFCYDVALEYLESS 1457
Db 1423 PEYRFFCYDVALEYLESS 1440

RESULT 3
Q68DT8 PRELIMINARY; PRT; 1440 AA.
ID Q68DT8
AC Q68DT8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein DKFZp686C2268.
GN Name=DKFZp686C2268;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium carcinoma cell line;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaiipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CE749277; CAH18132.1; -.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR000367; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
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DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPc; 2.
DR SMART; SM00404; PTPc motif; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00660; MAM_2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hypothetical protein.
SQ SEQUENCE 1440 AA; 162129 MW; 41BA5E4D6E0C0359 CRC64;

Query Match 97.2%; Score 7589.5; DB 2; Length 1440;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1420; Conservative 12; Mismatches 7; Indels 19; Gaps 3;

QY 1 MD-VAAALPAFVALWLLYPWLLGSLGQPSAGGCTPDDGPGACDYHQDLYDDFEWVHV 59
Db 1 MDTTAAALPAFVALWLLSPWLLGSAQGPAGGCTPDDGPGACDYHQDLYDDFEWVHV 60
QY 60 SAQSPHYLPPMPGSGSYMVVDSSNHDGCEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 119
Db 61 SAQSPHYLPPMPGSGSYMVDSSNHDGCEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120
QY 120 GTNLILVRVNGKPLANPINWVTGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSYI 179
Db 121 GTNLILVRVNGKPLANPINWVTGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSYI 180
QY 180 AIDDIQVLSYPCDSKSPHFLRLGDEVNAGONATQCIATGRDAVNKMLWLRNGEDIPV 239
Db 181 AIDDIQVLSYPCDSKSPHFLRLGDEVNAGONATQCIATGRDAVNKMLWLRNGEDIPV 240
QY 240 AOTKNINHRRFAASFRLOEVTKTDDLYRCVCTQSERGSGVSNFAQLIVREPRPTAPPOL 299
Db 241 AOTKNINHRRFAASFRLOEVTKTDDLYRCVCTQSERGSGVSNFAQLIVREPRPTAPPOL 300
QY 300 LGVGPTVILLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPTDYE 359
Db 301 LGVGPTVILLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPTDYE 360
QY 360 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKLTIAETQARRIAVDWSLGNITRC 419
Db 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKLTIAETQARRIAVDWSLGNITRC 420
QY 420 HTFNVTICYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 479
Db 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 480
QY 480 TIIQTDEDVPGVPVKSLQGTSFENKIFLNKKEPLEPNGIITQYEVSVSSIRSPDPAVPV 539
Db 481 TIIQTDEDVPGVPVKSLQGTSFENKIFLNKKEPLEDNPNGIITQYEVSVSSIRSPDPAVPV 540
QY 540 AGPQTQVSNLWNSTHVFHMLHPGTYTQFFTRASTVKFGPATAINVTNTISAPSLDYE 599
Db 541 AGPQTQVSNLWNSTHVFHMLHPGTYTQFFTRASTVKFGPATAINVTNTISAPSLDYE 600
QY 600 GVDASLNATATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECVQVPVTYQN 659
Db 601 GVDASLNATATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECVQVPVTYQN 660
QY 660 ALSGAPYFAAELPPGNLPEPAPFTVGDNRITKGFWMNPPPLAPRKGYNIYFOAMSVEKE 719
Db 661 AMSGAPYFAAELPPGNLPEPAPFTVGDNRITKGFWMNPPPLAPRKGYNIYFOAMSVEKE 720
QY 720 TKTCQVRIATKAAATEEPEVTPDPAKQTDTRVVVKIAGISAGILVFLILLVIVIVKSKL 779
Db 721 TKTCQVRIATKAAATEEPEVTPDPAKQTDTRVVVKIAGISAGILVFLILLVIVIVKSKL 780
QY 780 AKKRKDMGNTROEMTHVMNADRSYADQSTLHABDPLSLTFMDQHNFSRPLNDPLVPT 839
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Db 781 AKKRDANGNTRQEWTHWVNDMSYADQSTLHAEDEPLSITFMDQHNFSRY----- 832

Qy 840 AVLDEHSATASRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHINLMKTSDSYGF 899

Db 833 ----ENHSATASRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHINLMKTSDSYGF 888

Qy 900 KEEVESFEGOSASWDVAKDONAKRYGNIIAYDHSRVILQVEDDPSDDYINANYID 959

Db 889 KEEVESFEGOSASWDVAKDONAKRYGNIIAYDHSRVILQVEDDPSDDYINANYI- 947

Qy 960 IWLVRDGYQRPESHYATQGPVHETVDFWRVMVQEQSACIWMVNLNVEGVKCYKWPD 1019

Db 948 ----DGVRPESHYATQGPVHETVDFWRVMVQEQSACIWMVNLNVEGVKCYKWPD 1002

Qy 1020 DTEVYGFKVTCEMEPLAEYVTRFTLRRGYNEIREVKQFHTGMPDHGVPVHATGLL 1079

Db 1003 DTEVYGFKVTCEMEPLAEYVTRFTLRRGYNEIREVKQFHTGMPDHGVPVHATGLL 1062

Qy 1080 SFTIRVKLSNPPSAGPIVHCSAGRTGCVIVIDIMLDMAERGVVDIYNCVKALRSRR 1139

Db 1063 SFTIRVKLSNPPSAGPIVHCSAGRTGCVIVIDIMLDMAERGVVDIYNCVKALRSRR 1122

Qy 1140 INMVQTEBQYIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDSQTNSSHLKDEFOTLN 1199

Db 1123 INMVQTEBQYIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDSQTNSSHLKDEFOTLN 1182

Qy 1200 SVTPRLQAECDSCIACLPNDHDKNFMPLPDRCLPFLITIDGSSNYINAALMDSYROP 1259

Db 1183 SVTPRLQAECDSCIACLPNDHDKNFMPLPDRCLPFLITIDGSSNYINAALMDSYROP 1242

Qy 1260 AAFITVQYPLNTVKDFWRLVYDYGCTSIWMLNEVDLSQGPQYWPPEGMLRYGPIQVEK 1319

Db 1243 AAFITVQYPLNTVKDFWRLVYDYGCTSIWMLNEVDLSQGPQYWPPEGMLRYGPIQVEK 1302

Qy 1320 MSCSMDCDVNIRIFRICNLTRPQBYLWQFOFYLGWASHREVPGSKRSFLKLILQVEKW 1379

Db 1303 MSCSMDCDVNIRIFRICNLTRPQBYLWQFOFYLGWASHREVPGSKRSFLKLILQVEKW 1362

Qy 1380 QEECEGEGRTHIHLNGGGRSGMFCAGIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1439

Db 1363 QEECEGEGRTHIHLNGGGRSGMFCAGIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1422

Qy 1440 PEQYRFCYDVALEYLESS 1457

Db 1423 PEQYRFCYDVALEYLESS 1440

RESULT 4

PTPK_HUMAN STANDARD; PRT; 1439 AA.

AC Q15262; Q14763;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Receptor-type protein-tyrosine phosphatase kappa precursor

DE (EC 3.1.3.48) (R-PTP-kappa).

GN Name=PTPRK; Synonyms=PTPK;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RA MEDLINE=96279245; PubMed=8663237; DOI=10.1074/jbc.271.28.16712;

RA Fuchs M., Mueller T., Lerch M., Ullrich A.;

RT "Association of human protein-tyrosine phosphatase kappa with members

RT of the armadillo family.";

RL J. Biol. Chem. 271:16712-16719(1996).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Forebrain;

RX MEDLINE=97199372; PubMed=9047348; DOI=10.1016/S0378-1119(96)00684-1;

RA Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.;

RT "Molecular cloning and chromosomal localization of a human gene homologous to the murine R-PTP-kappa, a receptor-type protein tyrosine phosphatase.";

RL Gene 186:77-82(1997).

CC -1- FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis. Forms complexes with beta-catenin and gamma-catenin/plakoglobin. Beta-catenin may be a substrate for the catalytic activity of PTP-kappa.

CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein; at adherens junctions.

CC -1- TISSUE SPECIFICITY: High levels in lung, brain and colon; less in liver, pancreas, stomach, kidney, placenta and mammary carcinoma.

CC -1- PIM: This protein undergoes proteolytic processing.

CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 2B subfamily.

CC -1- SIMILARITY: Contains 4 fibronectin type III domains.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -1- SIMILARITY: Contains 1 MAM domain.

CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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CC -----

DR EMBL; Z70660; CAA94519.1; -.

DR EMBL; L77886; AAC37599.1; -.

DR HSP; P28827; IRPM.

DR Genew; HGNC:9674; PTPRK.

DR MIM; 602545; -.

DR GO; GO:0005887; C: integral to plasma membrane; TAS.

DR GO; GO:0005001; F: transmembrane receptor protein tyrosine phosphatase; TAS.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR008957; FN_III-like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR000998; MAM.

DR InterPro; IPR000387; TYR_phosphatase.

DR InterPro; IPR000242; Tyr_PP.

DR Pfam; PF00041; fn3; 2.

DR Pfam; PF00047; ig; 1.

DR Pfam; PF00629; MAM; 1.

DR Pfam; PF0102; Y_phosphatase; 2.

DR PRINTS; PR00020; MAMDOMAIN.

DR PRINTS; PR00700; PRTYPHPTASE.

DR PROSITE; PS50853; FN3; 3.

DR PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE; PS00740; MAM_1; 1.

DR PROSITE; PS50060; MAM_2; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

KW Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;

KW Receptor; Repeat; Signal; Transmembrane.

FT SIGNAL 1 26

FT CHAIN 27 1439

FT Receptor-type protein-tyrosine phosphatase kappa.

FT Extracellular (Potential).

FT Potential.

FT Cytoplasmic (Potential).

FT MAM.

FT Ig-like C2-type.

FT Fibronectin type-III 1.

FT Fibronectin type-III 2.

FT Fibronectin type-III 3.

FT Fibronectin type-III 4.

FT Protein-tyrosine phosphatase 1.

FT Protein-tyrosine phosphatase 2.

FT	ACT_SITE	1082	1082	Phosphocysteine intermediate (By similarity).
FT	ACT_SITE	1376	1376	Phosphocysteine intermediate (By similarity).
FT	DISULFID SITE	216	270	Potential.
FT	CARBOHYD	641	644	Cleavage site (Probable).
FT	CARBOHYD	101	101	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	140	140	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	211	211	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	416	416	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	424	424	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	436	436	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	462	462	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	552	552	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	586	586	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	590	590	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	607	607	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	690	690	N-linked (GlcNAc. .) (Potential).
FT	CONFLICT	9	9	L -> V (in Ref. 2).
FT	CONFLICT	158	158	S -> T (in Ref. 2).
FT	CONFLICT	284	284	A -> P (in Ref. 2).
FT	CONFLICT	422	422	T -> S (in Ref. 2).
FT	CONFLICT	672	674	AEL -> CRT (in Ref. 2).
FT	CONFLICT	715	715	S -> T (in Ref. 2).
FT	CONFLICT	732	732	A -> AA (in Ref. 2).
FT	CONFLICT	1366	1366	E -> K (in Ref. 2).
SQ	SEQUENCE	1439	1439	AA; 162087 MW; BED529AF7C9F4451 CRC64;
Query Match				
Best Local Similarity 97.1%; Score 7582; DB 1; Length 1439;				
Matches 1420; Conservative 13; Mismatches 5; Indels 20; Gaps 4;				
QY	1	MD-VAAAAALPAFVALWLLYPMLLSALGQFSAGGCTFDDGPGACDYHQDLYDDPEWVHV	59	
Db	1	MDTAAALPAFVALLLSPVLLLSAQQFSAGGCTFDDGPGACDYHQDLYDDPEWVHV	60	
QY	60	SAQEPHYLPPEMPOGYSYVVDSSNDHDPGEKARLQLPTWKENDTHCIDFSYLLYSOKGLNP	119	
Db	61	SAQEPHYLPPEMPOGYSYVVDSSNDHDPGEKARLQLPTWKENDTHCIDFSYLLYSOKGLNP	120	
QY	120	GTNLTLVRVNGKPLANPTWNTGFGROWLRAELAVSTFWPNEYOVIFEAESVGGSGYI	179	
Db	121	GTNLTLVRVNGKPLANPTWNTGFGROWLRAELAVSTFWPNEYOVIFEAESVGGSGYI	180	
QY	180	AIDDIQVLSYPCDKSPHFLRLGDVENVAGQATFQCIATGRDAVHKLWLQRRNGEDIPV	239	
Db	181	AIDDIQVLSYPCDKSPHFLRLGDVENVAGQATFQCIATGRDAVHKLWLQRRNGEDIPV	240	
QY	240	AQTKINHRRFAASFLQEVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRPTAPPQL	299	
Db	241	AQTKINHRRFAASFLQEVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRPTAPPQL	300	
QY	300	LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE	359	
Db	301	LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE	360	
QY	360	IRVLLTRPGEGTGLPGPLLTRTKCAEPMRPTKTKIAEQARRIAVDWESLGYNITRC	419	
Db	361	IRVLLTRPGEGTGLPGPLLTRTKCAEPMRPTKTKIAEQARRIAVDWESLGYNITRC	420	
QY	420	HTFNVTICVHYPRGHNESPADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE	479	
Db	421	HTFNVTICVHYPRGHNESPADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE	480	
QY	480	TLIQDDEVPVGPVVKSLGTSFENKI FLNWKPELEPGIITQYEVSYSSIRSFDPAPVP	539	
Db	481	TLIQDDEVPVGPVVKSLGTSFENKI FLNWKPELEPGIITQYEVSYSSIRSFDPAPVP	540	
QY	540	AGPPQTVSNLNMSTHVVHMLHPGTTYQFFIRASTVKGFGPATAINVTNNISAPSLPDYE	599	
Db	541	AGPPQTVSNLNMSTHVVHMLHPGTTYQFFIRASTVKGFGPATAINVTNNISAPSLPDYE	600	
QY	600	GVDAASNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQN	659	

Db	601	GVDAASNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQN	660	
QY	660	ALSGAGPYFAAELPPGNLPEPPAPFTVGDNRITYKGFNPNPLAPRKGNYIYQAMSSVEKE	719	
Db	661	AMSGAGPYFAAELPPGNLPEPPAPFTVGDNRITYKGFNPNPLAPRKGNYIYQAMSSVEKE	720	
QY	720	TKTCQVRIATKAATEPEPIPDPAKQTDVVKIAGISAGILVFILLVIVIVKSKL	779	
Db	721	TKTCQVRIATK-AATEPEPIPDPAKQTDVVKIAGISAGILVFILLVIVIVKSKL	779	
QY	780	AKREKDWNTQEMTHVMAMDRSYADQSTLHAEDPLSLTFMDQHNPSPLPNDPLVPT	839	
Db	780	AKREKDWNTQEMTHVMAMDRSYADQSTLHAEDPLSLTFMDQHNPSPLPNDPLVPT	831	
QY	840	AVLDENHSATAESSRLLDVPRYLCEGTSPYQTLQHPAIRVADLLQHINLMKTSDSYGF	899	
Db	832	---ENHSATAESSRLLDVPRYLCEGTSPYQTLQHPAIRVADLLQHINLMKTSDSYGF	887	
QY	900	KEEYESFEGSASWDVAKKQONRAKRYGNI IAYDHSRVILQPVDDPSSDIYINANYID	959	
Db	888	KEEYESFEGSASWDVAKKQONRAKRYGNI IAYDHSRVILQPVDDPSSDIYINANYI-	946	
QY	960	IWLVDGVQRPSPHYATQGPVHETVDFWRMVWQESACI VMVTNLVEVGRVKCYKWPD	1019	
Db	947	-----DGYQRPSPHYATQGPVHETVDFWRMVWQESACI VMVTNLVEVGRVKCYKWPD	1001	
QY	1020	DTEYVGDVKVTCVEMEPLAEYVVRFTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLL	1079	
Db	1002	DTEYVGDVKVTCVEMEPLAEYVVRFTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLL	1061	
QY	1080	SFIRRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRR	1139	
Db	1062	SFIRRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRR	1121	
QY	1140	INMVQTEQYIFIHDAILEACLGCETAI PVCEPKAAVDFMIRIDSQTNSSHLKDEFOFLN	1199	
Db	1122	INMVQTEQYIFIHDAILEACLGCETAI PVCEPKAAVDFMIRIDSQTNSSHLKDEFOFLN	1181	
QY	1200	SVTPRLQAEACSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQP	1259	
Db	1182	SVTPRLQAEACSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQP	1241	
QY	1260	AAFTVQYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCPOYWPPEGMLRYGPIQVEK	1319	
Db	1242	AAFTVQYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCPOYWPPEGMLRYGPIQVEK	1301	
QY	1320	MSCSMDCDVINRIFRICNLTRPQEGYLMVQFQYLGWASHREVPGSKRSFLKLILOVEKW	1379	
Db	1302	MSCSMDCDVINRIFRICNLTRPQEGYLMVQFQYLGWASHREVPGSKRSFLKLILOVEKW	1361	
QY	1380	QEECEGEGRITIIHCLNGGGRSGMFCAGI GIVVMVKRQNVVDVFAVKTLRNSKPNMVEA	1439	
Db	1362	QEECEGEGRITIIHCLNGGGRSGMFCAGI GIVVMVKRQNVVDVFAVKTLRNSKPNMVEA	1421	
QY	1440	PEQRFYCDVALEYLESS 1457		
Db	1422	PEQRFYCDVALEYLESS 1439		
RESULT 5				
Q68FM4				
ID	Q68FM4	PRELIMINARY;	PRT;	1486 AA.
AC	Q68FM4;			
DT	25-OCT-2004 (TReMBLrel. 28, Created)			
DT	25-OCT-2004 (TReMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TReMBLrel. 28, Last annotation update)			
DE	Ptprm protein.			
GN	Name=Ptprm;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			

RN
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Collins P.S., Wagner L., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN
 RP
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC079621; AAH79621.1;
 DR InterPro; IPR003961; FN_III;
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000998; MAM.
 DR InterPro; IPR003595; PTPC_motif.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00629; MAM; 1.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR PRINTS; PR00700; PTPYPPHTASE.
 DR SMART; SM00060; FN3; 3.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00137; MAM; 1.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC_motif; 2.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Glycoprotein.
 SQ
 Query Match 61.8%; Score 4822.5; DB 2; Length 1486;
 Best Local Similarity 60.4%; Pred. No. 2.4e-317;
 Matches 896; Conservative 208; Mismatches 320; Indels 59; Gaps 9;
 QY 22 LIGSALQFSGAGGCTFDGACDCHQDLYDDEFWHVHSAQEYHLYLPENPGSGYMVVDS 81
 DB 14 LLTAAGETSGGCLFDEPYSTCGYQADDEDFWNEQVNTLTKTPTSDPFWPMSGFMVNT 73
 QY 82 SNHDPGKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGFTNLIVRVKNGPLANPWNVT 141
 DB 74 SKRPEGQRAHLLLPQKENDTHCIDFHYFVSSKSNAPGLLVVYKVNNGPLNPNWIS 133
 QY 142 GFTGRDLRLAEAVSTFWPNEYQVIFAEVSGRSGYIADDDIQVLSYPCDKSPHFRLRG 201
 DB 1203 SLYYDMNKLDPTQNSSQIKKEEFRTLNWVTPTLRVEDCSIALPRNHEKNRCKMDILPPDR 1262

Db 134 GDPTRTWRAELAISTFWPNFYQVIFEV-VTSGHQGYLAIDEVKVLGHPCTRTTTHFLRIQ 192
 QY 202 DVEVNAGQATFOCIATGRDAVHNKMLQRRNGEDIIPVAQTKNINHRFAASFFRLQEVTK 261
 Db 193 NVEVNAGQATFOCIATGRDAVHNKMLQRRNGEDIIPVAQTKNINHRFAASFFRLQEVTK 252
 QY 262 TDQDLYRCVTSQSRGVSQSNPAQLIVREPPRPPIAPPOLLGVGPYLLIQLNANSIIGDGP 321
 Db 253 RDAGKYRCMCTEGGVGISNYAELVWKEPVPPIAPPOLLGVGPYLLIQLNANSIIGDGP 312
 QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPPDEYEVIRVLLTRPGEGGTLGPPPLIT 381
 Db 313 IVAREVEYCTASSWDRQPDVSTSYKIGHLDPPDEYEVIRVLLTRPGEGGTLGPPPLIT 372
 QY 382 RTKCAEPMRPTKTLKIAEQARRIADVWSLGNITRCHTFNVTICYHYFRGHESRAD- 440
 Db 373 RTKCADPMRGPRLKLEVEVKSQRTIRWEPPGVNVTCHSVNLTVHYGYVGGOEQVREE 432
 QY 441 -CLDMDPKAPQHVNVNHLPPYTNVSLKMLNPNPEGRKESEETIQTDDSDVPGVPVKSLQG 499
 Db 433 VSWDTONSHPQHTITNLSPYTNVSVKILANPEGRKESBELTQTQDDELDPCAVPTESTQG 492
 QY 500 TSPENKIFLNWKEPLEPENGIIIOYEVSYSSIRSPDPAVPVAGPPQTVSNLWNSTHVFMH 559
 Db 493 SAFEKIFLQWRREPTQYGVITLYEITYKAVSSFPDEIDLSNOSGRVSKLGNETHFLFFG 552
 QY 560 LHPGTTYQFFIRASTVKFGFPAATINVTINISAPSLPDYEGVDASLNETAETITVILRPA 619
 Db 553 LYFGTTYFTIRASTAKGFOPPATNQFTTKISAPSMAYE-FETPLNQDNTVTVMLKPA 611
 QY 620 QAKGAPISAYQIVVQQLHPHRTKREAGAMECYQVPTYQNALSGGAPYFAAEAPPGNLP 679
 Db 612 QSRGAPVSVYQIVVEBERPRRTKTKTEILKCYVPPIHFQNASILNSQYFAAEAPPADSLQ 671
 QY 680 EPAPFTGDNRTYKGFWNPPPLAPRKGNIIYFOAMSSVEKETKTCQVRIAKAA----- 732
 Db 672 AAQFTTIGDNKTYNGWNTPLPHKSYRIYIYQAASTRANGETKDKCVRVATKAAIIVTQLT 731
 QY 733 -----ATEPEVPIPDPAKOTDRVVKIAGISAGILVFILLVIVIVVK 776
 Db 732 TPYIRIAPAGDGLTCAVTPKVPPEKQTDHTVKIAGIAGILLVIFLGVVLVWKK 791
 QY 777 SKLAKKRKADMGNTROEMTHVNAMDRSYADQSTLHAEDPLSLTFMDQHNFSR----- 830
 Db 792 RKLAKKRKETMSSTRQEMTVVNSMDKSYAEQGTNCDE---AFSFMGTHNLNGRSVSPS 848
 QY 831 -----LPN-----DPLVPTAVLDENHATAESSRLLDVPRY-LCEGTESPTQG 873
 Db 849 SFTMTKNTLTSTSVNSYYPDPFVPTAILDETHMASDTSLSAQPHYTYKREAAADVPYQTG 908
 QY 874 QLHPAIRVADLLQHLNLMKTSDSYGFKEEYESFFEGOSASWDVAKDONAKRYGNIIA 933
 Db 909 QLHPAIRVADLLQHLNLMKTSDSYGFKEEYESFFEGOSASWDVAKDONAKRYGNIIA 968
 QY 934 YDHSRVLQFVEDDPSDDINANYIDWLRYDGYQRPISHYIATQGPVHETVYDFWRVMWQ 993
 Db 969 YDHSRVLQFVEDDPSDDINANYIDWLRYDGYQRPISHYIATQGPVHETVYDFWRVMW 1022
 QY 994 EQSACIWMVNLVEGVRKCYKWPDDTEVVGDFKVTCTVEMEPLEAVVTVFTLRRGYN 1053
 Db 1023 ENTASIMVNLVEGVRKCYKWPDDTEVVGDFKVTCTVEMEPLEAVVTVFTLRRGYN 1082
 QY 1054 EIREVQKQFTGPDHGVPHATGLLSFTRRVKLSNPSPSAGPIVHVCSAGAGTGCYIVI 1113
 Db 1083 EIREVQKQFTGPDHGVPHATGLLSFTRRVKLSNPSPSAGPIVHVCSAGAGTGCYIVI 1142
 QY 1114 DIMLDMAREGVVDIYNCVKALRSRRINMVQTEQYIFIHDAILEACLCCGTAIPVCEFK 1173
 Db 1143 DIMLDMAREGVVDIYNCVKALRSRRINMVQTEQYIFIHDAILEACLCCGTAIPVCEFK 1202
 QY 1174 AAYFDMIRIDSQNSHLKDEPOTLNSVTPRLQAEBCSIACLPRNHDKNRPMMLPPDR 1233
 Db 1203 SLYYDMNKLDPTQNSSQIKKEEFRTLNWVTPTLRVEDCSIALPRNHEKNRCKMDILPPDR 1262

QY 1234 LPFLITIDGSSNYINAALMDSYQPAFIIVTQYPLNTVDFWRLVYDYCTSIIVMLNE 1293
Db 1263 LPFLITIDGSSNYINAALMDSYQPSAFIVTQYPLNTVDFWRLVLDYHCTSIIVMLND 1322
QY 1294 VDLGQCQYWPPEGMLRYGIQVECMSCMDGVINRIFRICNLTRPQEGYLMVQQFOY 1353
Db 1323 VDPALQCFQYWPENGVRHGGIQLQVEFVSADLEEDIISRIPIYNASRPQDGRMVQQFOF 1382
QY 1354 LGWASHREVPKSGSFLKLLIQVEKWQBECEGRTIIHCLNGGGRSGMFCATGIVVEM 1413
Db 1383 LGWPMYRDPVPSKGSFLKLLIQVEKWQBECEGRTIVHCLNGGGRSGTFCATGIVCEM 1442
QY 1414 VKRQNVDPVFAVKTIRNSKKNVPEAPQYFCYDVALEYLES 1456
Db 1443 LRHQRTVDVFAVKTIRNKNKNMVDLLDQYKFCYDVALEYLNS 1485
RESULT 6
PTPM_HUMAN STANDARD; PRT; 1452 AA.
AC P28827;
AT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)
DE (R-PTP-mu).
GN Name=PTPRM; Synonym=PTPRL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;
RA Gebbink M.F.B.G., van Eten I., Hateboer G., Suijkerbuijk R.,
RA Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.,
RT "Cloning, expression and chromosomal localization of a new putative
RT receptor-like protein tyrosine phosphatase.";
RL FEBS Lett. 290:123-130(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.
RX MEDLINE=98010572; PubMed=9346878; DOI=10.1074/jbc.272.44.27505;
RA Hoffmann K.M., Tonks N.K., Barford D.,
RT "The crystal structure of domain 1 of receptor protein-tyrosine
RT phosphatase mu.";
RL J. Biol. Chem. 272:27505-27508(1997).
CC -!- FUNCTION: May play a key role in signal transduction and growth
CC control.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 2B subfamily.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X58288; CAA41226.1; -.
DR PIR; S17669; S17669.
DR PDB; IRPM; X-ray; A/B=879-1156.
DR Genew; HGNC:9675; PTPRM.
DR MIM; 176888; -.
DR GO; GO:0005887; C-integral to plasma membrane; TAS.

GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS50853; FN3; 3.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW 3D-structure; Glycoprotein; Hydrolase; Immunoglobulin domain;
KW Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 1452 Receptor-type protein-tyrosine
FT DOMAIN 21 742 Phosphatase mu.
FT TRANSMEM 743 764 Extracellular (Potential).
FT DOMAIN 765 1452 Potential.
FT DOMAIN 22 184 Cytoplasmic (Potential).
FT DOMAIN 186 277 Ig-like C2-type.
FT DOMAIN 281 371 Fibronectin type-III 1.
FT DOMAIN 379 477 Fibronectin type-III 2.
FT DOMAIN 482 581 Fibronectin type-III 3.
FT DOMAIN 589 671 Fibronectin type-III 4.
FT DOMAIN 923 1153 Protein-tyrosine phosphatase 1.
FT DOMAIN 1213 1447 Protein-tyrosine phosphatase 2.
FT ACT_SITE 1095 1095 Phosphocysteine intermediate (By
FT ACT_SITE 1389 1389 similarity).
FT ACT_SITE 1389 1389 Phosphocysteine intermediate (By
FT DISULFID 206 260 similarity).
FT CARBOHYD 72 72 Potential.
FT CARBOHYD 92 92 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 131 131 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 249 249 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 406 406 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 414 414 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 454 454 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 534 534 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 544 544 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 598 598 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 651 651 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 681 681 N-linked (GlcNAc . .) (Potential).
FT STRAND 880 881
FT TURN 882 884
FT HELIX 885 905
FT TURN 906 906
FT TURN 916 919
FT HELIX 921 926
FT TURN 930 931
FT HELIX 936 938
FT STRAND 939 941
FT TURN 946 947
FT TURN 949 952
FT STRAND 953 961
FT TURN 962 963

[illegible]

RC TISSUE=Lung;
RX MEDLINE=92008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;
RA Gebbink M.F.B.G., van Eeten I., Hateboer G., Suijkerbuijk R.,
RA Beijersbergen R., Gaurs van Kessel A., Moolenaar W.H.;
RT "Cloning, expression and chromosomal localization of a new putative
RT receptor-like protein tyrosine phosphatase.";
RL FEBS Lett. 290:123-130(1991).
CC -!- FUNCTION: May play a key role in signal transduction and growth
CC control.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Most abundant in lung, less in brain and
CC heart.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 2B subfamily.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X58287; CAA41225.1; -.
DR PIR; S17670; S17670.
DR HSP; P28827; IREP.
DR MGD; MGI:102694; Ptpm.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR00387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS50853; FN3; 3.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00740; MAM 1; 1.
DR PROSITE; PS50060; MAM 2; 1.
DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
DR PROSITE; PS50056; TYR PHOSPHATASE 2; 2.
DR PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.
KW Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;
KW Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 1452
FT Receptor-type protein-tyrosine
FT phosphatase mu.
FT Extracellular (Potential).
FT Potential.
FT Cytoplasmic (Potential).
FT MAM.
FT Ig-like C2-type.
FT Fibronectin type-III 1.
FT Fibronectin type-III 2.
FT Fibronectin type-III 3.
FT Fibronectin type-III 4.
FT Protein-tyrosine phosphatase 1.
FT DOMAIN 923 1153

FT	DOMAIN	1213	1447	Protein-tyrosine phosphatase 2.
FT	ACT_SITE	1095	1095	Phosphocysteine intermediate (By similarity).
FT	ACT_SITE	1389	1389	Phosphocysteine intermediate (By similarity).
FT	DISULFID	206	260	Potential.
FT	CARBOHYD	72	72	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	92	92	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	131	131	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	249	249	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	406	406	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	414	414	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	454	454	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	534	534	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	544	544	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	598	598	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	651	651	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	681	681	N-linked (GlcNAc. .) (Potential).
SQ	SEQUENCE	1452	1452	AA; 163594 MW; F99D0FC67922CF1E CRC64;

Query Match 61.4%; Score 4793.5; DB 1; Length 1452;
Best Local Similarity 61.3%; Pred. No. 2.4e-315;
Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

Qy	22	LLGSALGQFSAGGCTEDDGPACDYNHODLYDDFEMVHVSQAQEPHYLPPEMQSGSMVVD	81
Db <td>14</td> <td>LLTAAAGETSGGCLFDEPYSTCGYQADEDDFNEQVNTUTKPTSDPMWSSGSMVNT</td> <td>73</td>	14	LLTAAAGETSGGCLFDEPYSTCGYQADEDDFNEQVNTUTKPTSDPMWSSGSMVNT	73
Qy <td>82</td> <td>SNHDPGSKARLQLPTMKENDTHCIDFSLYSQKGLNPGLTNILVRVKNKGLANPIMVNT</td> <td>141</td>	82	SNHDPGSKARLQLPTMKENDTHCIDFSLYSQKGLNPGLTNILVRVKNKGLANPIMVNT	141
Db <td>74</td> <td>SGKEGQRAHLLLPQKXENDTHCIDFHYFVSSKSNAPGLLVVKNVNGPLGNINIS</td> <td>133</td>	74	SGKEGQRAHLLLPQKXENDTHCIDFHYFVSSKSNAPGLLVVKNVNGPLGNINIS	133
Qy <td>142</td> <td>GFTGRDLRAELAVSTFWPNEYSQVFEAEVSGSGSYIAIDDIQVLSVPCDKSHFLRLG</td> <td>201</td>	142	GFTGRDLRAELAVSTFWPNEYSQVFEAEVSGSGSYIAIDDIQVLSVPCDKSHFLRLG	201
Db <td>134</td> <td>GDPTRTWRAELAISTFWPNFYQVFEV-VTSHGQGLAIDDEVKVLGHPCRTTTHFLRIQ</td> <td>192</td>	134	GDPTRTWRAELAISTFWPNFYQVFEV-VTSHGQGLAIDDEVKVLGHPCRTTTHFLRIQ	192
Qy <td>202</td> <td>DVEYNAGQATFOCIATGRDAVHNKWLQRENGEDI PVAOTKTNINHRFAFASRLQVTK</td> <td>261</td>	202	DVEYNAGQATFOCIATGRDAVHNKWLQRENGEDI PVAOTKTNINHRFAFASRLQVTK	261
Db <td>193</td> <td>NVEYNAGQATFOCSAIGRTVAGDRLMLQGLIDVDRDLKEIKVTSRRFISAFNVNTTK</td> <td>252</td>	193	NVEYNAGQATFOCSAIGRTVAGDRLMLQGLIDVDRDLKEIKVTSRRFISAFNVNTTK	252
Qy <td>262</td> <td>TDQLYRCVCTSERGSGVSNFAQLIVREPPPIAPPQLLGVGPTVLLQLNANSIIGDGP</td> <td>321</td>	262	TDQLYRCVCTSERGSGVSNFAQLIVREPPPIAPPQLLGVGPTVLLQLNANSIIGDGP	321
Db <td>253</td> <td>RDAGYRCMCTEGVGISNVAELVVKPEVPPIAPPQLASVGATVLTQLNANSINGDGP</td> <td>312</td>	253	RDAGYRCMCTEGVGISNVAELVVKPEVPPIAPPQLASVGATVLTQLNANSINGDGP	312
Qy <td>322</td> <td>IILKEVYRMTSGSWTETHAVNAPYKLUHLDPTEYBIRVLLTRPGEGGTGLPGPLIT</td> <td>381</td>	322	IILKEVYRMTSGSWTETHAVNAPYKLUHLDPTEYBIRVLLTRPGEGGTGLPGPLIT	381
Db <td>313</td> <td>IVAREVEYCTASGSWDRQPVDSYKIGHLDPDTEYBISVLLTRPGEGGTGSPGALRT</td> <td>372</td>	313	IVAREVEYCTASGSWDRQPVDSYKIGHLDPDTEYBISVLLTRPGEGGTGSPGALRT	372
Qy <td>382</td> <td>RTKCAEPMRTPTLKIAEIQAARIADVDSIGYNTTRCHTFNVTICVHYFRGHNESRAD</td> <td>440</td>	382	RTKCAEPMRTPTLKIAEIQAARIADVDSIGYNTTRCHTFNVTICVHYFRGHNESRAD	440
Db <td>373</td> <td>RTKCADPMRGPRKLEVEVSKSQITIRWSPFGYNVTRCHSYNLTVHYQVGGQGVREE</td> <td>432</td>	373	RTKCADPMRGPRKLEVEVSKSQITIRWSPFGYNVTRCHSYNLTVHYQVGGQGVREE	432
Qy <td>441</td> <td>-CLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEETIIQTDDEVPQVPVKSLQG</td> <td>499</td>	441	-CLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEETIIQTDDEVPQVPVKSLQG	499
Db <td>433</td> <td>VSWTDNSHPQHTITNLSPYTNVSVKLIAMNPEGRKESQELTVQTDDELPGAFTESIQG</td> <td>492</td>	433	VSWTDNSHPQHTITNLSPYTNVSVKLIAMNPEGRKESQELTVQTDDELPGAFTESIQG	492
Qy <td>500</td> <td>TSFNKPIFNWKEPLENGIITQYEVSVSSTRSDPAVPVAGPPQTVNLNWNSTHHVFMH</td> <td>559</td>	500	TSFNKPIFNWKEPLENGIITQYEVSVSSTRSDPAVPVAGPPQTVNLNWNSTHHVFMH	559
Db <td>493</td> <td>SAFEKIFLOWREPTQTVGITVETIYKAVSSFDPEIDLNSQSGRVSGLGNETHFLPFG</td> <td>552</td>	493	SAFEKIFLOWREPTQTVGITVETIYKAVSSFDPEIDLNSQSGRVSGLGNETHFLPFG	552
Qy <td>560</td> <td>LHRTTYQFFIRASTVKGFGPATINVTNLSAPSLDPYEGVDASLNETATITVLLRPA</td> <td>619</td>	560	LHRTTYQFFIRASTVKGFGPATINVTNLSAPSLDPYEGVDASLNETATITVLLRPA	619
Db <td>553</td> <td>LYPGTYSFTIRASTAGFGPATNQFTTKLSAPSMPAYE-FETPLNQTDNTVTVMLRPA</td> <td>611</td>	553	LYPGTYSFTIRASTAGFGPATNQFTTKLSAPSMPAYE-FETPLNQTDNTVTVMLRPA	611
Qy <td>620</td> <td>QAKGAPISAYQIVVVEQLPHRTKREAGAMECYQVPVTVQNALSGGAPYFAAELPGLNLP</td> <td>679</td>	620	QAKGAPISAYQIVVVEQLPHRTKREAGAMECYQVPVTVQNALSGGAPYFAAELPGLNLP	679
Db <td>612</td> <td>QSRGAPSVYQIVVVEERPRTKTTELKCYVPPIHFQNASILNSQYFFAAEFADSLQ</td> <td>671</td>	612	QSRGAPSVYQIVVVEERPRTKTTELKCYVPPIHFQNASILNSQYFFAAEFADSLQ	671
Qy <td>680</td> <td>EPAPFTVDNRTYKGFNPNPLAPRGYNYIQPQAMSSVEKETQTCVCIATKAAATEEPEV</td> <td>739</td>	680	EPAPFTVDNRTYKGFNPNPLAPRGYNYIQPQAMSSVEKETQTCVCIATKAAATEEPEV	739
Db <td>672</td> <td>AAQPTTIGDNKTYGYNWNTPLPHKSYRIYQAASRANGETKIDCVRVATKGAFTPKP</td> <td>729</td>	672	AAQPTTIGDNKTYGYNWNTPLPHKSYRIYQAASRANGETKIDCVRVATKGAFTPKP	729
Qy <td>740</td> <td>IPDPAKQTDVRVVKTAGISAGILVFILLLVIVIVKSKLAKKRDKAMGNTREQMTMVN</td> <td>799</td>	740	IPDPAKQTDVRVVKTAGISAGILVFILLLVIVIVKSKLAKKRDKAMGNTREQMTMVN	799

730 VPEPEKDTHTVKTAGVIAGLLEFVILGLVVLVKKRKLAKRKETMSSTRQMTVMVN 789
800 AMRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDP-----LVPTAVL-DENH 846
790 SMDKSYAEQGTNCDE---AFSEFMGTHNLGRSVSSPSSFTMTKTTLSTSPVNSYYPDETH 846
847 SATAESRLLDVPRY-ICEGTESPYQGLHPAIRVADILLOHNLMTSISYGEKEYES 905
847 TMSADTSSLAQPHYTKKREADVQYQGLHPAIRVADILLOHNLMTSISYGEKEYES 906
906 FFEQOSASWVAKKDNKRNRYNIIAYDHSRVLQVDEDDPSDDYINANYIDWLRYD 965
907 FFEQOSAPWSAKDENMKRNRYNIIAYDHSRVLQVDEDDPSDDYINANYIDWLRYD 960
966 GYQRPSHYIATQGVFVHTVYDFWVMWQBSACIVYIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1025
961 GYHRPNHYIATQGVFVHTVYDFWVMWQBSACIVYIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1020
1026 DFKVTCEMEPLARYVVRTTLERGVNIREVKQFHTGWPDHGVPHATGLLSFIRRV 1085
1021 DIKVTLLDTLLAEYVIRTEFAVEKRGIIHEIREIRQFHTGWPDHGVPHATGLLGFRVQ 1080
1086 KLSNPPSAGPIVHCSAGAGRTGCVYIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1145
1081 KXSPPNAGPIVHCSAGAGRTGCVYIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1140
1146 EEOVFIFHDAILEACLCGETAIPCEPKAAYFDMRIDSTNSHLKDEFQTLNSVTPRL 1205
1141 EEOVFIFHDAILEACLCGETSIPASQVRSYLYDNKLDPTQNSQIKBEFTLNWVTPRL 1200
1206 QABDCSTACLPNRHDKNRPMMLPPDRCLPLFITIDGESSNYINAAALMDSYRQPAFIVT 1265
1201 RVEDCSIALPRNHEKRNKMDILLPPDRCLPLFITIDGESSNYINAAALMDSYRQPAFIVT 1260
1266 QYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPOYWPBEGMLRGPIQVECMSCMD 1325
1261 QHPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPOYWPBEGMLRGPIQVECMSCMD 1320
1326 CDVNRIFRINLFRPOEGLVLMVOQFOYLGWASHREVPGRKSRFLKILQVKKWQECSE 1385
1321 EDIISRIFRINLFRPOEGLVLMVOQFOYLGWASHREVPGRKSRFLKILQVKKWQECSE 1380
1386 GEGRTIHLCLNGGSGMFCAGIVBWMVRQNVVDVFAVKTILRNSKPNMVEAPEQYRF 1445
1381 GEGRTVHCLNGGSGMFCAGIVBWMVRQNVVDVFAVKTILRNSKPNMVEAPEQYRF 1440
1446 CYDVALEYLES 1456
1441 CYEVALEYLNS 1451

RESULT 8

Q86V60 PRELIMINARY; PRT; 1390 AA.
ID Q86V60
AC Q86V60
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PTPRM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBITaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownshtein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
Kryzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051651; AAH51651.1; -;
DR HSP; P28827; IRPM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00740; MAM 1; 1.
DR PROSITE; PS00650; MAM 2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolase.
SQ SEQUENCE 1390 AA; 156936 MW; D8173543CDD9F79 CRC64;
Query Match 60.6%; Score 4732.5; DB 2; Length 1390;
Best Local Similarity 62.2%; Pred. No. 3.1e-311;
Matches 872; Conservative 205; Mismatches 296; Indels 29; Gaps 9;
Qy 71 MPOGSVMYVDSNHDCEKARLQPTMKENDTHCIDPSYLLYSQKGLNPGTLNLLVRVK 130
Db 1 MPGSFMLVNASGRPEQRAHLLLPQKENDTHCIDPHYFVSSKSNPPGLNLYVVKNN 60
Qy 131 GPLANPNTVNTGFTGRDNLAEAVSTFWPNEVQVIFAEVSGRSGYIADIDQVLSYP 190
Db 61 GPLGNFNWISGDPARTWNAELAISTFWNFQVIFEV-ITSGHQYLAIDEVKKVLGHP 119
Qy 191 CDKSPHFLRLGDEVNAGQWATFQCITATGSDAVHKLWLQRRNGEDIPVATQKNINRRF 250
Db 120 CTRTPHFLRIQNVENVNAGQWATFQCSAIGRTVAGDRLWLQCIDVRDAPLKEIKVTSRRF 179
Qy 251 AASFRLOEVTKTDQDLRYRCVTSQSRGSGVSNFAQLIVREPRPIAPQOLLGVGPTLLIQ 310
Db 180 IASFNVVNTTKRDAGKYRCMIRTEGGVGISNYAELVVKPEVPFIAPPQLASVGTATLMIQ 239

Db 84 AHLIFQALSENDTHCLQSFYFWYGRDGHSPOTLSAYVVRMGPGVGSVAWNASGSHGRQWH 143
Qy 150 RAEIAVSTFWNEYQVIFAEVSGRSGYIAIDIOVLSPYCDKSPHFLRGLDVEVNAGQ 209
Db 144 QAEIAVSLFWPSEYQVLFVAVISSERRGYLGLDILLNLYPCSKAPHFSLRGLDVEVNAGQ 203
Qy 210 NATQCCATGDAVHKLMLORRNGEDI PVAQTGNINHRRAASPRLOEVTKTODLIYRC 269
Db 204 NATPQCAAGKAABERFLMORQSEGVVPAASVXHSRRELFATFOLDDEVSKGQDLYRC 263
Qy 270 VTQSESGVSNFAQLVREPRPIAPPOLLGVGPTVLLIOLNANSIIGDOPILKEVEY 329
Db 264 VTQSESGVSNFAELIVKEPPTIAPPOLLRASTVLLIOLNANSIIGDOPVIRKIEY 323
Qy 330 RMTSGSWETHAVNAPTYKMLHLPDDEYEIRVLLTRPGEGLTGPPLLTRTKCAEPM 389
Db 324 RMTSGPSEVHAVNMQTYKMLHLPDDEYEIRVLLTRPGEGLTGPPLISRTKCAEPM 383
Qy 390 RTPKTLIAEIQARRIADVHESLGNITRCHTFNWTICYHYF--RGHNSRADCLMDMPK 447
Db 384 RAPKGLAFSEIQSRLQTLQWEPGLNYLTRCHTYSVSLCYRYLVGSLNQTFRECAKMER 443
Qy 448 APOHVAHLPPYTNVSLKMLITNPEGRKESEETIIQDDEVPGVPVVKSLQGTSEFNKIP 507
Db 444 ANRTIKNLLPYRNIHVKLLISNPEGRKEGKVTFQDDEVPGGIASESLTFTPLEDMIF 503
Qy 508 LNKKEPLENGIITQYEYSXSSIRSFDPVAVAGPQPTVSLMNSTHHVFMHLHPGTTYQ 567
Db 504 LKWEPEVPEGLIITQYEISYQSISSDPANVPGPRRTVSKLRNETHVFSNLHPGTTYL 563
Qy 568 FFIRASTVKGEPATATNVTNISAPSLPDYEGVDASINETAATTITVLLRPAQAKGAPIS 627
Db 564 FSVRAARTKGFGQALTAEITTNISAPTF-DYGDMPSPGLSESTITVLLRPAQGRGAPIS 622
Qy 628 AYQIVVQLPHRTRKAGAMECYQVPTVYONALSGGAPYVFAALPPGNLPPEPAPTVG 687
Db 623 TYQVIVEDPRKIKRELGGQECFPVLPITFDDAMSRGSHVHFGAELPASSUTEAKPTVG 682
Qy 688 DNRTYKGFNPPLAPRGYNIYFOAMSSVEKETKTQCVRIATKAATAEETEEVDPDAKQT 747
Db 683 DNQYSGVNPPLPEKKAYLIYFOAMSNLKGTELNCIRIARKAACKESKPL-EVSQHS 741
Qy 748 DRVVKIAGISA-GILVFIILLVIVIVKSKLAKKRDAMGNTRQEMTHVMNAMDYSYA 806
Db 742 EEMGLILGICAGGLVLLIILGAIIVIRKGPVNMTK-ATINVRHEKTHMSAIDRSFT 800
Qy 807 DQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPTAVLDENHSATAESRLL-DVPRYLCEG 865
Db 801 DQSTLQEDERLGLSFMDSHNSR-----GDORSVNVNSSLGSPRRQGR 849
Qy 866 TESPYQTGQLHPAIRVADLLQHINLMKTSDSYGKBEYSEFQGSASWDVAKKQDNRAK 925
Db 850 KGSPIHTGQLHPAVRVADLLQHINQMKTAEYGFQBEYSEFFEG----WASKK-KDKTK 904
Qy 926 NRYGNIITAYDHSRVILOPVEDDPSSDIYANIDYLRDGYORPSSHYIATQGPVHETV 985
Db 905 GRQDHVSTYDRHVKLHPLLDGPNDSVINANYI-----DGYHRSNHFIAITQGPKEQMVY 958
Qy 986 DFWRMWQESACIWMVNLVCEVRVKCYKWPDDTEVYGFKTCVMEPELAYVVRTF 1045
Db 959 DFWRMWQECSSIVMTIKLVEGRVKCSKWPDDSEMYGDIKTLVKSEKLAEYAVRTF 1018
Qy 1046 TLERRGYNEIREVKQFHTGVPDGVPHATGLLSFIRRVKLSNPPSAGPIVVHCSAGAG 1105
Db 1019 ALERGVYSARHEVVKQFHTSWPEGVPHATGLLAFIRRVKASTPPDAGPIVHCSAGTG 1078
Qy 1106 RTGCVIIVIDIMLDAEREGVVDIYCNVKALSRIRNMVQTESEQYIFIHDAILEACLCGET 1165
Db 1079 RTGCVIIVLDMDAECEGVVDIYCNVKTLCSRRINMIQTESEQYIFIHDAILEACLCGET 1138
Qy 1166 AIPVCEKAAFYDMIRDSQTNLSHLKDEFTLNSVTPRLQAECDSCATCLPRNHDKRFM 1225
Db 1139 SIPASEFPKTYKEMVRIEPOSNSQLREEFQTLNSVTPHLDVERCSIALLPNRNRNRS 1198

Qy 1226 DMLPPDRCLPLITIDGESSNYINAAWLDSTYQPAAFIVTQYPLPNTVQFWRLVYDYG 1285
Db 1199 DVLPPDRCLPLISVDGDSNNYINAAWLDSTYKSAAFIVTLHLPLQNTTDFWRLVYDYG 1258
Qy 1286 TSIVMLNEVDLSQ--CPOYWPBEGMLRGPIQVECKMSCMDCDVINRFRICNLTRPO 1342
Db 1259 TSIVMLNQLNOSANPCLQYWPBEGMLRGPIQVECKMSCMDCDVINRFRICNLTRLO 1318
Qy 1343 EGYLMVQOQFOYLWASHREVPVSGSKRSLKLITQVEKQWEECEGEGRITIIHCLNGGGRSG 1402
Db 1319 EGHLMVRFQYLRNSAYEDTFDSKSLHLHLLAQVERWQK--ESDGRVTVHCLNGGGRSG 1376
Qy 1403 MFCAIGVIVEMVRQNVVDVHFAVTKLRLNKNPNVVEAPEQYRPFYCDVALEYLES 1456
Db 1377 TYCASTMILEMIKHNADIFYAAKTLRLNKNPNVVEAPEQYRPFYCDVALEYLES 1430
RESULT 10
O00197 PRELIMINARY; PRT; 1436 AA.
AC O00197;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor protein tyrosine phosphatase hPTP-J precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skelletal muscle;
RX MEDLINE=9723402; PubMed=9070223; DOI=10.1006/bbrc.1997.6004;
RA Wang B., Kishihara K., Zhang D., Hara H., Nomoto K.;
RT "Molecular cloning and characterization of a novel human receptor
RT protein tyrosine phosphatase gene, hPTP-J: down-regulation of gene
RL expression by PMA and calcium ionophore in Jurkat T lymphoma cells.";
RL Biochem. Biophys. Res. Commun. 231:77-81(1997).
DR EMBL; J07327; AB51343.1; -.
DR IPIR; J07327; J07327.
DR HSP; P28827; IRPM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3_3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIIL.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTEC; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00740; MAM; 1; 1.
DR PROSITE; PS00060; MAM; 2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolase; Receptor; Signal.

FT SIGNAL 1 18 Potential.
FT CHAIN 19 1436 receptor protein tyrosine phosphatase
FT hFTP-J.
SQ SEQUENCE 1436 AA; 161092 MW; C05B86FF7A9412D9 CRC64;
Query Match 59.1%; Score 4619; DB 2; Length 1436;
Best Local Similarity 60.4%; Pred. No. 1.6e-303;
Matches 866; Conservative 203; Mismatches 329; Indels 36; Gaps 12;
QY 32 AGGCTFD--DGPAGCDYHQDLYDDFEWVHVSAQEPHYLPPEMPGSGYMWVDSNHDPE 88
DB 24 AAGCTFEASDPAVCEYSQAQYDDQWEQVRHFGTRAPADLPHGSYLVMTVSHAPGQ 83
QY 89 KARLQLPWKENDTHCIDFSLYLSQKGLNPGTINILVRNKGPLANFIMVNTGTRDM 148
DB 84 RAHVIFQISENDTHCVQFSLYSRDGHSPGTLGVYRVVNGPGLGSVANNMTSGHGRW 143
QY 149 LRAELAVSTFWNEQVIFEAESVGRSGYIAIDDIQVLSYPCDKSPHFLRLGDVEVNAG 208
DB 144 HQAELAVSTFWNEQVIFEAELISDRRGYMGDLIDILLSVPCAKAPHSRLGDVEVNAG 203
QY 209 QNATFCIATGRDAVHNKMLQRRNGEDIPVAQTKNHNRRPAASFRLOEVTKTDDLYR 268
DB 204 QNASFCMAAGRAEAERFLQROSGALVPAAGVRHISHRRFLATFPPLAAVSRAEQDLYR 263
QY 269 CVTQSERGSCUNFAQLIVREPRPIAPOLLICVGTPTVLLIQLNANSIIGDPIILKEVE 328
DB 264 CVSQAPRGAGVSNFAELIVKEPPTIAPPQLLRAGPTVLIQLNNTSIIGDPIVKEIE 323
QY 329 YMTSGSTETHAVNAPTVMKWLHDPDTEYERVLTLTRPGEGTGLPGPPLITRTKCAEP 388
DB 324 YMAEGPNAEVAVSLQTYKMLHLPDTEYELSVLTLTRPGDGTGRPGPPLISRTKCAEP 383
QY 389 MRPKTLKIAEQARRIADVMSLGNITRCHTFNVTICYHYFRG--HNESRADCLMDP 446
DB 384 MRAPKGLAFAEIQAQLTLQWEPLGVNTRCHTYSVSLCYHTVLTGSSHNQIRECVKTEQ 443
QY 447 KAPQHVNHLPYTVNLSKMLTNEGRKESSEITIIQDDEVPVPVKSLOGTSFENKI 506
DB 444 GVSRTYKLNLPYRNHVHLVLTNEGRKEGKEVTFQDDEVPFGIAAESLTFTFLEDMI 503
QY 507 FLNWKPELEPNGIITQYEVSYSSIRSDPAVPVAGPQTVSNLWNTSHRVFHLHPGTTY 566
DB 504 FLKWEPPQPNGLITQYELISYQSISSDPAVNVPGPRTISKLNETHVFSNLHPGTTY 563
QY 567 QFFIRASTVKGCPATINVTNINSAPSLPDYEGVDASLNETATTITVLLRPAQAGAPI 626
DB 564 LFSVRAATKGFQAALTBITTNISAPSF-DYADMPSPLGESENTITVLLRPAQGRGAPI 622
QY 627 SAYQIVVEQLHPHRTKREAGMECYQVPTYQNALSGGAPYFAAELPGNLPPEAPPTV 686
DB 623 SVYQVIVEERARRURLEPGGQDCFPVPLTFAALARGHLVFGAELAASSLPEAMPPTV 682
QY 687 GNRNRYKGNWPNPLAPRKGNINYIFQAMSVKXETKTCQVRIATKAAATEEPEVIPPAPQ 746
DB 683 GNGQTYRGFWNPPLERKXAYLYFQAASHLKGDTLNCIRIARKACKESKPL-EVSOR 741
QY 747 TDRVVKIAGISA-GILVFIILLLLWIVIVKSKLAKRKDAMGNTRQEMTHVMVNAWDRSY 805
DB 742 SEEMGLILGICAGGLAVLILLGAILIIVIRKGPVNMVK-ATVNYRQEKTHMWSADVRSF 800
QY 806 AQOSTLHAEEDPLSLTMDQHNFSRPLPNDPLVPTAVLDENHSATAESRL--DVRPLYCE 864
DB 801 TDQSTLQEDERLGLSPMDTHGYSTR-----GQDRSGGVTEASLSLGGSPRRPGC 849
QY 865 GTESPYOTQOLHPAIRVADLLOHINLMKTSDSYGFKEEYESFFEGQSGASWDVAKDQNR 924
DB 850 RKGSPTHQOLHPAVRVAADLLOHINQMKTAGYGFKEEYESFEG----WDATKKDKVK 905
QY 925 KNRGNIATYDHSRVILQPVEDDPSDYINANYIDIWLRYDGYQRPVSHVATQGPVHETV 984
DB 906 GSRQEPMPAYDRHRVKLHMLGDPNADYNANYI-----DGYHRSNHPFIATQGPKEPV 959

QY 985 YDFRMVWYQEQSACIVMVTNLVEGRVKCYKYVPPDDTEVYGDVKTCVMEPLAEYVVRT 1044
DB 960 YDFRMVWYQEQHSSIVMITKLVEGRVKCSRYNWDSDTYGDIKIMLVKTTAEYVVRT 1019
QY 1045 FTLERRGYNEIREVKQFHTGWPDPGHVPYHATGLLSFIRRVKLSNPSPSAGPIVHCSAGA 1104
DB 1020 FALERRGYSARHEVRQFHTAWPEHGVYHATGLLAFIRRVKASTPPDAGPIVHCSAGT 1079
QY 1105 GRTCYIVIDIMLMDAEREGVDIYNCKALRSBRINNVQTEEQYIFTHDAILEACLCGE 1164
DB 1080 GRTCYIVLVDMLDMAECGVVDIYNCKTLCRSRVNMIQTEEQYIFTHDAILEACLCGE 1139
QY 1165 TAIPTVCFKAAYPOMRIDSTNSHLKDEPOTLNSVTPRLQAEDCSACIAPRHHDKNRF 1224
DB 1140 TTIPVSEFKATYKEMIRIDPQSNSSQLREEFQTLNSVTPPLDVECSIALPRNEDKNRS 1199
QY 1225 MDMLPPDRCLPFLITIDGESNNYINAAIMDSYRQAPAPIVTOYPLPNTVKDFWRLVYDG 1284
DB 1200 MDVLPDRCLPFLISTDGSNNYINAAITDSYTSAAPIVTLHPLQSTTPDFWRLVYDG 1259
QY 1285 CTSIWMLEVDLSQ---CPQYWPBEGMLRVGPITOECMSCMDCDVINRFRICNLTRP 1341
DB 1260 CTSIWMNLQNLQNSAWPCLQYNPEPGRQYGLMEVFMSGTADLVARVFRVQNISRL 1319
QY 1342 QEGVLMYQFOYLGWASHREVPVSGRSFKLILQVEKMQEBCGEGRITIIHCLNGGGRS 1401
DB 1320 QEGHLLVNHVFOFLWSAYRDTDPDSKAPFLHLLAEVDKQW--AESGDGRTIVHCLNGGGRS 1377
QY 1402 GMFCAIGIVEMVVRQNVVDVHVAVKTLRNSKPNMVEAPEQYRFCYDVALEYL 1455
DB 1378 GTFCACATVLEMRCHNLVDVFFAAKTLRNYKPNMVTMDQYHFCYDVALEYL 1431
RESULT 11
Q92850 PRELIMINARY; PRT; 1436 AA.
AC Q92850;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor protein tyrosine phosphatase psi.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Banville D., Masson S., L'Abbe D., Stocco R., Shen S.-H.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00289; AAB07074.1; -.
DR HSP; P28827; IRPM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF0102; Y_phosphatase; 2.
DR PRINTS; PR00014; ENTYPRII.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolase; Receptor.


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DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3.3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEI1.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3.3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS00853; FN3.3.
DR PROSITE; PS00660; MAM 2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydroxylase.
SQ SEQUENCE 1436 AA; 161157 MW; 8D406DE4948643FF CRC64;

Query Match      58.98; Score 4597; DB 2; Length 1436;
Best Local Similarity 60.08; Pred. No. 4.9e-302;
Matches 861; Conservative 208; Mismatches 330; Indels 36; Gaps 12;

QY 32 AGCTFDGPG---ACDYHODLYDDFEWVHVSQAEPHYLPPEMPOGSMVYVDDSNHDPGE 88
DB 24 AAGCTFEASDPVPCFEFSQAQYDDFQEQVIRHPGTRTPEDLPHGAYLWVNASQAPQG 83
QY 89 KARLQPTMKENDTHCIDFSYLSYQKGLNPGLTILNLRVKNKGLPLANINVTGFTGRDW 148
DB 84 RAHIIIFQTLSENDTHCQVFSYLYSRDGHSGPTLGVVYRVNGGPGLSAVNMWMTGSHGQW 143
QY 149 LRAELAVSTWPNQYQVIFEAVSQSGSGYIAIDDIQVLSYPCDKSFHFLRLGDVEYNAG 208
DB 144 HQAELAVSTWPNQYQVIFEAISPDHKGITGLDILLFSYPCAKAPHFSRLGDEYNAG 203
QY 209 QNATFOCIATGRDAVHNKMLQRRNGEDIPVAOTPKNINHRFFAASPRQLQVTKDQDLYR 268
DB 204 QNASFCQMAAGRAAEHFFLQKQSGVLVPAAGVRHISHRRFLATFFLASVGRSEQDLYR 263
QY 269 CVTQSERGSGVNSPAQLIVREPPIAPPOLLQGVGPTLLIQLNANSIIGDGPILKEVE 328
DB 264 CVSQAPRGAGVNSFAELIVKEPPTPIAPPOLLQVRAGPTLLIQLNANSIIGDGPVIRKEIE 323
QY 329 YRMTSGSWTETHAVNATPYKLWHLDPDTEYIEIRVLLTRPGEQGLPGPPLITRTKCAEP 388
DB 324 YRMARGPWAHVAVNLQTKLWHLDPDTEYIEISVLLTRPGDGGTGRPGPPLISRTKCAEP 383
QY 389 MRPKTLKIAEQARRTAVDWESIGYNTSCHFNVTICVHYPRG--HNESRADCLMDWP 446
DB 384 TRAPKGLAFAEIQARQULTQWEPYGVNTRCHTVAVSLCYRYTLGGSHNQTIRECVKMER 443
QY 447 KAPQHVNVHLPPYTNVSKMLINPEGRKESEETIIQTDDEDVPGVPVVKSLQGTSEFNKI 506
DB 444 GASRYTIKNLLPFRNIHVRLILNTPGKGEKVTFQTDDEDVPGGIAESLTFTPLEDMI 503
QY 507 FLNWKPLENGIITQEVSYSSIRSPDPAVPVAGPQPTVSNLWNSHTHVFMHLHPGTTY 566
DB 504 FLKWEPEQEPNGIITQEVSYSSQTESDPAVNVPGPRTTISKLRNETHYVFSNLHPGTTY 563
QY 567 QFFIRASTVKGFGPATINVTNLSAPSLPDYEGVDASINETATITIVLARPAQACAPI 626
DB 564 LFSVRAKTSFGGQAALTEITTNISAPSF--DYADMPSPGSESENTITVLLRPAQGRAPI 622
QY 627 SAYQIVVQEQHPHRTKREAGACEYQVPVTVYQNALSGCAPYFAAELPPGNLPEPAPFTV 686
DB 623 SVTVQVVEBERPRLRREPQAGQCFVPLTFETALAGLVHYFGAELAAASLLEAMPFTV 682
QY 687 GDNRTYKGFNPPPLAPRKGYNIYFQAMSSVEKTKTQCVRATKAAATEPEVIPDPAKQ 746

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RESULT 14

P70125

ID P70125 PRELIMINARY; PRT; 1436 AA.

AC P70125;

DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Receptor protein tyrosine phosphatase-lambda.

GN Name=Ptpu; Synonyms=ptp-lambda;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Cheng J., Armanini M., Phillips H., Dowbenko D., Daimaru L.,

RA Lasky L.A.

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U55057; AAB17895.1; -.

DR HSSP; P28827; 1RPM.

DR MGD; MGI:1321151; Ptpu.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR000998; MAM.
 DR InterPro; IPR000387; TYR phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00629; MAM; 1.
 DR Pfam; PF00102; y_phosphatase; 2.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 3.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00137; MAM; 1.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00853; FN3; 3.
 DR PROSITE; PS00600; MAM 2; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
 KW Glycoprotein; Hydrolase; Receptor.
 SQ SEQUENCE 1436 AA; 161199 MW; EFFAAE52C6903F02 CRC64;

Query Match 58.8%; Score 4591; DB 2; Length 1436;
 Best Local Similarity 59.9%; Pred. No. 1.2e-330;
 Matches 859; Conservative 210; Mismatches 330; Indels 36; Gaps 12;

QY 32 AGGCTFDDGPG---ACDTHQDLYDDFWVHYSAQBPVLPPEMPOGSMYVDSSNHDGPE 88
 DB 24 AAGCTFEASDPVPCFSQAQYDDFQNEQVRIHFGTTPEDLPAGVLMWNASQHTFGQ 83
 QY 89 KARLQPTMKENDTRCIDFSYLLYSQKGLNPGTILNVLVKNKGLPIANPIWVNTGTGRDW 148
 DB 84 RAHIIIFQTLSENDTHCVQFSYFLYSRDSGHSPTGLGVVYVKNVGGPLGSVAVNMTGSHGRQW 143
 QY 149 LBAELAVSTFWPNEQVIFEAUSGGRGYTAIDDIQVLSYPCDKSPHFLRLGDVEVNAAG 208
 DB 144 HQAELAVSTFWPNEQVIFEAUSGGRGYTAIDDIQVLSYPCDKSPHFLRLGDVEVNAAG 203
 QY 209 QNATFQCIATGRDAVHNKMLQRRNGEDIPVAQTKNINHRFAASFRLEQVTKDQDLYR 268
 DB 204 QNASFQCHWAGRAAEHFFLQSQGVLPAGVGHISHRRFLATFPLASVGRSQDLYR 263
 QY 269 CVTQSGRSGVSNFAQLIVREPPRIAPQLLGVGPTYLLIQLNANSIIGDGPILKVEVE 328
 DB 264 CVSQAPRGAGVSNFAELIVKEPPTPIAPQLLRAGPTVLIQLNTNSIIGDGPVIRKEIE 323
 QY 329 YMTSGSWTETHAVNAPTKLWHLDPDTEYERVLTRPGEGTGLPGPPLITRCKAEP 388
 DB 324 YRMARGPWAHVAVNLQTYKLWHLDPDTEYERVLTRPGEGTGLPGPPLISRTCKAEP 383
 QY 389 METPKTLTAETQARRIAVDWESLGNITRCHTFENVITCYHYFRG--HNESRADCLMDP 446
 DB 384 TRAPKGLAPAEIQAQLTLQNEPLGVNTRCHTYAVSLCYRTLGSNQTIRECVKWER 443
 QY 447 KAPOHVNHLPPYTNVSLKMLTNPGRKSEBETIIQTDEDPGPPVPVKSLQGTSPENKI 506
 DB 444 GASRYTIKNLLFPRIHVRILLTNPGRKEGKVEVTFQTDDEPVGGLAAESLFTPLEDMI 503
 QY 507 FLNWKPEPLNGLIITQYEVSYSSISRFDPAVPAGPQTVNLMWSTHVFVHLLPGTYY 566
 DB 504 FLKWEPEQPNGLIITQYEVSYSSISRFDPAVPAGPQTVNLMWSTHVFVHLLPGTYY 563
 QY 567 QFFIRASTVKGFGPATAINVTNINAPSPLDYGVDASLNATATTITVLLRPAQAKGAPI 626
 DB 564 LFSVARTSKRGQAALTEITTNISAPSF-DYADMPSPLGESENTITVLLRPAQGRGAPI 622

QY 627 SAYQIVVQQLPHRTKREAGAMECYQVPTVYQNALSGAPYFAAEPLPGNLPAPPTV 686
 DB 623 SVYQVVVEERPRRLRREPQAGQCFSLPITFETALRGLVHYFGAEAAASLLAMPFTV 682
 QY 687 GDNRTYKGFNPPPLAPKGYNIYFQAMSSVKEKTKTCQVRIATKAAATEEPEVDPFAKQ 746
 DB 683 GDMQTYGFWNPPLEPKAYLIVFQAASHLKGTRLCINRIARKAACKESKRPL-EVSR 741
 QY 747 TDRVVKIAGISA-GILFIILLVIVVVKSKLAKRKKDAMGNTRQEMTHWVAMDRSY 805
 DB 742 SEEMGLILGICAGGLAVLILLGAILIIRKKGPNMTK-ATVNYROEKTHMSAVDRSF 800
 QY 806 ADQSTLHAEDPLSLTMDQHNFSRPLNDPLVPTAVLDENHSATAESRLL-DVPRYLCE 864
 DB 801 TDQSTLQEDERLGLSFMDAPGYSR-----GDQRGGVTEASSLGGSPRRPCG 849
 QY 865 GTESPYQTQLHPAIRVADLLQHINLMKTSDSYGFKEEYESFFEGQSASMDVAKDQNR 924
 DB 850 RKGSPYHTGQLHPAVRVADLLQHINQMKAEGYGFQKQYESFFEG---WDATKKDKLK 905
 QY 925 KNRGNIIADHSRVILQPVEDDPSSDIYINANYIDIMLYRDGYORPSHYIATQPVHETV 984
 DB 906 GGRQEPVSAYDRHHVHLHPMLADPDADYISANYI-----DGYHRSNHFIIATQGPKEMI 959
 QY 985 YDFWRWYQBSACIWMVTNLVEGRVKCYKYPDDTEVYGDGFKVTCVEMEPLEAYVVRT 1044
 DB 960 YDFWRWYQBSACIWMVTNLVEGRVKCYKYPDDTEVYGDGFKVTCVEMEPLEAYVVRT 1019
 QY 1045 FTLERRGYNEIREVKQHFHTGWPDPHGVPIYHATGLLSFIRRVKLSNPPSAGPIVHCSAGA 1104
 DB 1020 FALERGYSAHREVQHFHTAWPEHGVPIYHATGLLAFIRRVKASTPPDAGPIVHCSAGT 1079
 QY 1105 GRTCYIVIDIMDMAEREGVVDIYNCVKALRSRRINNVQTEQYIFIHDAILEACLCGE 1164
 DB 1080 GRTCYIVLDVMDMAECEGVVDIYNCVKALRSRRINNVQTEQYIFIHDAILEACLCGE 1139
 QY 1165 TAIPVCEFAAYFDMIRIDSQTSNLSHLKDEPQTLNSVTPRLOAEDCSACLPRNHDKNRF 1224
 DB 1140 TTIPVNEFRATYREMIIDPQSSQSUREEFTLNSVTPRLOAEDCSACLPRNHDKNRS 1199
 QY 1225 MDMLPPRCPLPFLITIDGESSNYNAALMDSYROPAAFIQYPLPNTVKDFWRLVYDYG 1284
 DB 1200 MDVLPDRCLPFLISSDGPNNYNAALTDSTYSAAFIVTLHPLOSTTPDFWRLVYDYG 1259
 QY 1285 CTSIVMLNEVDLSQG---CPQYWPBEGMLRYGPIQVECMSCMCDVINRIFRICNLTRP 1341
 DB 1260 CTSIVMLNQLNQSNSAWPCLQYWPBEGRQQYGLMEVEFVSGTANEDLVSRVFRVQNSRL 1319
 QY 1342 QEGYLMVQOFOYLGNASHREVPGSKRSFLKLLQVEKMQBCECEGERTIICHLNGGGRS 1401
 DB 1320 QEGHLLVRHFQFLRWSAYRDTFDSRKAFHLHLAEVDKMQ--AESGDGRTVVHCLNGGGRS 1377
 QY 1402 GMFCAIGIVBWKRONVVDVFAVKTLRNSKPNMVEAPEQYRCFYCDVALEYLES 1456
 DB 1378 GTFCACATVLEIRCHSLVDVFFAKTLRNYKPNMVEVTDQYHFCDYDALEYLEA 1432

RESULT 15
 PTPT_MOUSE
 ID_PTPT_MOUSE STANDARD; PRT: 1454 AA.
 AC Q99M80; Q99M81; Q99M82; Q9JIZ1; Q9JIZ2; Q9JKC2; Q9JLPO;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)
 DE (R-PTP-T) (RPTP-rho) (mRPTrho) (RPTPmam4).
 GN Name=PtpT;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]


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FT VARSPLIC 1007 1007 /FTid=vsp 007805.
FT R -> RHPAETHVGTATIGRAASPCM (in isoform
FT 2).
FT CONFLICT 13 16 /FTid=vsp 007806.
FT CONFLICT 21 21 Missing (in Ref. 1).
FT CONFLICT 34 37 R -> P (in Ref. 1).
FT CONFLICT 87 87 GCSC -> RGVP (in Ref. 1).
FT CONFLICT 254 254 A -> T (in Ref. 4; AAF82401).
FT CONFLICT 266 266 A -> S (in Ref. 4; AAF82401).
FT CONFLICT 602 602 I -> V (in Ref. 4; AAF82401).
FT CONFLICT 822 822 T -> S (in Ref. 4; AAF82401).
FT CONFLICT 825 825 A -> T (in Ref. 4; AAF82401).
FT CONFLICT 844 845 G -> S (in Ref. 4; AAF82401).
FT CONFLICT 1016 1016 TD -> N (in Ref. 4; AAF82401).
FT CONFLICT 1049 1049 D -> A (in Ref. 4; AAF82401).
FT CONFLICT 1050 1050 Y -> H (in Ref. 1).
FT CONFLICT 1076 1076 H -> N (in Ref. 4; AAF82401).
FT CONFLICT 1103 1103 L -> V (in Ref. 4; AAF82401).
FT CONFLICT 1259 1259 R -> K (in Ref. 1).
FT CONFLICT 1266 1266 F -> L (in Ref. 4; AAF82401).
FT CONFLICT 1269 1269 L -> I (in Ref. 4; AAF82401).
FT CONFLICT 1269 1269 T -> S (in Ref. 4; AAF82401).
SQ SEQUENCE 1454 AA; C60464F7B423F8A8 CRC64;

Query Match 58.6%; Score 4579; DB 1; Length 1454;
Best Local Similarity 57.8%; Pred. No. 8.3e-301; Mismatches 333; Indels 42; Gaps 8;
Matches 841; Conservative 239;

QY 21 PLLGSALQFAGGCTFDGACDYHQDL-YDDFEWVHVSAQEPHYLPPEMPOGSSVMV 79
DB 22 PPLPGAGQAQAGGCSFDEHVSNCYSVALGTNGFTWEQINTWEKPMPLDPAVPTGSMV 81

QY 80 DSSNHPGKARLQLPWKENDTHCIDFSYLLYSQKLNPGTLNLVWVKNKGPLANPIWN 139
DB 82 NSSGRASGOKAHLPLTKENDTHCIDPHYFSSDRSGPAGNALVYVKNVGGPQGNPVNM 141

QY 140 VTGFTGRDMLRAELAVSTFWPEYQVIFPEAEVSGSGSYIAIDDTQVLSYPCDKSPHLR 199
DB 142 VSGVTEGWKVAELAISTFWPHFYQVIFESVSLKGHPGYIAVDEVRVLAHPCRKAPHFLR 201

QY 200 LGDEVNAGQATFOCIATGRDAVHKNLWLRNGEDIPVATQKNHRRFAASPRLOEV 259
DB 202 LQNEVNVQATFOCIAGGKWSQDKLWQWNGRDTALMVRVNVNRRFSATVSVADT 261

QY 260 TKTDQDLRCVTSQSRGVSNAFQILVREPRPIAPQLLGVTYLLIQLNANSIIGD 319
DB 262 SQRISIKYKCVIRSDGSGVSNAELIVKEPPTIAPPELLAVGATYLWIKPNANSIIGD 321

QY 320 GPIILKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYRVLTRPGEGGTGLPGPPL 379
DB 322 GPIILKEVEYRTTGTWABTHIVDSFNPYKLMHLDPDVEYRVLTRPGEGGTGP GPPL 381

QY 380 ITRTKCABPMRPTKTLKAEIOARRIADVWESLGNITRCHTFNVITCVHYFRGHNESRA 439
DB 382 TRTKCABDPVGPQNVIEIVDRQITLQWEPFGVAVTRCHSYNLTVQYQV--FNQOQY 439

QY 440 DCLDMDPKAPQHVNVHLPPTYNVLSUKMLITNPEGRKESEETIQTDEDVPGVPVKSQ 499
DB 440 EAEVEIQTSSHVTLRGLRPFMTIRLLLSNPEGRMESEELVVQTEEDVPGAVPLESIQ 499

QY 500 TSPENKIPLNWKEPLEPGNIIITOYEVSYSSTRSPDPVAVPGPPQTVSNLWNSTHVPMH 559
DB 500 GPFEKIVIQWPPNETNGVITLYINYKAVGSLDPSADLSSQKGVFKLRNETHFLFVG 559

QY 560 LHPGTYTOFFIRASTVKGFPATANVTNINISAPSLPDYEGVDASINETATTITVLLRPA 619
DB 560 LYPGTYTFTIKASTAGKGGPPVTRIAIKISAPMPEYD-ADTFLNETDTITVMLKPA 618

QY 620 QAKGAPI1SAYQIVBQLPHRTRKRBAGAMECYQVPVTTYONALSGGAPYFFAAELPPGNLP 679
DB 619 QSRGAPVSVYQLVWKEERLQKRRADIIECFSPVSVRNASNLDSLHYFAAELKPSNLP 678
QY 680 EPAPTVGDNRTYKGFNWPPLAPRKGYNITVFOAMSSVEKETKTQCVRATKAAATEEP 739
```

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DB 679 VTQPFVTGDNKTYNGYWNPPSLPKSYIIFQALSKANGETKINCVRLATKAGPMGSAQV 738
QY 740 IP-----DPAKQTRVVKIAGISAGILVFIILLVIVIVIVVIVVIVVIVVIVVIVV 781
DB 739 TPGTPPLCLLTASTQNSNTVEPEKQVDNTVMAGVIAGLLMFIILLGVMLTIKRRKLAK 798
QY 782 KRKDMAGNTRQEMTHMNMADRSDADQSTLHAEDPLSLTFMDQHNFSRPLFNDPLVPTAV 841
DB 799 KQKETQSGAOREM-GPVASTDKPTAKLGTNRNDEGFSSSQDVNGFTDGSRGELSQTFLT 857
QY 842 LDENHSATBESSRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHLINMLKTSDSYGFKE 901
DB 858 I-QTH-----PYRTCDPVMSYPRDQQAIRVADLLQHLITOMKRGQGYGFKE 904
QY 902 EYESFFEQSASWDVAKQONRAKNRYGNIITAYDHSRVILQFVEDDPSDDSYINANYIDW 961
DB 905 EYEALPEGQTASWDATAKEDENRNKNRYGNIISYDHSRVLLVLDGDPHSDSYINANYI--- 961
QY 962 LYRDGQRPISHYIATQGVPHETVYDFWRMWOESACIVMTNLVVEGRVKCYKWPDDT 1021
DB 962 ---DGYHRPHRYIATQGMQETVXDQFWRMIWQENSASIVMWVNLVVEGRVKCYKWPDDT 1018
QY 1022 EYVGDEKVTCEMEPLAEYVYVTRFTLERRGYNEIREVKOPHFTGPDHGVPHATGLLSF 1081
DB 1019 EYVGDIKVTIETPLAEYVIRFTVQKKGYHEIRELRFLFTSWPDHGVPCYATGLLGF 1078
QY 1082 IRRYKLNPPFSAGPIVHCSAGAGTCYIVIDIMDMAEREGVVDIYNCVKALRSRIN 1141
DB 1079 VRQVKFLNPPBAGPIVHCSAGAGRTGCFIAIDTMDMAENEGVVDIENCVRELRAQRVN 1138
QY 1142 MVQTEBOYIFHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTSNSSLKDEPOTLNSV 1201
DB 1139 LVQTEBOYVFDHDAILEACLCGNTAIPVCEPRSYINISRLDPQTSNQQIKDEPOTLNV 1198
QY 1202 TPLQAEDCSFACLPNRHDKNRFMDLPPDRCLPFLITIDGESSNYINAAIMDSVRQPA 1261
DB 1199 TPRVRPDCSGLLPNRHDKNRSMDVLPDLRCLPFLISVDGESSNYINAAIMDSHQPA 1258
QY 1262 FIVTQYPLPNTVKDFWRLVVDYDGTCTSVMLNEVDLSQGCQYWPBEGMLRYGPIQVECMS 1321
DB 1259 FVVTQHPPLPNTVADFWRLLVDFDNCSSVVMLENDTAQLCMQYWPBKTSGCYGPIQVEFVS 1318
QY 1322 CSMDCDVINRIFRINLTPRQEGHLMVQOQFOYLGWASHREVPBGSKRSFLKLILQVEKQ 1381
DB 1319 ADIDEDITHIRIFRICNMRARPODGYRIVQHLQYIGWPAYRDTPPSKRSLLKVVRLKQ 1378
QY 1382 BCEBEGRTIITHCLNGGSGMFCAGIGIVBVMKQNVVDVFAVKTLLRNSKPNMVEAPE 1441
DB 1379 QYDREGRTVVHCLNGGSGRTFCAICSVCEMIQQNIIDVFIHVKTLLRNNKSNMVE 1438
QY 1442 QYREFCYDVALEYLES 1456
DB 1439 QYKFVYVVALEYLSS 1453
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Search completed: June 1, 2005, 13:55:00
Job time : 177.044 secs

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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:31:52 ; Search time 145.589 Seconds
(without alignments)
3822.724 Million cell updates/sec

Title: US-09-887-669-2
Perfect score: 7709
Sequence: 1 MDITAAALPAFVALLLSP.....EAPQRFYCDVVALEYLESS 1439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7692	99.8	1439	2	AAR63632 Human rec
2	7688	99.7	1439	7	ADJ68478 Human hea
3	7656.5	99.3	1440	2	AAY29591 Human pro
4	7656.5	99.3	1440	8	ADI23886 Human PTP
5	7571	98.2	1457	5	ABB57308 Mouse isc
6	7524	97.6	1457	2	AAR63633 Murine re
7	7174	93.1	1407	2	AAR63631 Murine re
8	4818	62.5	1452	4	AAM79159 Human pro
9	4807	62.4	1452	8	ADI80761 Human pro
10	4806	62.3	1452	6	ABR58629 Human can
11	4784	62.1	1452	7	ADJ68277 Human hea
12	4777.5	62.0	1455	4	AAM80143 Human pro
13	4602.5	59.7	1436	7	ADB79775 Rat putat
14	4586.5	59.5	1436	2	AAM41361 Receptor
15	4575.5	59.4	1462	5	ABB97521 Novel hum
16	4564	59.2	1463	6	ABJ37035 Human bre
17	4564	59.2	1463	7	ADB75519 Prostate
18	4564	59.2	1520	5	ABJ05584 Breast ca
19	4555	59.1	1499	4	AAM25768 Human pro
20	4374.5	56.7	1442	7	ADJ68999 Human hea
21	4287	55.6	1430	2	AAM49907 Human pan
22	2493.5	32.3	623	4	AAM25675 Human pro
23	2210.5	28.7	815	4	AAM25875 Human pro
24	1529.5	19.8	1501	2	AAR72858 Rat recep
25	1513	19.6	1254	8	ADN02662 Liver dis

26	1512	19.6	1796	6	AAE37971 Human kin
27	1509	19.6	1897	3	AAY81785 Human pro
28	1509	19.6	1897	3	AAY56100 LAR tyros
29	1509	19.6	1897	3	AAB19712 Human pro
30	1509	19.6	1897	7	ADD18740 Human dis
31	1509	19.6	1897	8	ADJ33670 Human leu
32	1509	19.6	1907	8	ADP18674 Human pro
33	1506.5	19.5	1266	8	ADQ66041 Novel hum
34	1506	19.5	1948	7	ADD18742 Human dis
35	1505.5	19.5	1907	4	AAU14143 Human nov
36	1505.5	19.5	1912	8	ADR40183 Human pro
37	1505	19.5	1949	7	ADE57117 Human pro
38	1505	19.5	1949	7	ADE57121 Human pro
39	1505	19.5	1949	7	ADD47019 Human pro
40	1505	19.5	1949	7	ADD47015 Human pro
41	1493	19.4	1291	2	AAR75201 Tyrosine
42	1491	19.3	1495	5	ABB57380 Rat mucoc
43	1491	19.3	1496	7	ADE57115 Rat Prote
44	1491	19.3	1496	7	ADE57119 Rat Prote
45	1491	19.3	1496	7	ADD47013 Rat Prote

ALIGNMENTS

RESULT 1
AAR63632
ID AAR63632 standard; protein; 1439 AA.

XX AC AAR63632;
XX DT 21-OCT-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 26-OCT-1995 (first entry)
XX DE Human receptor-type protein tyrosine phosphatase (RPTP) kappa.
XX DE Receptor-type protein tyrosine phosphatase protein; cellular signal;
XX KW RPTPase-kappa; PTPase.
XX OS Homo sapiens.
XX OS Unidentified.
XX FH Location/Qualifiers
XX Domain 207..277
XX Domain /label = Ig-like domain
XX Domain 755..774
XX Domain /label = alpha helical transmembrane domain
XX WO9424161-A1.
XX PD 27-OCT-1994.
XX PF 20-APR-1994; 94WO-US004377.
XX PR 21-APR-1993; 93US-00049384.
XX PR 01-JUL-1993; 93US-00087244.
XX PA (UTNY-) UNIV NEW YORK MEDICAL CENT.
XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX PI Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;
XX PI WPI; 1994-341769/42.
XX DR N-PSDB; AAQ72913.
XX PT Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)
XX PT protein and DNA - useful to identify cpds. which bind to RPTP-k and
XX PT modulate enzymatic activity. Also inhibition of type II RPTP homo.philic
XX PT binding (Engl).
XX PS Claim 4; Fig 15; 144pp; English.

CC The novel receptor-type protein tyrosine phosphatase protein or
 CC glycoprotein is termed *PTP kappa* (also known as *PTPase-kappa*). Human
 CC breast cancer cell line SK-BR-3 was examined by PCR using primers
 CC corresp. to conserved sequences within the PTP catalytic domain shared
 CC by all identified PTPases. Several known PTPases were revealed together
 CC with some novel members of the PTPase family. One of the novel sequences,
 CC designated MCP7 (Mammary carcinoma-derived PTPase clone 7) was highly
 CC represented in all 121 clones examined. The MCP7 PCR fragment was used to
 CC screen a SK-BR-3 cDNA library. The results are AAQ72913 and its deduced
 CC AA sequence AAR63632. The AA sequence displays the structural
 CC organization of a type II transmembrane PTPase. The N-terminal
 CC hydrophobic stretch of 20-26 AAs is typical of signal peptides. A second
 CC region consisting of hydrophobic residues (see FT) is predicted to be a
 CC single alpha-helical transmembrane domain. It is followed by a short
 CC region of mainly basic residues characteristic of a transfer stop
 CC sequence. The amino-terminal portion of the putative extracellular domain
 CC contains a sequence motif, a so-called WAM domain, spanning a region of
 CC about 170 residues. This motif is followed by one possible Ig-like domain
 CC (see FT). (Updated on 25-MAR-2003 to correct FN field.)

Revised record issued on 21-OCT-2004 : Correction to feature table key

Sequence 1439 AA;

Query Match 99.8%; Score 7692; DB 2; Length 1439;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTTAAALPAFVALLLSPPLIGSAGQSAGGCTFDGPGADYHQDLYDFEWHV 60
 DB 1 MDTTAAALPAFVALLLSPPLIGSAGQSAGGCTFDGPGADYHQDLYDFEWHV 60
 QY 61 SAQEPHYLPPEMPOGQSYMIVDSSDHPGKARLQPTMKENDTHCIDFSYLLSQKGLNP 120
 DB 61 SAQEPHYLPPEMPOGQSYMIVDSSDHPGKARLQPTMKENDTHCIDFSYLLSQKGLNP 120
 QY 121 GTLNTLVRVKGPLANPTVNWVGTGROWLRAELAVSTFWPNEYQVIFEAEVSGRSGYI 180
 DB 121 GTLNTLVRVKGPLANPTVNWVGTGROWLRAELAVSTFWPNEYQVIFEAEVSGRSGYI 180
 QY 181 AIDDIQVLSYPCDKSPHFLRGDGVNAGONATFOCIATGRDAVHVKLWLRNGEDIPV 240
 DB 181 AIDDIQVLSYPCDKSPHFLRGDGVNAGONATFOCIATGRDAVHVKLWLRNGEDIPV 240
 QY 241 AQTQKINHRRFAASFRLOEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPRIAPPQL 300
 DB 241 AQTQKINHRRFAASFRLOEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPRIAPPQL 300
 QY 301 LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 360
 DB 301 LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 360
 QY 361 IRVLLTRPGCGTGLPGPLIIRTKCAEPMRPTKTKIAEIOARRIAVDWESLGYNITRC 420
 DB 361 IRVLLTRPGCGTGLPGPLIIRTKCAEPMRPTKTKIAEIOARRIAVDWESLGYNITRC 420
 QY 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE 480
 DB 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE 480
 QY 481 TTIQTDDEDVPGVPVKSLQGTSTFENKIFLNWKEPLDPNGIITQYEISYSSIRSFDPAPVP 540
 DB 481 TTIQTDDEDVPGVPVKSLQGTSTFENKIFLNWKEPLDPNGIITQYEISYSSIRSFDPAPVP 540
 QY 541 AGPPTQVSNLWNSTHHVFHLLHPGTYQFFIRASTVKGPGPATAINVTNINISAPTLPDYE 600
 DB 541 AGPPTQVSNLWNSTHHVFHLLHPGTYQFFIRASTVKGPGPATAINVTNINISAPTLPDYE 600
 QY 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELPHRTRKREAGAMECYQVPVYQN 660
 DB 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELPHRTRKREAGAMECYQVPVYQN 660
 QY 661 AMSGGAPYYFAELPPGNLPEPAPFTVGNRTYQGFNPPPLAPRKGNYIFYQAMSSVEKE 720

DB 661 AMSGGAPYYFAELPPGNLPEPAPFTVGNRTYQGFNPPPLAPRKGNYIFYQAMSSVEKE 720
 QY 721 TKTQCVRIATKAATEEPEVIPPDPKAKQTRDVVKVIAGISAGILVFIILLVLIWVKSKLA 780
 DB 721 TKTQCVRIATKAATEEPEVIPPDPKAKQTRDVVKVIAGISAGILVFIILLVLIWVKSKLA 780
 QY 781 KKRKDMAGNTRQETHMVMNADRSYADOSTLHAEPLSLITFMDQHNFSPRYENHSATAES 840
 DB 781 KKRKDMAGNTRQETHMVMNADRSYADOSTLHAEPLSLITFMDQHNFSPRYENHSATAES 840
 QY 841 SRLLDVPRYLCEGPESPVQGLHPARVADLLQHILMLKMTSDSYGFKEEYESFEQOSA 900
 DB 841 SRLLDVPRYLCEGPESPVQGLHPARVADLLQHILMLKMTSDSYGFKEEYESFEQOSA 900
 QY 901 SWDVAKKQDNRAKNRYGNIITAYDHSRVILQVEDDPSDDYINANYIDGYQRPISHYATQG 960
 DB 901 SWDVAKKQDNRAKNRYGNIITAYDHSRVILQVEDDPSDDYINANYIDGYQRPISHYATQG 960
 QY 961 PVHETVDFWRMIWQESACIWMVTNLVEGRVKCYKYPDDTEYIGDFKTCVMEPELA 1020
 DB 961 PVHETVDFWRMIWQESACIWMVTNLVEGRVKCYKYPDDTEYIGDFKTCVMEPELA 1020
 QY 1021 EYVVRTFTLBERGYNEIREVKQPHFTGPDHGVPHATGLLSFIRRVKLSNPPSAGPIVW 1080
 DB 1021 EYVVRTFTLBERGYNEIREVKQPHFTGPDHGVPHATGLLSFIRRVKLSNPPSAGPIVW 1080
 QY 1081 HCSAGAGRTGCYIVIDIMDMAEREGVVDIYNCVKALRSRRINNMVQTEEQYIFIHDAILE 1140
 DB 1081 HCSAGAGRTGCYIVIDIMDMAEREGVVDIYNCVKALRSRRINNMVQTEEQYIFIHDAILE 1140
 QY 1141 ACLCGETAIPVCEPKAAYFDMIRIDSTNSHLLKDEFTQTLNSVTPRLOAEDCSACLPRN 1200
 DB 1141 ACLCGETAIPVCEPKAAYFDMIRIDSTNSHLLKDEFTQTLNSVTPRLOAEDCSACLPRN 1200
 QY 1201 HDKKNRFMDMLPPDRCLPLITIDGESSNYINAAIMDSYRQPAAFIVTQYPLPNTVKDFWR 1260
 DB 1201 HDKKNRFMDMLPPDRCLPLITIDGESSNYINAAIMDSYRQPAAFIVTQYPLPNTVKDFWR 1260
 QY 1261 LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRGPQVECMSCMDCDINRIFRICNL 1320
 DB 1261 LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRGPQVECMSCMDCDINRIFRICNL 1320
 QY 1321 TRPEGYLWVQOQYOLGWASHREVPGRSKRSLKILQVEKQEWKEGEGRTIHCINGG 1380
 DB 1321 TRPEGYLWVQOQYOLGWASHREVPGRSKRSLKILQVEKQEWKEGEGRTIHCINGG 1380
 QY 1381 GRSGMFCAGIIVBWKQNVVDVHFVAVKTLRNKPNMVEAPEQYRVCYDVALEYLESS 1439
 DB 1381 GRSGMFCAGIIVBWKQNVVDVHFVAVKTLRNKPNMVEAPEQYRVCYDVALEYLESS 1439
 RESULT 2
 ADJ68478
 ID ADJ68478 standard; protein; 1439 AA.
 XX ADJ68478;
 AC
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human heat mitochondrial protein as a therapeutic target SeqID284.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX Homo sapiens.
 XX WO2003087768-A2.

XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX PI Warnock DE;
XX DR WPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX PS Claim 1; SEQ ID NO 284; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, neurotropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytosolic activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.
XX SQ Sequence 1439 AA;

Query Match 99.7%; Score 7688; DB 7; Length 1439;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1436; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTTAAALPAFVALLLSWPLLSAQGQFSAGGCTFDGPGACDYHQDLYDDFEWVHV 60
DB 1 MDTTAAALPAFVALLLSWPLLSAQGQFSAGGCTFDGPGACDYHQDLYDDFEWVHV 60
QY 61 SAQEPHYLPPEMPOGYSYIVDSSDHPGKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120
DB 61 SAQEPHYLPPEMPOGYSYIVDSSDHPGKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120
QY 121 GTNLILVRNKGPLANFIVNVTGTRDMLRAELAVSTFWPNEYQVIFEAESVSGRSYI 180
DB 121 GTNLILVRNKGPLANFIVNVTGTRDMLRAELAVSTFWPNEYQVIFEAESVSGRSYI 180
QY 181 AIDDIQVLSYPCDKSPHFLRGDVEVNAGQATPCCIATGRDAVHNKMLQRRNGEDIPV 240
DB 181 AIDDIQVLSYPCDKSPHFLRGDVEVNAGQATPCCIATGRDAVHNKMLQRRNGEDIPV 240
QY 241 AQTKNINHRFAASFRLOEVTKTDQDLYRCVTSQERGSVSNFAQLIVRPPPIAPPOL 300
DB 241 AQTKNINHRFAASFRLOEVTKTDQDLYRCVTSQERGSVSNFAQLIVRPPPIAPPOL 300
QY 301 LGVGPYLLIQLNANSIIGDGPPIILKEVEYEMTSGSWTETHAVNAPTYKMLHLDPDTEYE 360
DB 301 LGVGPYLLIQLNANSIIGDGPPIILKEVEYEMTSGSWTETHAVNAPTYKMLHLDPDTEYE 360
QY 361 IRVLLTRPGSGGTGLPGPPLITRTKCAEPMTPTKTKIAEIQAARRIADVWESLYNITRC 420
DB 361 IRVLLTRPGSGGTGLPGPPLITRTKCAEPMTPTKTKIAEIQAARRIADVWESLYNITRC 420

QY 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPEGRKESEE 480
DB 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPEGRKESEE 480
QY 481 TIIQTODEVPGPVKSLQGSTPENKIFLANKKPLDPNGLIITQVEISYSIRSDPAVPV 540
DB 481 TIIQTODEVPGPVKSLQGSTPENKIFLANKKPLDPNGLIITQVEISYSIRSDPAVPV 540
QY 541 AGPPQTVSNLWNSTHVFHMLHPCTTYQFFIRASTVKGFGPATAINVTWISAPTLPDYE 600
DB 541 AGPPQTVSNLWNSTHVFHMLHPCTTYQFFIRASTVKGFGPATAINVTWISAPTLPDYE 600
QY 601 GVDASLNETAATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTVQN 660
DB 601 GVDASLNETAATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTVQN 660
QY 661 AMSGGAPYFAAELPCNLPPEPAPFTVGDNRVTYQGFNWPPLAPRKGNIIYFQAMSSVEKE 720
DB 661 AMSGGAPYFAAELPCNLPPEPAPFTVGDNRVTYQGFNWPPLAPRKGNIIYFQAMSSVEKE 720
QY 721 TKTQCVRIATKAATERPEVIPPDAKOTDRVVKIAGISAGILVFILLVILIVKSKLA 780
DB 721 TKTQCVRIATKAATERPEVIPPDAKOTDRVVKIAGISAGILVFILLVILIVKSKLA 780
QY 781 KKRKDMGNTRQBMTHMVNAMDRSYADQSTLHAEDPLSITFMDOHNSPRYENHSATAES 840
DB 781 KKRKDMGNTRQBMTHMVNAMDRSYADQSTLHAEDPLSITFMDOHNSPRYENHSATAES 840
QY 841 SRLLDVPRLYCEGTSPYQGLHPAIRVADLLQHNLMKTSDSYGKBEYESFEQOSA 900
DB 841 SRLLDVPRLYCEGTSPYQGLHPAIRVADLLQHNLMKTSDSYGKBEYESFEQOSA 900
QY 901 SWDVAKKQDNRAKNRGNIIYADHSRVILQVDEDDPSDDYINANYIDGYORPSHYIATQ 960
DB 901 SWDVAKKQDNRAKNRGNIIYADHSRVILQVDEDDPSDDYINANYIDGYORPSHYIATQ 960
QY 961 PVHETVYDFWRMIWQBSQACIVMVTNLVEGRVKCYKYPDDTEVYGDVKVTCVMEPLA 1020
DB 961 PVHETVYDFWRMIWQBSQACIVMVTNLVEGRVKCYKYPDDTEVYGDVKVTCVMEPLA 1020
QY 1021 EYVVRFTLRRGYNEIREVKQFHFTGWPDPHGPYHATGLLSFIRRVKLSNPPSAGPIV 1080
DB 1021 EYVVRFTLRRGYNEIREVKQFHFTGWPDPHGPYHATGLLSFIRRVKLSNPPSAGPIV 1080
QY 1081 HCSAGAGRTCYIVDMLDMAEREGVVDIYNCVKALRSRRINNVQTEEOYIFTHDAILE 1140
DB 1081 HCSAGAGRTCYIVDMLDMAEREGVVDIYNCVKALRSRRINNVQTEEOYIFTHDAILE 1140
QY 1141 ACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAEDECSIACLPRN 1200
DB 1141 ACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAEDECSIACLPRN 1200
QY 1201 HDKRNFMMDLPPDRCLPFLITIDGESSNYINAAIMDSYRQAPAFIVTQYPLNTVKDFWR 1260
DB 1201 HDKRNFMMDLPPDRCLPFLITIDGESSNYINAAIMDSYRQAPAFIVTQYPLNTVKDFWR 1260
QY 1261 LVVDYDGTCTSVMLNEVDLSQGCPOYWPBEGMLRGPIQVECMSCSMDCCVINRIFCNL 1320
DB 1261 LVVDYDGTCTSVMLNEVDLSQGCPOYWPBEGMLRGPIQVECMSCSMDCCVINRIFCNL 1320
QY 1321 TRPQEGYLMVQQPYQLGWASHREVPGSKRSFLKILIQVEKWQBEWKEGERTIIHCLNGG 1380
DB 1321 TRPQEGYLMVQQPYQLGWASHREVPGSKRSFLKILIQVEKWQBEWKEGERTIIHCLNGG 1380
QY 1381 GRSGMFCAGIIVVEMVKRQNVDFVFAVKTLRNSKPNWVEAPQYRCYDVALEYLESS 1439
DB 1381 GRSGMFCAGIIVVEMVKRQNVDFVFAVKTLRNSKPNWVEAPQYRCYDVALEYLESS 1439

RESULT 3
AAAY29591
ID AAAY29591 standard; protein; 1440 AA.

XX AC AAV29591;
XX 14-OCT-1999 (first entry)
XX Human protein phosphatase k.
XX Human; protein phosphatase k; HPTPK.
XX Homo sapiens.
XX KR98026246-A.
XX 15-JUL-1998.
XX 08-OCT-1996; 96KR-00044614.
XX 08-OCT-1996; 96KR-00044614.
XX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX Hah HJ, Kil MC, Yang Y, Byun GH;
XX WPI; 1999-335582/28.
XX N-PSDB; AAZ08539.
XX Human protein phosphatase, base sequence thereof and amino acid sequence
PT thereof.
XX Disclosure; Fig 1a-d; 14pp; Korean.
XX The present sequence represents human protein phosphatase k (HPTPK)
XX Sequence 1440 AA;
Query Match 99.3%; Score 7656.5; DB 2; Length 1440;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1431; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
QY 1 MDTTAAALPAFVALLLSPWLLGSAQGSAGCTFDGPGACDYHQDLYDDFEWVHV 60
DB 1 MDTTAAALPAFVALLLSPWLLGSAQGSAGCTFDGPGACDYHQDLYDDFEWVHV 60
QY 61 SAQEPHYLPPEMQSGSYMIVDSSDHPGKARLQLPTWKENDTHCIDFSYLLYSQKGLNP 120
DB 61 SAQEPHYLPPEMQSGSYMIVDSSDHPGKARLQLPTWKENDTHCIDFSYLLYSQKGLNP 120
QY 121 GTLNILVRVNGPLANPIWNTGFTGRDWRRAELAVSTFWPNEYQVIFEAESVSGRSYI 180
DB 121 GTLNILVRVNGPLANPIWNTGFTGRDWRRAELAVSTFWPNEYQVIFEAESVSGRSYI 180
QY 181 AIDDIQVLSYPCDKSPHFRLRLGDEVNAGONATFCIATGRDAVHNKWLQRRNGEDIPV 240
DB 181 AIDDIQVLSYPCDKSPHFRLRLGDEVNAGONATFCIATGRDAVHNKWLQRRNGEDIPV 240
QY 241 AQTKNINRRFAASFRLOEVTKTDQDLYRCVTSQSGSVSNFAQLIVREPRPTAPPQL 300
DB 241 AQTKNINRRFAASFRLOEVTKTDQDLYRCVTSQSGSVSNFAQLIVREPRPTAPPQL 300
QY 301 LGVGFTYLLIQNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYE 360
DB 301 LGVGFTYLLIQNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYE 360
QY 361 IRVLLTRPEGGTGLPGPLPITRTKCAEFMRTPKTKIAEQARRIAVDWESLGYNITRC 420
DB 361 IRVLLTRPEGGTGLPGPLPITRTKCAEFMRTPKTKIAEQARRIAVDWESLGYNITRC 420
QY 421 HTFNVTICVHYPRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLITNPEGRKESEE 480
DB 421 HSFNVTICVHYPRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLITNPEGRKESEE 480
QY 481 TTIQTDEDVPGVPVKSLQGTSPENKIFLNWKEPLDPNGIITQYEISYSSIRSPDPAVPV 540
DB 481 TTIQTDEDVPGVPVKSLQGTSPENKIFLNWKEPLDPNGIITQYEISYSSIRSPDPAVPV 540

DB 481 TTIQTDEDVPGVPVKSLQGTSPENKIFLNWKEPLDPNGIITQYEISYSSIRSPDPAVPV 540
QY 541 AGPPQTVSNLWNSTHHVFMHLHPGTTTQFFIRASTVKGFGPATAINVTNTNISAPTLDPYE 600
DB 541 AGPPQTVSNLWNSTHHVFMHLHPGTTTQFFIRASTVKGFGPATAINVTNTNISAPTLDPYE 600
QY 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQPVVTYQN 660
DB 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQPVVTYQN 660
QY 661 AMSGAPYFAAELPPGCLPEPAPFTVGDNRITYQGFNWPPLAPRKGNYIFQAMTSVEKE 720
DB 661 AMSGAPYFAAELPPGCLPEPAPFTVGDNRITYQGFNWPPLAPRKGNYIFQAMTSVEKE 720
QY 721 TKTCQVRIATK-AATEBEPIVDPKAKOTDRVVKIAGISAGILVIFILLVILVKKSKL 779
DB 721 TKTCQVRIATK-AATEBEPIVDPKAKOTDRVVKIAGISAGILVIFILLVILVKKSKL 780
QY 780 AKREKADMGNTROEMTHVMNAMDRSYADQSTLHAEDPLSITFMDOHNPSPRYENHSATAE 839
DB 781 AKREKADMGNTROEMTHVMNAMDRSYADQSTLHAEDPLSITFMDOHNPSPRYENHSATAE 840
QY 840 SSRLLDVPYLCGCTESPYQTQLHPAIRVADLLQHINLMKTSYSGFKSEYSEFFEGQS 899
DB 841 SSRLLDVPYLCGCTESPYQTQLHPAIRVADLLQHINLMKTSYSGFKSEYSEFFEGQS 900
QY 900 ASMDVAKKQNRKRNKRNIIAYDHSRVILQPVDEDDSSDIYINANYIDGYPORPHYIATQ 959
DB 901 ASMDVAKKQNRKRNKRNIIAYDHSRVILQPVDEDDSSDIYINANYIDGYPORPHYIATQ 960
QY 960 GPVHETVDFWRMIWQOSACIWMVTNLVEGRVKYKYPDDTEVVGDFKVCVEMEPL 1019
DB 961 GPVHETVDFWRMIWQOSACIWMVTNLVEGRVKYKYPDDTEVVGDFKVCVEMEPL 1020
QY 1020 AEYVVRFTLERRGYNEIREVKQFHTGWPDPHGVPHYATGLLSFIRRVKLSNPPSAGPIV 1079
DB 1021 AEYVVRFTLERRGYNEIREVKQFHTGWPDPHGVPHYATGLLSFIRRVKLSNPPSAGPIV 1080
QY 1080 VHCASAGRTGCTYIVDIMLDMAREGVVDIYNCVKALRSRRINNVQTEEQYIFIHDAI 1139
DB 1081 VHCASAGRTGCTYIVDIMLDMAREGVVDIYNCVKALRSRRINNVQTEEQYIFIHDAI 1140
QY 1140 EACLCGETATPVCEFKAAEDMIRIDISQTNSSHLKDBFQTLNSVTPLQAECDSCJACLP 1199
DB 1141 EACLCGETATPVCEFKAAEDMIRIDISQTNSSHLKDBFQTLNSVTPLQAECDSCJACLP 1200
QY 1200 NHDKNRFDMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFW 1259
DB 1201 NHDKNRFDMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFW 1260
QY 1260 RLVTYDGTCTSIVMNLNEVDLSQGCQYWPPEGMLRYGPIQVCEMCSMDVDINRIFRICN 1319
DB 1261 RLVTYDGTCTSIVMNLNEVDLSQGCQYWPPEGMLRYGPIQVCEMCSMDVDINRIFRICN 1320
QY 1320 LTRPQEGVLMVQQYQILGWASHREVPKRSFLKLIQVEKWQEBWKEGERTIIHCLNG 1379
DB 1321 LTRPQEGVLMVQQYQILGWASHREVPKRSFLKLIQVEKWQEBWKEGERTIIHCLNG 1380
QY 1380 GGRSGMCAIGIVVMVKRQNVVDVFAVKTLRNSKPNMVEAPEQYRFCYDVALEYLESS 1439
DB 1381 GGRSGMCAIGIVVMVKRQNVVDVFAVKTLRNSKPNMVEAPEQYRFCYDVALEYLESS 1440
RESULT 4
ADI23886
ID ADI23886 standard; protein; 1440 AA.
XX ADI23886;
AC ADI23886;
XX 22-APR-2004 (first entry)
XX Human PTPRK protein SEQ ID NO:4.
XX

KW antisense oligonucleotide; human;
 KW protein tyrosine phosphatase receptor type K; PTPRK; cytosolic;
 KW antidiabetic; antidiabetic; antisense gene therapy; diabetes;
 KW inflammation; hyperproliferative disorder; cancer; chromosome 6.
 XX
 OS Homo sapiens.
 XX
 PN W0204005312-A1.
 XX
 PD 15-JAN-2004.
 XX
 XX 27-JUN-2003; 2003WO-US016237.
 XX
 XX 03-JUL-2002; 2002US-00189429.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Cowsett LM, Freier SM;
 XX
 DR WPI; 2004-083493/08.
 DR N-PSDB; AD123748.
 XX
 XX New antisense oligonucleotide, having a sequence targeted to a nucleic
 PT acid encoding PTPRK, useful for preparing a composition for treating
 PT diabetes, inflammation or hyperproliferative disorder, e.g., cancer.
 XX
 PS Example 13; SEQ ID NO 4; 150pp; English.
 XX
 CC The present invention describes an antisense oligonucleotide (I), having
 CC a sequence comprising 8-80 base pairs, targeted to a nucleic acid
 CC encoding protein tyrosine phosphatase receptor type K (PTPRK), that
 CC specifically hybridizes with the nucleic acid encoding PTPRK, and inhibits
 CC expression of PTPRK. Also described: (1) a composition comprising the
 CC compound and a carrier or diluent; (2) a method of inhibiting the
 CC expression of PTPRK in cells or tissues; (3) a method of treating an
 CC animal having or suspected of having a disease or condition associated
 CC with PTPRK; and (4) a method for screening for an antisense compound. (1)
 CC has cytostatic, antiinflammatory and antidiabetic activities, and can be
 CC used in antisense gene therapy. The antisense oligonucleotide (I) can be
 CC used for preparing a composition for treating diabetes, inflammation or
 CC hyperproliferative disorder, e.g., cancer. The present sequence
 CC represents human PTPRK, which is used in an example from the present
 CC invention. The human PTPRK gene is located on chromosome 6, more
 CC specifically to 6q22.2-23.1.
 XX
 SQ Sequence 1440 AA;

Query Match 99.3%; Score 7656.5; DB 8; Length 1440;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1431; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 MDTTAAALPAFVALLLSFWPLLSAQGQFSAGGCTFDDPGACDYHQDLXDDEFWVHV 60
 DB 1 MDTTAAALPAFVALLLSFWPLLSAQGQFSAGGCTFDDPGACDYHQDLXDDEFWVHV 60

QY 61 SAQEPHYLPPEMPOGSGYMI VDSDDHDPGEKARLQPTMKENDTHCIDFSYLLXSQKGLNP 120
 DB 61 SAQEPHYLPPEMPOGSGYMI VDSDDHDPGEKARLQPTMKENDTHCIDFSYLLXSQKGLNP 120

QY 121 GTNLILVRNKGPLANIPWNTGTGRDNLRAELAVSTFWPNEQVIFAEVSGRSGYI 180
 DB 121 GTNLILVRNKGPLANIPWNTGTGRDNLRAELAVSTFWPNEQVIFAEVSGRSGYI 180

QY 181 AIDDIQVLSYPCDKSPHFLRGLGDEVNAGQATFQCIATGRDAVHNKMLQRRNGEDIPV 240
 DB 181 AIDDIQVLSYPCDKSPHFLRGLGDEVNAGQATFQCIATGRDAVHNKMLQRRNGEDIPV 240

QY 241 AQTKNINHRFAAFRLQEVTKTDODLYRCVTSERGSYVSNFAQLIVREPPPIAPPOL 300
 DB 241 AQTKNINHRFAAFRLQEVTKTDODLYRCVTSERGSYVSNFAQLIVREPPPIAPPOL 300

QY 301 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLVHLDPDTEYE 360

DB 301 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLVHLDPDTEYE 360
 QY 361 IRVLLTRPGSGGTCLPGPPLITRTKCAEPMTPTKTLKIAIEIQARRIAVDWESLYNITRC 420
 DB 361 IRVLLTRPGSGGTCLPGPPLITRTKCAEPMTPTKTLKIAIEIQARRIAVDWESLYNITRC 420
 QY 421 HTFNVTICHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLINTNPEGRKSEEE 480
 DB 421 HSFNVTICHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLINTNPEGRKSEEE 480
 QY 481 TIIQTDEDVPGVPVKSLOQTSFENKIFLNKKEPLDPNGIITQVEISYSIRSFDPAVPV 540
 DB 481 TIIQTDEDVPGVPVKSLOQTSFENKIFLNKKEPLDPNGIITQVEISYSIRSFDPAVPV 540
 QY 541 AGPPQTVSNLWNSHTHVFMHLPGTQYQFFIRASTVKFGCPATAINVTNISAPTLDPYE 600
 DB 541 AGPPQTVSNLWNSHTHVFMHLPGTQYQFFIRASTVKFGCPATAINVTNISAPTLDPYE 600
 QY 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 660
 DB 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 660
 QY 661 AMSGGAPYFAAELPGNLPPEPAPFTVGDNRVTQGFNWPPLAPRKGYNIYFOAMSSVEKE 720
 DB 661 AMSGGAPYFAAELPGNLPPEPAPFTVGDNRVTQGFNWPPLAPRKGYNIYFOAMSSVEKE 720
 QY 721 TKTQCVRATK-AATBEPEVIPDPAKQTDNRVVIAGISAGILVFILLVILVVKSKL 779
 DB 721 TKTQCVRATKAAATEEPEVIPDPAKQTDNRVVIAGISAGILVFILLVILVVKSKL 780
 QY 780 AKRKDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRYENHSATAE 839
 DB 781 AKRKDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRYENHSATAE 840
 QY 840 SSRLLDVRVLCGTSPTQGTGOLHPAIRVADILLOHNLMTKSDSYGKGEYESFFRSGS 899
 DB 841 SSRLLDVRVLCGTSPTQGTGOLHPAIRVADILLOHNLMTKSDSYGKGEYESFFRSGS 900
 QY 900 ASWDVAKQONRAKRYGNI IAYDHSRVILQPVDEDPSSDIYINANYIDGQRPSHYIATQ 959
 DB 901 ASWDVAKQONRAKRYGNI IAYDHSRVILQPVDEDPSSDIYINANYIDGQRPSHYIATQ 960
 QY 960 GPVHETVDFWRMIWQESACI VVWVNLVEVRVKYKYPWDDTEVVGDPKVCVMEPL 1019
 DB 961 GPVHETVDFWRMIWQESACI VVWVNLVEVRVKYKYPWDDTEVVGDPKVCVMEPL 1020
 QY 1020 AEYVVRFTTLERGYNEIREVKQFHTGPDHGVPHATGLLSFIRVKLSNPPSAGPIV 1079
 DB 1021 AEYVVRFTTLERGYNEIREVKQFHTGPDHGVPHATGLLSFIRVKLSNPPSAGPIV 1080
 QY 1080 VHCAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVOTEEQYIFIHDAIL 1139
 DB 1081 VHCAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVOTEEQYIFIHDAIL 1140
 QY 1140 EACLCCETAIPVCEFAAAYFDMIRIDSQTNSSHLKQEFOTLNSVTPRLQADCSIACLPR 1199
 DB 1141 EACLCCETAIPVCEFAAAYFDMIRIDSQTNSSHLKQEFOTLNSVTPRLQADCSIACLPR 1200
 QY 1200 NHDKNRFDMLPPDRCLPLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLNTVXDFW 1259
 DB 1201 NHDKNRFDMLPPDRCLPLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLNTVXDFW 1260
 QY 1260 RLVDYDGTCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVECMSCSDCVINRI FRICN 1319
 DB 1261 RLVDYDGTCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVECMSCSDCVINRI FRICN 1320
 QY 1320 LTRPQEGYLMVQVQFYLGWASHREVPFGSKSFLKLILQVEKQWSEKGEGRITIIHCLNG 1379
 DB 1321 LTRPQEGYLMVQVQFYLGWASHREVPFGSKSFLKLILQVEKQWSEKGEGRITIIHCLNG 1380
 QY 1380 GGRSGMFCAGIIVEMVKRQNVDFVHAKVTLRNSKPNMVEAPEQYRCDVALEYLESS 1439
 DB 1381 GGRSGMFCAGIIVEMVKRQNVDFVHAKVTLRNSKPNMVEAPEQYRCDVALEYLESS 1440

RESULT 5

ABB57308
ID ABB57308 standard; protein; 1457 AA.

XX AC ABB57308;

XX DT 07-MAR-2002 (first entry)

XX DE Mouse ischaemic condition related protein sequence SEQ ID NO:862.

XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX OS Mus musculus.

XX PN WO200188188-A2.

XX XX 22-NOV-2001.

XX PD 18-MAY-2001; 2001WO-JP004192.

XX PF 18-MAY-2000; 2000JP-00145977.

XX PR (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX PA Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX PI WPI; 2002-034733/04.

XX DR N-PSDB; AB199774.

XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
expression levels of particular genes defined in the specification or by
determining the expression profile of a gene group comprising these
genes.

XX PS Claim 2; Page 2155-2161; 2690pp; English.

XX CC The present invention describes a method for examining ischaemic
conditions, comprising measuring the expression levels of particular
genes (I) in a test sample or determining the expression profile of a
gene group in the sample comprising genes selected from (I). The method
is useful for examining the ischaemic condition (e.g. compressive
ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
expression levels of particular genes (AB199202 to AB199912, encoding the
protein sequences in ABB57020 to ABB57374) or by determining the
expression profile of a gene group comprising these genes. The expression
levels or expression profiles produced by these genes are used as an
indicator when screening for ischaemic condition-improving drugs or
therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR
primers for a mouse ischaemic condition related sequence, which are used
in the exemplification of the present invention

SQ Sequence 1457 AA;

Query Match 98.2%; Score 7571; DB 5; Length 1457;

Best Local Similarity 97.3%; Pred. No. 0;

Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

QY 1 MDTTAAALPAFVALLLLSPWLLGSAQGFSGAGGCTFDDGACDYHODLYDDPEWHV 60
DB 1 MD-VAAALPAFVALLLLYPWLLGSAQGFSGAGGCTFDDGACDYHODLYDDPEWHV 59
QY 61 SAQEPHYLPPEPQGSYMTVDSDDHPGKARLQLPTMKENDTHCIDFSYLLYSOKGLNP 120
DB 60 SAQEPHYLPPEPQGSYMTVDSDDHPGKARLQLPTMKENDTHCIDFSYLLYSOKGLNP 119
QY 121 GTILNLRVKNKGLANPIWNTGFTGRDMLRAELAVSTFWPNEYQVIFPAEVSGRSGYI 180
DB 120 GTILNLRVKNKGLANPIWNTGFTGRDMLRAELAVSTFWPNEYQVIFPAEVSGRSGYI 179
QY 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFQCIGTATGRDAVHNKMLQRRNGEDIPV 240

DB 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFQCIGTATGRDAVHNKMLQRRNGEDIPV 239
QY 241 AQTKNINHRRFAASFRLOEVTKTQDLYRCVTQSERGSGVSNFAQLIVREPRPIAPPOL 300
DB 240 AQTKNINHRRFAASFRLOEVTKTQDLYRCVTQSERGSGVSNFAQLIVREPRPIAPPOL 299
QY 301 LGVGPTVLLIQLNANSIIGDGPITLKEVEYHMTSGSWTETHAVNAPTIVKWLHLPDPTBE 360
DB 300 LGVGPTVLLIQLNANSIIGDGPITLKEVEYHMTSGSWTETHAVNAPTIVKWLHLPDPTBE 359
QY 361 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPTKLIAEIQARRIAVDWSLGYNITRC 420
DB 360 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPTKLIAEIQARRIAVDWSLGYNITRC 419
QY 421 HTFNWTCYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGEKESSE 480
DB 420 HTFNWTCYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGEKESSE 479
QY 481 TTIQTDREDVPGVPVKSILQGTSPFNKIPLNKEPLDPNGIITOYEISYSSIRSPDPAPVP 540
DB 480 TTIQTDREDVPGVPVKSILQGTSPFNKIPLNKEPLDPNGIITOYEISYSSIRSPDPAPVP 539
QY 541 AGPPQTVSNLWNSTHVFHMLHPCGTYQFFIRASTVKGFGPATAINVTNINISAPSLDYE 600
DB 540 AGPPQTVSNLWNSTHVFHMLHPCGTYQFFIRASTVKGFGPATAINVTNINISAPSLDYE 599
QY 601 GVDASLNETATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVTON 660
DB 600 GVDASLNETATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVTON 659
QY 661 AMSGAPYFAELPPGGLPEPAPFTVGDNRTYOGFWNPPLAPRKGYNIYQAMSSVSKE 720
DB 660 ALSGAPYFAELPPGGLPEPAPFTVGDNRTYOGFWNPPLAPRKGYNIYQAMSSVSKE 719
QY 721 TKTQCVRIATK-AAATERPEVIPPAPKQTDRTVVKVIAGISAGILVFLILLVILVVKSKL 779
DB 720 TKTQCVRIATKAAATERPEVIPPAPKQTDRTVVKVIAGISAGILVFLILLVILVVKSKL 779
QY 780 AKKQKDMGNTRQEMTHMVNMDRSYADQSTLHAEPLSLITFMDQHNPSRY----- 831
DB 780 AKKQKDMGNTRQEMTHMVNMDRSYADQSTLHAEPLSLITFMDQHNPSRPLNDPLVPT 839
QY 832 ----ENHSATAESRLLDVPRYLCGTEPSPQTGQLHFAIRVADLQHINLMKTSDSYGF 887
DB 840 AVLDEHNSATAESRLLDVPRYLCGTEPSPQTGQLHFAIRVADLQHINLMKTSDSYGF 899
QY 888 KEEVESFFEGQSASWDVAKQDNRAKNRYGNI IAYDHSRVILQPVEDDPSSDIYINANYI- 946
DB 900 KEEVESFFEGQSASWDVAKQDNRAKNRYGNI IAYDHSRVILQPVEDDPSSDIYINANYI 959
QY 947 ----DGVRPSHYIATQGPVHETVYDFWRMIWQESACIWMVTNLEVEGRVKCYKYPD 1001
DB 960 IWLVRDGYQRPESHVIATQGPVHETVYDFWRMIWQESACIWMVTNLEVEGRVKCYKYPD 1019
QY 1002 DTEVYGDGPKVTCVMEPLAEYVVRFTTLERGYNEIREVKOPHETGPDHGVPHYATGLL 1061
DB 1020 DTEVYGDGPKVTCVMEPLAEYVVRFTTLERGYNEIREVKOPHETGPDHGVPHYATGLL 1079
QY 1062 SFIRRVKLSNPPSAGPIVVHCSAGAGRTGCYIVIDIMLDMAREGVDIYNCVKALRSR 1121
DB 1080 SFIRRVKLSNPPSAGPIVVHCSAGAGRTGCYIVIDIMLDMAREGVDIYNCVKALRSR 1139
QY 1122 INMVQTEQYIFIHDAILEACLCGETAIPVCEFFAAAYFDMIRIDISQTNSSHLKDFQTLN 1181
DB 1140 INMVQTEQYIFIHDAILEACLCGETAIPVCEFFAAAYFDMIRIDISQTNSSHLKDFQTLN 1199
QY 1182 SVTPQLQADCSIACLPRNHDKNRPMWMLPPDRCLPELITIDGSSNYINAAALMDSYROP 1241
DB 1200 SVTPQLQADCSIACLPRNHDKNRPMWMLPPDRCLPELITIDGSSNYINAAALMDSYROP 1259
QY 1242 AAFIVTQPLPNTVDFWRLVYDYCTSI VMLNEVDLSQGCQPYWPBEGMLRYGPIQVEC 1301


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Db 780 AKRKDAMGNTREQETHMVMNADMSYADQSTLHAEDPLSLTFMQHNFSPRLPNDPLVPT 839
Qy 832 ----ENHSATAESRLLDVPRYLCEGTSPYQTQLHPAIRVADLLQHINLMKTSDSYGF 887
Db 840 AVLDSNHSATAESRLLDVPRYLCEGTSPYQTQLHPAIRVADLLQHINLMKTSDSYGF 899
Qy 888 KEEVESPEEGOSASDWAKDONRAKRYGNI IAYDHSRVTLQVDDPSSDYINANYI - 946
Db 900 KEEVESPEEGOSASDWAKDONRAKRYGNI IAYDHSRVTLQVDDPSSDYINANYID 959
Qy 947 -----DGQRSHYIATQPVHETVYDFWRMIWQESACI VAVTNLVEGVKVCYKWPD 1001
Db 960 IWLVRDGYQRSHYIATQPVHETVYDFWRMVWQESACI VAVTNLVEGVKVCYKWPD 1019
Qy 1002 DTEVYDGFVKTCVEMEPLAEYVVRFTFLRRGYNEIREVKQFHTGWPDHGVPHATGLL 1061
Db 1020 DTEVYDGFVKTCVEMEPLAEYVVRFTFLRRGYNEIREVKQFHTGWPDHGVPHATGLL 1079
Qy 1062 SFIRRVKLSNPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSR 1121
Db 1080 SFIRRVKLSNPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSR 1139
Qy 1122 INMWQTEQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOFLN 1181
Db 1140 INMWQTEQYIFIHDPILLEASLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOFLN 1199
Qy 1182 SVTPRLQAEDCSIACLPNRHDKNRFMDMLPPDRCLPFLITIDGSSNYINAAALMDSYRQ 1241
Db 1200 SVTPRLQAEDCSIACLPNRHDKNRFMDMLPPDRCLPFLITIDGSSNYINAAALMDSYRQ 1259
Qy 1242 AAFIVTQPLNTVKDFRLVYDYGCTSI VMLNEVDLSQGCPOQWPPEGMLRYGPIQVE 1301
Db 1260 AAFIVTQPLNTVKDFRLVYDYGCTSI VMLNEVDLSQGCPOQWPPEGMLRYGPIQVE 1319
Qy 1302 MSCSMDCDVINRIPRICNLTRPOEGLVMVQOFOYLGWASHREVPGRKSFKLILQVEKW 1361
Db 1320 MSCSMDCDVINRIFRICNLTRPOEGLVMVQOFOYLGWASHREVPGRKSFKLILQVEKW 1379
Qy 1362 QBEWKEGEGRTIIHCLNGGSGMFCAGIVVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1421
Db 1380 QEECEGEGRTIIHCLNGGSGMFCAGIVVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1439
Qy 1422 PEQYRFDVDALEYLESS 1439
Db 1440 PEHYRFDLPDLYLESS 1457

RESULT 7
ID AAR63631 standard; protein; 1407 AA.
XX AC AAR63631;
XX DT 21-OCT-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 08-JUN-1995 (first entry)
XX DE Murine receptor-type protein tyrosine phosphatase protein (RPTP- kappa).
XX KW Receptor-type protein tyrosine phosphatase protein; cellular signal;
XX KW RPTase-kappa; enzyme.
XX OS Mus musculus.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Peptide 1..25
XX FT Region 210..270
XX FT FT /label= signal
XX FT FT /label= IG-like repeat
XX FT FT 703..724
XX FT FT /label = Transmembrane
XX FT FT 877..1108
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FT Domain /label = PTPase 1
FT 1168..1404
FT /label = PTPase 2
XX MO9424161-A1.
XX PD 27-OCT-1994.
XX XX 20-APR-1994; 94WO-US004377.
XX PF 21-APR-1993; 93US-00049384.
XX PR 01-JUL-1993; 93US-00087244.
XX XX (UNY-) UNIV NEW YORK MEDICAL CENT.
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX XX Schlessinger J, Sap JW, Ullrich A, Vogel W, Fuchs M;
XX WPI; 1994-341769/42.
XX XX
XX NB: It appears that one line, comprising 50AAs is missing from Figure 3
XX (cf AAR63631). The novel receptor-type protein tyrosine phosphatase
XX protein or glycoprotein is termed RPTP kappa (also known as RPTase-
XX kappa). The first approx. 170AAs of RPTP kappa show similarity (26%
XX overall identity) to a region in the Xenopus cell surface protein A5 with
XX -like repeats (residues 296-681). The tandem repeat of two PTPase
XX homologues is typical for most RPTases. A feature of RPTP kappa is the
XX extended distance between its transmembrane domain and the start of the
XX first phosphatase homology domain. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX Revised record issued on 21-OCT-2004 : Correction to feature table key
XX Sequence 1407 AA;
XX Query Match 93.1%; Score 7174; DB 2; Length 1407;
XX Best Local Similarity 92.9%; Pred. No. 0;
XX Matches 1355; Conservative 18; Mismatches 15; Indels 70; Gaps 5;
Qy 1 MDTTAAALPAFVALLLLSPWLLGSAQGFSAQGSCTFDDGPGACDHYQDLVDDFEWHV 60
Db 1 MD-VAAALPAFVALLWLLYPWLLGSAQGSCTFDDGPGACDHYQDLVDDFEWHV 59
Qy 61 SAQEPHYLPPEMPOGSGYMIYVDSDDHDFGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120
Db 60 SAQEPHYLPPEMPOGSGYMWVDSSNHDHGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 119
Qy 121 GTNLILVRNKGPLANPINVNTGTRDWRRAELAVSTFWPNEQVIFPEAEVSGRSYI 180
Db 120 GTNLILVRNKGPLANPINVNTGTRDWRRAELAVSTFWPNEQVIFPEAEVSGRSYI 179
Qy 181 AIDDIQVLSYPCDKSPHFLRGDVEVNAGONATFCQIATGRDVAHNKLVORRNGEDIPV 240
Db 180 AIDDIQVLSYPCDKSPHFLRGDVEVNAGONATFCQIATGRDVAHNKLVORRNGEDIPV 239
Qy 241 AQTKNINHRFAASFRLQEVTKTDQDLVRCVTSQSERGSGVSNFAQLIVREPRPIAPPQL 300
Db 240 AQTKNINRRFAASFRLQVKYTKTDQDLVRCVTSQSERGSGVSNFAQLIVREPRPIAPPQL 299
Qy 301 LGVGPTVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTLYKLWHLDDPTIYE 360
Db 300 LGVGPTVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTLYKLWHLDDPTIYE 359
Qy 361 IRLVLLTRPGEGGTGLPGPPLITRTKCAEPMPTKTLKIAEQARRIADVDSLSGYNITRC 420
XX
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Db 360 IRVLLTRPGGGTGLPPPLITRTTKCAEPHRTPTKTKIAEIQARRIAVDWESLGYNITRC 419
Qy 421 HTFNVTTCYHYFRGHNSKADCLMDPKAPQHVNNHLPPTYNVSLKMLTNPEGRKESEE 480
Db 420 HTFNVTTCYHYFRGHNSRADCLMDPKAPQ----- 450
Qy 481 TIIQTDEVDVCPVPVKSQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRSPDPAPVP 540
Db 451 -----SPEHKIFLHWKEPLEPNGIITQVEISYSSIRSPDPAPVP 489
Qy 541 AGPPQTVSNLWNSHHVFMHLPGTQYQFFIRASTVKGFGPATVNTTNSISAPTLDPYE 600
Db 490 AGPPQTVSNLWNSHHVFMHLPGTQYQFFIRASTVKGFGPATVNTTNSISAPTLDPYE 549
Qy 601 GVDASLNETATTITVLLRPAQAAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTTYQ 660
Db 550 GVDASLNETATTITVLLRPAQAAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTTYQ 609
Qy 661 AMSGGAPYYFAAELPPGNLPEPAPFTVGDNRITVQGFNPPPLAPRKGNIIYFOAMSSVEKE 720
Db 610 ALSGGAPYYFAAELPPGNLPEPAPFTVGDNRITVQGFNPPPLAPRKGNIIYFOAMSSVEKE 669
Qy 721 TKTCQVRIATK-AATEPEVIPPAPKOTDRVVKTAGISAGILVFILLLVILVIVKSKL 779
Db 670 TKTCQVRIATKAAATEPEVIPPAPKOTDRVVKTAGISAGILVFILLLVILVIVKSKL 729
Qy 780 AKRKKDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRY----- 831
Db 730 AKRKKDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRPLNDPLVPT 789
Qy 832 -----ENHSATAESRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHLNLMKTSYGF 887
Db 790 AVLDEHNSATAESRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHLNLMKTSYGF 849
Qy 888 KEYESFFEGQSASWDVAKKQDQNRKNRYGNIITAYDHSRVILQVDEDDPSDDVINYI- 946
Db 850 KEYESFFEGQSASWDVAKKQDQNRKNRYGNIITAYDHSRVILQVDEDDPSDDVINYI 909
Qy 947 -----DGYQRPSPHYIATQGPVHETVDFWRMIWQESACIWMVNLVEGRVKCYKWP 1001
Db 910 IWLRYDGYQRPSPHYIATQGPVHETVDFWRMIWQESACIWMVNLVEGRVKCYKWP 969
Qy 1002 DTEVYGDVKTCVEMEPLASYVVRFTFLRRGNYNEIREVKQFHTGHPDGVPHATGLL 1061
Db 970 DTEVYGDVKTCVEMEPLASYVVRFTFLRRGNYNEIREVKQFHTGHPDGVPHATGLL 1029
Qy 1062 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCIYVIDIMLMDAEREGVVDIYNCVKALRSR 1121
Db 1030 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCIYVIDIMLMDAEREGVVDIYNCVKALRSR 1089
Qy 1122 INNVQTEEQYIFHDAILEACLCGETAIPVCEPKAAAFDMIRIDQSNSSHLKDFOTLN 1181
Db 1090 INNVQTEEQYIFHDAILEACLCGETAIPVCEPKAAAFDMIRIDQSNSSHLKDFOTLN 1149
Qy 1182 SVTPRLOAEDCSIACLPRNHDKNRMDLPPDRCLPELITIDGESSNYINAALMDSYQ 1241
Db 1150 SVTPRLOAEDCSIACLPRNHDKNRMDLPPDRCLPELITIDGESSNYINAALMDSYQ 1209
Qy 1242 AAFIVQYPLPNTVKDFWRLVYDGTSTIYMLNEVDLSQCPQWPBEGMLRGPTQVE 1301
Db 1210 AAFIVQYPLPNTVKDFWRLVYDGTSTIYMLNEVDLSQCPQWPBEGMLRGPTQVE 1269
Qy 1302 MSCMDCDVNIRIFRICNLTRPOEGLMVQOQFVLGWASHREVPGRKSLKILQVEKW 1361
Db 1270 MSCMDCDVNIRIFRICNLTRPOEGLMVQOQFVLGWASHREVPGRKSLKILQVEKW 1329
Qy 1362 QEBWKEGEGRTIICHLGGGRSGMFCAGIIGVEMVKRQNVVDVFAVKTLRNSKPNVEA 1421
Db 1330 QEBWKEGEGRTIICHLGGGRSGMFCAGIIGVEMVKRQNVVDVFAVKTLRNSKPNVEA 1389
Qy 1422 PEQYRFDYVALEYLESS 1439
Db 1390 PEQYRFDYVALEYLESS 1407

RESULT 8

AAM79159

ID AAM79159 standard; protein; 1452 AA.

XX AAM79159;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 1821.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

XX WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PR 20-JUN-2000; 2000US-00598075.

XX PR 19-JUL-2000; 2000US-00620325.

XX PR 01-SEP-2000; 2000US-00654936.

XX PR 15-SEP-2000; 2000US-00663561.

XX PR 20-OCT-2000; 2000US-00693325.

XX PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

XX PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX DR WPI; 2001-476283/51.

XX DR N-PSDB; AAK52292.

XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy.

XX PS Claim 20; Page 4196-4199; 6221pp; English.

XX CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activity/inhibit activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
sequence listing were missing at the time of publication

SQ Sequence 1452 AA;

* Query Match 62.5%; Score 4818; DB 4; Length 1452;

* Best Local Similarity 60.8%; Pred. No. 0;

Matches 890; Conservative 207; Mismatches 324; Indels 42; Gaps 8;

Qy 4 TAAALPAFVALLLLSPWLLGSAQGFSAAGCTFDDGPGACDYHODLYDDFEWVHYSAQ 63

Db 3 TLGTCTATAGLLL-----TAAGTFFSGGCLFDEPYSTCTGYSOEGDDFNWEQNTL 54

Qy 64 EPHYLPPEMQSGSYMTIVDSGDHPGKARLQLPTMKENDTHCIDFSYLLYSQKLNPGTL 123

Db 55 TKPTSDPMPGSGFVNLVNASRPEGORAHLLLPOLKENDTHCIDPHFVSSKSNPPGLL 114
Qy 124 NILVRVNGKPIANFVNTVGTGTRDWDRAELAVSTFWPNEYQVIFAEVSGRSGYIAID 183
Db 115 NVYKVNNGPLGNPWNISGDPTRTNRAELAISTFWPNFYQVIFEV-ITSHQGYLAD 173
Qy 184 DIQVLSYPCDKSPHFLRLGDVENVAGONATQCIATGDEAVHKLMLQRRNGEDI PVAQT 243
Db 174 EVKVLGHFCTTHPLRLIQNVENVAGOPATFQCSAIGRTVAGDRLWLQGDIVROAPLKEI 233
Qy 244 KNIHRRFAAFLQEVTKTDQDLYRCVTOESRSGVSNFAQLIVRPPRPIAPQLLGV 303
Db 234 KVTSSRRFIASFVNTTKRAGKRCMRTEGGVGSINYAELVKEPPVPIAPQLASV 293
Qy 304 GPTYLLIQNLANSIIGDGPFIILKEVEYRMTSGSTETHAVNAPTYKMLHLPDPTYEIRV 363
Db 294 GATYLLIQNLANSINGDGPFI VAREVEYCTASGSMNDROPVDSTSYKIGHLPDPTYEISV 353
Qy 364 LLTRPGEGETGLPGPPLITRTKCAPMPRTPKTLKIAEQARRIADVMSLGYNITRCHTF 423
Db 354 LLTRPGEGETGSPGALTRTKADPMRGPRKLEVEVKSQITIRWEPFGYNVTRCHSY 413
Qy 424 NVTCYHYFRGHNEKAD--CLDMDPKAPQHVNHLPPTVNSVKMLNTNPEGRKESRET 481
Db 414 NLTVHYCYQVGQEQVREVSWDIENSHPOHTITNLSPTVNSVKLILMNPEGRKESQEL 473
Qy 482 IIQTDDEVPVPVKSLOQTSFENKIFLNWKEPLDPNGIITQYEISYSSIRSFPAPVPA 541
Db 474 IVQTDDELPGAVPTESIQGSTFEKIFLQWREPTQYGVITLYEITYKAVSSPDPEIDL 533
Qy 542 GPQTVNSLWNSHTVFMHLHPGITYQFFIRASTVKGFGPATINVTINISAPLTPDYEG 601
Db 534 NQSGRVSKLGNETHFLFGLYPGTYSFTIRASTAKGFGPATNQFTTKISAPSNPAYE- 592
Qy 602 VDASNETATTITVLLRPAQAKGAPISAVQIVBELHPHRTKREAGAMECYQVPVYQNA 661
Db 593 LETPLNQDNTVTVMLKPAHSGAPSVQIVVEERPRRTKTEILKCPVPIHFQNA 652
Qy 662 MSGGAPYFAALPLPGLNPEPAPFTVGNRTYQGFNPPPLAPRKGYNIYFOAMSVEKET 721
Db 653 SLLNSQYIFAABFADSLQAQPFITGDKNTYNGYWNTPLLPYKSYRIYFQAASRANGET 712
Qy 722 KTCQVRIATKAATESPEVIPPDAKOTDRVKIAGISAGILPILLVILLVILVKKSLAK 781
Db 713 KIDCVQVATKGAA--TPKEVPPEKQTDHTVKTAGVIAGILLFVIFLGVILWMLKRRKLAK 771
Qy 782 KKKDAMGNTROBMTMVMAMDRSYAQDSTLHAEDPLSITFMDOHNFSPRY----- 831
Db 772 KKKETMSSTRQEMTVVNSMDKSYAEQGTNCDE---AFSMDTHNLNRSVSSPSSFTWK 828
Qy 832 -----ENHSATAESSRLLDVPRY-LCEGTESPYQTQQLHPAIRVADLLQH 875
Db 829 TNLSTSVNSYYPDETHMTASDTSLSVQSHYTKKREPADVQYQGTQQLHPAIRVADLLQH 888
Qy 876 INLMKTSDSYGKEEYESFQCSASWDVAKQDQRAKRNQNIITAYDHSRVILQPVDEDD 935
Db 889 ITQMKCAEYGFKEEYESFQCSAPWDSAKDENMKRNQNIITAYDHSRVRLQTIEGD 948
Qy 936 PSSDYINANYIDGYORPSHYIATQCPVHETVDFWRMIWQEOSACIVMVTNLVEYGRVKC 995
Db 949 TNSDYINGNIIDGYHRPNHYIATQCPMQETIYDFWRMVHENTASIIWVTNLVEYGRVKC 1008
Qy 996 KYKVPDDTEYVDFKVKTCVMEPLAEYVVRVTRFTLERRGYNEIREVKQFHTGWPDPGVY 1055
Db 1009 KYKVPDDTEYKDKVLTLETALLAEYVIRTAFAVEKRGVHEIREIRQFHTGWPDPGVY 1068
Qy 1056 HATGLLSFTRRVKLNPPSAGPIVHCSAGAGRTCYIVIDIMLMAEREGVVDIYNVCK 1115
Db 1069 HATGLLGFVRQVKSPPSPSAGPLVHCSAGAGRTCFIVIDIMLMAEREGVVDIYNVCR 1128
Qy 1116 ALRSRRINNVQTEEQYIFTHDAILEACLGETAIPVCEPKAAYFMIDRSDOTNSHLKD 1175

Db 1129 ELRSRRVNMVQTEBEQYVFIHDAILEACLCDGTSPASQVRSRSLYYDMNKLDPQTNSSQIKE 1188
Qy 1176 EFQTLASVTRLOAEDCSIACLRNDHKNRPMWLPPDRCLPFLITIDGSSSNVINAALM 1235
Db 1189 EFTLNMVTPFLRVEDCSIALPRNHEKRCMDILLPPDRCLPFLITIDGSSSNVINAALM 1248
Qy 1236 DSVRQPAAFIVTOVPLPNTVKDFWRLVYDYGCTSIVMNLNEVDLSQGCPCQYWPBEGMLRYG 1295
Db 1249 DSYKQSAFIVTQHPLENTVKDFWRLVLDYHCTSVVNLNDVDPAQLCPQYWPENGVRHVG 1308
Qy 1296 PIQVECMSCMDCVNNRIFRINCLTRPBQGYLMVQFOGYLWASHREVPGSKSFKLKI 1355
Db 1309 PIQVEFVSADLEEDISIRIFRIYNAARPDQGYRMVQOQFLGWPMYRDTVPVSKESFLKLI 1368
Qy 1356 LOYKWOEEWKEGEGRTIIHCLNGGGRSGMFCAGIUVVMKRONVVDVHVAKTLSNSK 1415
Db 1369 RQVDKWOEEYNGEGRTVTVHCLNGGGRSGTFCALSICEMLRHQRTVDVHVAKTLSNRNK 1428
Qy 1416 PNVEAPEQYRVCYDVALEYLES 1438
Db 1429 PNWDLDDQYKFCYEVALEYLNS 1451
RESULT 9
ADI80761
ID ADI80761 standard; protein; 1452 AA.
XX AC ADI80761;
XX DT 15-APR-2004 (first entry)
XX DE Human protein tyrosine phosphatase receptor type mu protein sequence.
KW protein tyrosine phosphatase receptor type mu; PTPRM; cytostatic;
KW antidiabetic; gene therapy; expression pattern;
KW hyperproliferative disorder; cancer; metabolic disorder; diabetes;
XX infection; inflammation; tumour formation; human.
OS Homo sapiens.
XX OS Unidentified.
XX PN US2004014699-A1.
XX PD 22-JAN-2004.
XX PF 18-JUL-2002; 2002US-00200293.
XX PR 18-JUL-2002; 2002US-00200293.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowser LM, Dobie KW;
XX WPI; 2004-121596/12.
XX N-PSDB; ADI80645.
XX New antisense compound targeted to a nucleic acid molecule encoding
PT protein tyrosine phosphatase receptor type mu, useful for treating cancer
PT or diabetes or modulating expression of protein tyrosine phosphatase
PT receptor type mu.
XX Example 13; Page 33-38; 56pp; English.
XX This invention relates to a novel compound with an oligonucleotide 8-80
nucleotides in length targeted to a nucleic acid molecule encoding
CC protein tyrosine phosphatase receptor type mu (PTPRM) which specifically
CC hybridises with the nucleic acid molecule encoding PTPRM and inhibits the
CC expression of PTPRM or specifically hybridises with at least 8-nucleotide
CC portion of a preferred target region on a nucleic acid molecule encoding
CC PTPRM. The invention may be useful for the production of compositions
CC with a cytostatic or antidiabetic activity. In addition, the disclosed
CC sequences may be useful for gene therapy. The compound, particularly the
CC antisense oligonucleotide is useful in modulating the function of nucleic

CC acid molecules encoding PTPRM. The antisense compound can also be used as
 CC research tools and diagnostics. It can also be used as tools in
 CC differential and/or combinatorial analyses to elucidate expression
 CC patterns of a portion or the entire complement of genes expressed within
 CC cells and tissues. The compound can also be used for treating diseases or
 CC conditions associated with PTPRM, preferably hyperproliferative disorder,
 CC for example cancer or metabolic disorders, for example diabetes. The
 CC compound can also be used as prophylaxis, for example to prevent or delay
 CC infection, inflammation or tumour formation. The present sequence is that
 CC of the human protein tyrosine phosphatase receptor type mu (PTPRM) which
 CC is related to the invention.

XX
 SQ Sequence 1452 RA;

Query Match 62.4%; Score 4807; DB 8; Length 1452;
 Best Local Similarity 60.8%; Pred. No. 0;
 Matches 889; Conservative 206; Mismatches 326; Indels 42; Gaps 8;

QY 4 TAAALPAFVALLLLSWPLLGSAGQSFAGGCTPDGPGACDYHQDLYDDFEWVHSAQ 63
 DB 3 TLGCTLATLGLL-----TAAGTFSGGCLFDEPYSTCGYSQSGEDDFNWEQVNTL 54
 QY 64 EPHYLPEMPQGSYMIYDSDHDPGEKARLQLPKMKENDTHCIDFSYLLYSOKGLNPGTL 123
 DB 55 TKPTSDPMPSSGSLMVNAGRPEGQRAHLLLPOLKENDTHCIDFHYFVSKSNSPEGLL 114
 QY 124 NILRVNKGPLANIPNVGTGRDMLRABLAIVSTFWPNEYQVIFAEVSGGSGYIAID 183
 DB 115 NVYKVNNGPLGNIPWINSIGDPTWNRABLAIVSTFWPNEYQVIFEV-ITSGHQYLAI 173
 QY 184 DIQVLSVPCDSHFLRLGDEVNAGQATQCIATORDAVHKNLWJORNGEDIPVAQT 243
 DB 174 EVKVLGHPCRTTRFHLRIQVNEVNAQFATFQCSAIGRTVAGDRLMTQGDIVRDAPLKEI 233
 QY 244 KTNHRRFAASERLQEVTKDQDLRYCVTOSERGSGVSNFAQLIVREPPPIAPPOLLGV 303
 DB 234 KVTSSRRFIASFVNVTTKDAGKRCMIKEGVGSGVSNFAELVKEPPPIAPPQASV 293
 QY 304 GPTYLLIQLNANSIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYIRV 363
 DB 294 GATYLMIQLNANSINGDPIVAREVEYCTASGWNDRQPVDSYKIGHLDPDTEYISV 353
 QY 364 LLTRPBGEGTGLPPPLITTKCAEPWRTPKTKIABIQARRIAVDWESIGYINTRCHTF 423
 DB 354 LLTRPBGEGTGSRGPALRTKCADPMRGKLEWVEVSKRQITIRWEPPGYNVTRCHSY 413
 QY 424 NVTCICHYFRGHNESKAD--CLDMDPKAPOHVNVHLPPTYNVSLKMTLTPPEGRKSEET 481
 DB 414 NLIVHYCYQVGGEQVREEVSWDTEHSHQHTITNLSPYTNVSKLILMMPPEGRKSSQEL 473
 QY 482 IIQTDEDVPGVPVKSLQGSTFENKIFLNWKEPLDPNGIITQVEISYSSIRSFDPAPVPA 541
 DB 474 IVQTDDELPCAVPESIQGSTFEKIFLOWREPTQYGVITLYEITYKAVSSDPEDLS 533
 QY 542 GPQTVSNLWNSHHVPMHLPGTQYFFRASTVKGFPGPATAINVTNISAPLDPYEG 601
 DB 534 NQSGRVSKLGNETHFLPFLPGTYSFTIRASTAKGFGPPATNQFTTKISAPSPAYE- 592
 QY 602 VDAISLATATITVLRLPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVYNA 661
 DB 593 LETPLNQTNDTNTVLMKPAHSRGAPVSVYQIVVEEERPRETKTKTEILKCYVPPIHFQNA 652
 QY 662 MSGGAPYYFAELPPGNLPEPAPTVGDNRQTYQGFVWNPPLAPRKGYNIFYQAMSSVEKET 721
 DB 653 SLNLSQYFYFAEPADSLQAQPTTIGDNTYNGYWNTPLLPYKSYRIFYQAASRANGET 712
 QY 722 KTCQVRIATKAATEEPEVIPPDAKQDTRVVVKIAGISAGILVFIILLVLLVILVKKSKIAK 781
 DB 713 KIDCVQVATGAA--TPKPVPEPEKQTDHTVKIAGVIAGILLFVIFLGVLMVKRKLAK 771
 QY 782 KRQDAMGNITQETHVMNANDRSYADOSTLHAEDPLSITWDOHNSFPY----- 831
 DB 772 KRKETMSSTRQEMTMVNSMDKSYAEQGTNCDE---AFSEMDTHNLNGRSVSPSSFTMK 828

QY 832 -----ENHSATAESSRLLDVPRY-LCEGTSPYQTGQLHPAIRVADLLQH 875
 DB 829 TNLSTSPVNSYYPDETHTMASDTSLSVQSHYTKKREPADVQYQTGQLHPAIRVADLLQH 888
 QY 876 INLMKTSDSYKPEEYESFEGOSASWDVAKDONRAKNRYGNIIADHSRVILQPVDD 935
 DB 889 ITQMKCAEGYKPEEYESFEGOSAPWDSSAKDONRMKNRYGNIIADHSRVILQTIEGD 948
 QY 936 PSSDIYANANTIDGYQRPESHYIATQGPVHETVYDFWRMIWQESACIYVNTNLVSVGRVKC 995
 DB 949 TNSDINGNYIDGVHREHYIATQGPMEQIYDFWRMVWHTENTASIIWNTNLVEVGRVKC 1008
 QY 996 YKWPDDTEYVGDYKVTCEMEPLAEYVVRFTTLRRGYNEIREVKQFHFTGWPDPHGVY 1055
 DB 1009 CKYWPDDTEYIKDVKVTLIETELLAAYVIRTFAVEKRGVHEIREIROFHTGWPDPHGVY 1068
 QY 1056 HATGLLSFIRVKLSNPSPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGCVVDIYNCVK 1115
 DB 1069 HATGLLGFVRQVSKSPSPSAGPLVHCSAGAGRTGCYIVIDIMLDMAREGCVVDIYNCVR 1128
 QY 1116 ALASRRINMVQTEEQYIFIHDAILEACLCEGTAPVCEFAAYFDMIRIDSTQNSSHLKD 1175
 DB 1129 ELASRRINMVQTEEQYIFIHDAILEACLCEGTSPVSAQSVESLYYDMNKLDPQTNSSQIKE 1188
 QY 1176 EPTLNSVTPRLQACDSIACLPNHDKNRPMDLPPDRCLPFLITIDGSSSNYINAALM 1235
 DB 1189 EPTLNMVTPRLVEDCSIALPRNHEKNRPMDLPPDRCLPFLITIDGSSSNYINAALM 1248
 QY 1236 DSVROPAAFTVQYPLNTPVKDFWRLVYDYGCTSIYVNLNEVDLSQGCYQVWPEGMRLYG 1295
 DB 1249 DSYKQSPSAFTVQYPLNTPVKDFWRLVYDYGCTSIYVNLNEVDLPAQLCPQYWPENGVRHG 1308
 QY 1296 PIQVECMSCSMDCDVINRIENLTPRQBYGLMWQOQOYVLGWASHREVPKGSFELKI 1355
 DB 1309 PIQVEFVSADLEEDISRIYNAARPDQYRWVQOQFQLGWPMYRDTVPVSKRSFELKI 1368
 QY 1356 LQVEKQEEWKEGEGRTIHCINGGSGRSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSK 1415
 DB 1369 RQVDMQKEEYNGGEGPTVHCLNGGSGRSGTFCALISVCEMLRHQRTVDVFAVKTLRNK 1428
 QY 1416 PNWVEAPEQYRFDYVALEYLES 1438
 DB 1429 PNWDLDDQYKFCYEVALEYLNS 1451

RESULT 10
 ABR58629
 ID ABR58629 standard; protein; 1452 AA.
 XX ABR58629;
 XX AC
 XX AC
 XX AC
 DT 09-JUL-2003 (first entry)
 XX
 DE Human cancer related protein SEQ ID NO:286.
 XX
 KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.
 XX
 OS Homo sapiens.
 XX
 PN WC2003025138-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-US029560.
 XX
 PR 17-SEP-2001; 2001US-0323469P.
 PR 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX PA Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX PI Zlotnik A;
XX
XX MPI; 2003-354600/33.
XX DR N-PSDB; ACC72776.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 750; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX atherosclerosis and endometriosis. The nucleic acid is also useful in
XX drug screening, particularly for identifying agents for treating these
XX pathologies
XX
XX Sequence 1452 AA;
SQ

Query Match 62.3%; Score 4806; DB 6; Length 1452;
Best Local Similarity 61.4%; Pred. No. 0;
Matches 886; Conservative 206; Mismatches 318; Indels 34; Gaps 7;
23 LLGSAQGFSGAGCTFDGPGACDHYDLDDFEVHVHSAQEPHLPPEMPOGSMIVDS 82
14 LLLTAAGSTFGGCLFDPSTCYGVSQSEGDNFMEQVNTLTKTPTSDPMPSPGSLMUNA 73
83 SDHPGEKARLQLPWKENDTHCIDFVLLYSQKGNPCTLNILVRVKNKGLPIANVT 142
74 SGRPEGARHLLLPOLKENDTHCIDFVSVSKSNPPGLLNYYKVNKGLNPIWNIS 133
143 GFTGRDWLRABLAVSTFWPNEVQVIFAEVSGRSGYIAIDDIQVLSYPCDKSPHFLRG 202
134 GDPTRTNRAELAIATFWPNFYQVIFEV-ITSGHGYLAIDEVKVLGHPCRTTPHFLRIQ 192
203 DVEVNAGQATFQCATGRDAVHKLWLQRNGEDIPIVAQTKNINHRFPAASERLOEVTK 262
193 NVEVNAGQATFQCAIGRTVAGDRLMLQGDIVRDAPLKEIKVTSRRPIASFNVVNTTK 252
263 TDQDLRCVCTOSERSGVSNFAQLIVREPPRPRIAPPQLLGLVPTLLIQLNANSIIGDGP 322
253 RDAGKYRCMIRTEGGVGSINAEVLVKEPPVPIAPPQLASGATVYLWQLNANSINGDGP 312
323 IILKEVYRMTSGTETHAVNAPYKJWLHDDPDTEYEIRVLLTRPGGGTGLPGPLIT 382
313 IVAREVEYCTASGSWNRDPQVDSYKIGHLPDTEYBISVLLTRPGGGTSGPGALRT 372
383 RTKCAEPNRTPTKIAETQABRIADVESLGYNITRCHTNVTTCYHYFCHNESHKAD- 441
373 RTKCAADMRGPKRLEVEVSKQIITIRWEPFGYNTCHSYNLTVHYCYQVGGQVREE 432
442 -CLMDMPKAPQHVNVHLPPTYNVLSKMLITNPEGRKSEETIIQTDDEVPVGVKSLQG 500
433 VSWDTEHNSHPQHTITNLSPYTNVSVKLLMLNPEGRKESQELIVQTDDELPGAVPTESIQG 492
DB

QY 501 TSFENKIFLWKEPLDPNGIITQYEISYSSIRSSEDPAPVPVAGPPQTVQVSNLWNSHTHVFWH 560
DB 493 STFBEEKIFLOWREPTQYGVITLVEITYKAVSSPDEIDLSNQSGRVSUKLGNETHFLFFG 552
QY 561 LHPGTTYOFFIRASTKVGFGPATAINVTNISAPLTDYEGVDASLNETATITVLLRPA 620
DB 553 LYPGTTYFTIRASTAKGFGPPATNQPTTKISAFMPAYE-LETPLNQTDNTVTVMLKPA 611
QY 621 QAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVYONAMSGAPYFFAAELPPGNLP 680
DB 612 HSRGAPSVYQIVVEEERPRTKTKTEILKCYPIPHFQNASLLNSQSYFFAAEFPAADSIQ 671
QY 681 EPAPFTVDNRTYOGFNPPLAPRKGNYIYQAMSSVEKETKTCVRIATKAATEEPEVI 740
DB 672 AAQPFITGDNKTNGYWNTPLLPYKSYRIYFQNASRANGETKIDCVQVATGAA-TPKPV 730
QY 741 PPAKQTDVVKIAGISAGILVFIILLVLIIVKSKLAKKRDAMGNTQEMTHMVNA 800
DB 731 PEPEKQTDHTVKIAGIAGILLFVILFGLVVLWKKRLAKKRETSSTQEMTVWNS 790
QY 801 MDRSYAQDSTLHAEDPLSITFMDQHNSPRY- - - - -ENHS 835
DB 791 MDKSYAEQGTNCDE- - -AFSEMDTHNLNGRSVSPSSFTMTKNTLSTSVPSNYYDETHT 847
QY 836 ATAESSRLLDVPRY-LCEGTESPYQTQLHPAIRVADLLQHLINLMKTSDSYGFKEEYESF 894
DB 848 MASDTSLSVQSHYTKKREPADVYQTQLHPAIRVADLLQHTQMKCAEGYGFKEEYESF 907
QY 895 FEGQASQWVAKQONAKRNYGNIAYDHSRVLQPVDEDPSSDYINANTYIDGQRPESH 954
DB 908 FEGQASQWVAKQONAKRNYGNIAYDHSRVLQPVDEDPSSDYINANTYIDGQRPESH 967
QY 955 YIATQGPVHETVYDFWRMIWQESACIVMVTNLVEVGRVKCYKYPDPDTEVYVGDPKVTCV 1014
DB 968 YIATQGPVHETVYDFWRMIWQESACIVMVTNLVEVGRVKCYKYPDPDTEVYVGDPKVTCV 1027
QY 1015 EMEPLAEYVVRFTFLERRGYNEIREVQFHTGHPDHGVPYHATGLLSFIRKLSNPS 1074
DB 1028 ETELLAEYVIRTFVAVEKRGVHEIREIRQFHTGHPDHGVPYHATGLLGFRVQVSKSPPS 1087
QY 1075 AGPIVWHCSAGAGRTGCVIVIDIMDMAEREGVVDIYNCVKALRSRRINMVQTEQYIFI 1134
DB 1088 AGPIVWHCSAGAGRTGCVIVIDIMDMAEREGVVDIYNCVKALRSRRINMVQTEQYIFI 1147
QY 1135 HDAILEACLCGETAIPVCEFKAAFYDMIRIDSQTNSSHLKDEFOQLNSVTPLRQAECSII 1194
DB 1148 HDAILEACLCGETAIPVCEFKAAFYDMIRIDSQTNSSHLKDEFOQLNSVTPLRQAECSII 1207
QY 1195 ACLPRNHDKNRPFMDLPPDRCLPFLITIDGSSNVIINAAIMDSYQPAAFVTVQPLNPT 1254
DB 1208 ALLPRNHEKNRPFMDLPPDRCLPFLITIDGSSNVIINAAIMDSYQPAAFVTVQPLNPT 1267
QY 1255 VKDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYVWEGMLRYGPIQVECMSCSDCDVINRI 1314
DB 1268 VKDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYVWEGMLRYGPIQVECMSCSDCDVINRI 1327
QY 1315 FRIENLTPRQBYGLMWQOQFVYLGWASHREVPGSKRSFLKILQVEKWESEWKEGRTII 1374
DB 1328 FRIENLTPRQBYGLMWQOQFVYLGWASHREVPGSKRSFLKILQVEKWESEWKEGRTII 1387
QY 1375 HCLNGGSGRGMFCAIGIVEMVKQNVVDVFAVKTILNSKPNMVEAEQYRFFCYDVALE 1434
DB 1388 HCLNGGSGRGMFCAIGIVEMVKQNVVDVFAVKTILNSKPNMVEAEQYRFFCYDVALE 1447
QY 1435 YLES 1438
DB 1448 YLNS 1451
RESULT 11
ADJ68277
ID ADJ68277 standard; protein; 1452 AA.

Db 1189 EPTLNMVPTTLRVEDCSIALLPNNHKNRCWMDILPPDRCLPLFLITIDGESSNVINAALM 1248
Qy 1236 DSYQPAAFIVTQPLPNTVDFWRLVVDYDGTSTVLMNEVDLSQGCQYWPBEGMLRYG 1295
Db 1249 DSYQPSAFIVTQHPLPNTVDFWRLVLDVHCTSVMLNDVDPALQCPQYWPBEGVHRHG 1308
Qy 1296 PIVBECMSCMDCVINRIFRICNLTRPQEGVLMVQOQFYGLGWASHREVPGSKRSFLKLI 1355
Db 1309 PIVBFEVSADLEEDIIISRIFRYNAARPDQGRHVMVQOQFYGLGWPMDTTPVSKRSALLLI 1368
Qy 1356 LQVEKQWKEWKEGEGRTIIHCLINGGGRSGMFCAGIVVEMVKRQNVVDVFAVKTLRNSK 1415
Db 1369 RQVDKQWQEEYNGGEGPTVVHCLINGGGRSGTFCALSIVCEMLRHQRTVDVFAVKTLRNK 1428
Qy 1416 PNMVEAPEQYRCPYDVALEYLES 1438
Db 1429 PNMVDLLQYKFCYEVALEYLNS 1451
RESULT 12
AAW80143
ID AAW80143 standard; protein; 1455 AA.
XX AC AAW80143;
XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3789.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX OS Homo sapiens.
XX FN WO200157190-A2.
XX PD 09-AUG-2001.
XX PF 05-FEB-2001; 2001WO-US004098.
XX PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
XX PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
DR N-PSDB; AAK53276.
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX Claim 20; Page 437-438; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW7823-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX SQ Sequence 1455 AA;
Query Match 62.0%; Score 4777.5; DB 4; Length 1455;
Best Local Similarity 60.4%; Pred. No. 0;
Matches 885; Conservative 207; Mismatches 330; Indels 43; Gaps 9;
Qy 4 TAAALPAFVALLLSPMLLSAGOGFASAGCTFDDGPGACDYHQDLYDDPFWHVHSAQ 63
Db 3 TLGTCLATLALL-----TAAGTFSGGCLFDEPYSTCGYSQSEGGDFNWEQVNTL 54
Qy 64 EPHYLPPEMPOGYSYMIVDSSDHPDGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGTL 123
Db 55 TKPTSDPMPSPGSPMLVNASRPEGQRHALLLPOLKENDTHCIDFHYFVSKSNSPPGLL 114
Qy 124 NILVRNKGPLANPIVNTGTGRDWLRAELAVTFWPNFYQVIFPEAEVSGRSGYIAD 183
Db 115 NVYKVNNGPLGNPIWISGDPTRTNRAELAISTFWPNFYQVIFEV-ITSGHQGYLAID 173
Qy 184 DIOVLSYPCDKSPHFLRLGDVENVAGONATFOCIATGRDAVHNKILWLQRRNGEDIPVAQT 243
Db 174 EVKVLGHPCTRIPLHLRIQNVENVAGQFATFOCSAIGRTVAGDRMLWLOGIDVRAPLKEI 233
Qy 244 KNINHRFAASFRLOEYVTKTDQDLYRCVTOSESGSVSNFAQLIVREPRPIAPPQLGV 303
Db 234 KVTSSRFASFNVVNTTKRDAGKYRCMIRTEGGVIGSYAEVLVKEPPVPIAPPQLASV 293
Qy 304 GPTYLLIQLNANSIIGDPIILKEVEYMTSGSWTETHAVNAPYKLMHLPDPTDEYETRV 363
Db 294 GATYLIQLNANSINGDPIVAREVEYCTASGWNDRQVDVSTSYKIGHLPDPTDEYETSV 353
Qy 364 LLTRPGEGLCPGPLITRTKCAEPMRTPTKLTAEIQARRIAVDMSLGVNTRCHTF 423
Db 354 LLTRPGEGLTSGPGLTRTKCADPMRGPRLKEVVEVKSQITIRWEPFGVNTRCHSY 413
Qy 424 NVTCYHYFRGHNESKAD--CLDMDPKAPQVVAHLPPTVNVSLKMLITNPEGRSEBET 481
Db 414 NLTVHYCYVQGGQVREEVSWDTEHSPQHTITNLSPTVNVSVKLLMNPGRKESQBL 473
Qy 482 IIQTDDEVPVGVKSLQGSTFENKIFLNWKEPDPNGIITQYEISYSISIRSFDPAPVA 541
Db 474 IVQTDDELPGAVPPTESIQGSTFEKIFLQWREPTQTYGVITLYEITYKAVSFDPEIDL 533
Qy 542 GPQTVSNLWNSTHHFMHLHPGTTTYOFFIRASTVYKGPATAINVTTNISAPTLPDYEG 601
Db 534 NQGRVSKLGNETHFLFLFGLYPGTYSTIRASTAKGFGPPATQFTTKISAPSPAYE- 592
Qy 602 VDASINETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVYQNA 661
Db 593 LETPLNQDNTVTVMLKPAHSRGAPSVYQIVVEEERPRRTKTKTEILKCPVPPIHFQNA 652
Qy 662 MSGGAPYFAAEPLPPGNLPDEPAPFTVGNRTYQGFNPNPLAPRKGYNTYFQAMSSVEKET 721
Db 653 SLLNSQYFAAEFFPADSLQAAQPFPTIGDNKTYNGVWNTPLLPYKSYRYFQAAASRANGET 712
Qy 722 KTCQVRIATKATBEPEVIPPAPQOTDRVVKIAGISAGILVFILLVLLVILVKKSLAK 781
Db 713 KIDCVQVATKGA--TPKPEVPEPEXQTDHTVKIAGVIGILLFVILFLGVLLVKKRKLAK 771
Qy 782 KRKDAWGNTQRETMVMVNMAD--RSYADQSTLHAEDPLSITFMDQHNFSRY----- 831
Db 772 KRKETMSRQREIDILWIGELNGPRSYAQGTKLATRAFS--FMDTHNLNGRSVSSPSSFT 829
Qy 832 -----ENHSAEASSRLLDVPRY-LOEGTESPQTQQLHPAIRVADLL 873
Db 830 MKTNTLSTSVNSVYYPDETHTMASDTSSLVQSHTYTKKEGPADVPYQTQQLHPAIRVADLL 889
Qy 874 QHINLMKTSDSYGFKEEYESFFEGSASWDVAKQDNRAKNRYGNI IAYDHSRVILQPV 933

Db 890 QHITQMKCAGYGFKEEYESFEQSSAPWDSAKDENMKRYGNIAYDSRVLQTI 949
 Qy 934 DPSSDYINAYIDYQRPSHYIATQGFVHETVDFWRMIWQEQSACIWMVNLNVEGRV 993
 Db 950 GDTNSDYINGNYIDYHRPNHYIATQGPQSTIYDFWRWVWHENTASIMVNLNVEGRV 1009
 Qy 994 KCIYKWPDDTEYVGDYKTCVEMPELAYVVRTTLERAGNEIREVKQHFTGPDHGV 1053
 Db 1010 KCKYKWPDDTEYVGDYKTCVEMPELAYVVRTTLERAGNEIREVKQHFTGPDHGV 1069
 Qy 1054 PYHATGLLSFRRVKLSNPPSAGPIVHCSAGAGTCGYIIVIDIMLMAEREGVVDIYNC 1113
 Db 1070 PYHATGLLGFVRQVKSPPSAGPIVHCSAGAGTCGYIIVIDIMLMAEREGVVDIYNC 1129
 Qy 1114 VKALRSRRINNVQTEQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTNSSHL 1173
 Db 1130 VRELRSRRVNVQTEQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTNSSHL 1189
 Qy 1174 KDEQTLNSVTPRLOAEDCSIACLPRNHDKVRFDMLPPDRCLPFLITIDGESSNYINAA 1233
 Db 1190 KBEFTLNMVTPTRVEDCSIALPRNHEKNCMDILPPDRCLPFLITIDGESSNYINAA 1249
 Qy 1234 LMDSYROPAAFIYQYPLNTPVDFWRLVVDYDGTCTSIWMLNEVDLSQCPQYWEPEGMLR 1293
 Db 1250 LMDSYKQPSAFIVTQHPNTPVDFWRLVVDYDGTCTSIWMLNEVDLSQCPQYWEPEGMLR 1309
 Qy 1294 YGPIQVCMSCMDCDVINRIFRINLTPRQEGYLMVQOFOYLGWASHREVPKSRFLK 1353
 Db 1310 HGPIQVEFVSADLEDIISRFRIYNAARPDGYRMVQOFOYLGWASHREVPKSRFLK 1369
 Qy 1354 LIQVQKQEWKEGEGRTIHCINGGGRGSMFCAIGIVEMVKRQNVDFHAKVTLRN 1413
 Db 1370 LIQVQKQEWKEGEGRTIHCINGGGRGSMFCAIGIVEMVKRQNVDFHAKVTLRN 1429
 Qy 1414 SKNWEAPQYRCYDVALEYLS 1438
 Db 1430 NKNMVDLLDQYKFCYEVALEYLS 1454

RESULT 13

ADB79775
 ID ADB79775 standard; protein; 1436 AA.

XX ADB79775;

XX 04-DEC-2003 (first entry)

DE Rat putative receptor tyrosine phosphatase, SEQ ID 15.

XX Analgesic; pain; streptozocin-induced diabetes; rat.

XX Rattus norvegicus.

XX EPI279744-A2.

XX 29-JAN-2003.

XX 26-JUL-2002; 2002EP-00255249.

XX 27-JUL-2001; 2001GB-00018354.

XX 07-FEB-2002; 2002GB-00002910.

XX (WARN) WARNER LAMBERT CO.

XX Brookebank RA, Dixon AK, Lee K, Pinnock RD;

XX WPI; 2003-395407/38.

XX N-PSDB; ADB79776.

PT Use of isolated gene sequences and encoded polypeptides that are
 PT upregulated in the spinal cord in response to streptozocin-induced
 PT diabetes for screening compounds for the treatment of pain, or for

PT diagnosing pain.

XX Claim 1; Page 59-64; 334pp; English.

CC The present invention relates to nucleotide sequences which are useful in
 CC the screening of compounds for the treatment of pain, or for the
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the
 CC spinal cord in response to streptozocin-induced diabetes. The present
 CC sequence was used to illustrate the invention.

XX Sequence 1436 AA;

SQ Query Match 59.78; Score 4602.5; DB 7; Length 1436;
 Best Local Similarity 60.3%; Pred. No. 0;
 Matches 855; Conservative 214; Mismatches 329; Indels 19; Gaps 9;

Qy 33 AGCTCTDGPQ---ACDYHODLYDDFEWVHVSQAQEPHYLPPEMQSGYMIYDSDHDPGE 89
 Db 24 AAGCTFEASDPVVPCEFSQAQYDDFQEQVRHPGTRTPEDLPHGAYLWNASQHTPGQ 83
 Qy 90 KARLQLPTMKENDTHCIDFYSLLYSQKLNPGTLNILVRVNGKGLANPIMNVGTGTGRDW 149
 Db 84 RAHIIFQTLSENDTHCVQFSYFLYSRDGHSPTGLGVVVRVNGPLGSAVNMNMTSGHQW 143
 Qy 150 LRRLAVSTFWPNEYQVIFEAESVSGRSGVIAIDDIQVLSYPCDKSPHFLRLGDFEVNAG 209
 Db 144 HQAELAVSTFWPNEFQVLFELALISPDHKGVIGLDILLFSPYCAKAPHFSLGDFEVNAG 203
 Qy 210 QNATFOCIATGRADVHNKMLQRNGEDIPVAQTKNINHRREAFSLQSVTKTDDOLYR 269
 Db 204 QNASFQCMAGRAAEAEHFLQSGVGLVPAAGVRHISHRRFLATFFLASVGRSEQDLYR 263
 Qy 270 CVTQSERGSGVNSPAQLIVREPRPIAPPOLLGVGPTYLLIQLNANSIIGDPIILKEVE 329
 Db 264 CVSQAPGAGVNSFAELIVKEPPIAPPOLLRAGTYLLIQLNANSIIGDPIVIRKEIE 323
 Qy 330 YRMTSGSWTTHAVNAPTYKLMHLDPTTEYRVLTRPGEGGTLGPGPLITTKCAEP 389
 Db 324 YRMARGPWAHVAVNLQTYKLMHLDPTTEYRVLTRPGEGGTLGPGPLISRTKCAEP 383
 Qy 390 MRTPKTLKIAEIQARRIADVWESIGYNIIRCHTFNVTICYHYFRG--HNESKADCLMDP 447
 Db 384 TRAPKGLAFABEQARQLTLQWEPLGVNVTCHTYAVSLCYRYTLGGSHNQTIRECVKMER 443
 Qy 448 KAPQHVNVHLPPYTNVSLKMLTNPEGRKESEETIIQTDSDVPVGVVPSVQSGSFENKI 507
 Db 444 GASRYTIKNLLPFNINHVRLITNPEGRKEGKVTFTDEDVFGIAAESLITFTPLEDMI 503
 Qy 508 FLWKPELDPNGIITQYEISYSSIRSPDPVAVVAGPQTVSNLWNSHTHVMHLHPGTTY 567
 Db 504 FLKWEPPQEPNGLITQYEISYQSTESSDPAVNVPGPRTTISKLRNETHYVPSNLHPGTTY 563
 Qy 568 QPFRASVKGFGPATINVTNISAPTLDPYEGVDASINETATTIIVLIRPAQAKAPI 627
 Db 564 LFSVRARTSKGFGQAALTEITNISAPSF--DYADMPSLGESENTIIVLIRPAQGRAPI 622
 Qy 628 SAYQIVVEELHPHRTKREAGAMECYOVPTYQYAMSGGAPYFAELPPGNLPAPFTV 687
 Db 623 SVYQVVEERPRRLRREPQACQCFSVPLIFETALAGLVHYFGAELAAASLLEAMFTV 682
 Qy 688 GDNRTYQGFNPPPLAPRKGYNIYFOAMSSVEKETKTQCVRIATKAATEEPEVDPKAKQT 747
 Db 683 GDNQTYRGFWNPPEPRKAYLIYFOAASHLKGTRLCNIRIARKAACSKSRPLEVSQRS 742
 Qy 748 DRVVKIAGISA-GILVFIILLVILIVKSKLAKKRDAMGNTRQMTMWNAMDRSYA 806
 Db 743 EEMGLILGICAGGLAVLILLGAILIIVIRKGPVNMTK-ATVNYRQEKTHMMSAVDSFT 801
 Qy 807 DQSTLHAEDPLSITFMDQHNFSRYENHS--ATAESSRLDDVRYLCEGTESPYQTGLH 864
 Db 802 DQSTLQEDRLGLSFMADAPGYSRPGDQSGVTEASSLGGSPRRPCGRKGPSYHTQLH 861
 Qy 865 PAIRVADLLQHLINLMKTSDSYGFKEEYESFEQSSASWDVAKKDQNRKRYGNIAYDH 924

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Db 862 PAVRVADLLQHINQMKTAEYGFQKEYSFEG---WDATKKDKLKGGRQEPVSADR 917
Qy 925 SRVLQPVDDPSSYINAWYIDGQVRSHYIATQPGVHETVYDFWRMIWQEQSACIVMV 984
Db 918 HHVKLHPMLADPDADYISANVYIDGVRSHHFIATQGPKEIMYDFWRMVWQEQCASIWI 977
Qy 985 TNLVEGVKVCYKWPDDTEVYDGFKTCVEMEPALAEVVRFTLEREGYNEIREVKQFH 1044
Db 978 TKLVEGVKVCYKWPDDTEVYDGFKTCVEMEPALAEVVRFTLEREGYNEIREVKQFH 1037
Qy 1045 FTGWPDHGVYPYHATGLLSFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAR 1104
Db 1038 FTAWPEHGVYPYHATGLLAFIRRVKASTPPDAGPIVHCSAGAGRTGCVIVLDMMAEC 1097
Qy 1105 EGVVDIYNCVVALRSRRINMQTEQYIFIHDAILEACLCGETAIPVCFKAAVYDMIRI 1164
Db 1098 EGVVDIYNCVTKCSRRVNMIQTEQYIFIHDAILEACLCGETTIPVNEFRATYREMIRI 1157
Qy 1165 DSQTNSSHLKDFQTLNSVTPRLQAECDGSIACLRNHDKNRPMMLPDRCLPELITIDG 1224
Db 1158 DPQSNSSQLREEFQTLNSVTPRLDVECSIALPRNDRKNRSMVLPDRCLPELISSDG 1217
Qy 1225 ESSNINAAALMDSYRQPAAFIVTOYPLNVTVDVWRLVYDYGCTSIIVMLNEVDLSQG--- 1281
Db 1218 DPNVYINAAALTDYSTRSAFIVLHPLQSTPDPFWRLVYDYGCTSIIVMLNQLNQSNSAWP 1277
Qy 1282 CPQYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNLTRPQEGYLMVQVQYVLGMASH 1341
Db 1278 CLQYWPBEGRQYGLMEVEFVSGTANEDLVSRFVRQVNSSRLQEGHLLVRHFQFLRWASAY 1337
Qy 1342 REVPSKRSFLKLILOVEKQWQEWKEGEGRTIIHCLNGGSGRSGMCAIGIIVEMVKRONV 1401
Db 1338 RDTPSRKAFLHLAEVDKQAE--SGDGRTVVHCLNGGSGRSGTFCACATVLEMRCHSL 1395
Qy 1402 VDVFFAVKTLRNSKPNMVEAPQYRFCYDVDALEYLES 1438
Db 1396 VDVFFAAKTLRNYKNMVEWTDQYHFCYDVDALEYLEA 1432

RESULT 14
AAW41361
ID AAW41361 standard; protein; 1436 AA.
XX
AC AAW41361;
XX
26-MAY-1998 (first entry)
XX
Receptor protein tyrosine phosphatase lambda polypeptide.
XX
Receptor protein tyrosine phosphatase lambda; mouse; PTP lambda; therapy;
KW cognate ligand; paralytic disease; metastatic spread prevention;
KW epithelial development; neuronal structure development;
KW neuronal pathfinding.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 158
FT /label= unknown
FT /note= "encoded by TWI"
FT Misc-difference 340
FT /label= unknown
FT /note= "encoded by CAR"
FT Misc-difference 1208
FT /label= unknown
FT /note= "encoded by YGC"
XX
WO9744458-A1.
XX
27-NOV-1997.
XX
22-MAY-1997; 97WO-US009056.
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XX 24-MAY-1996; 96US-00652971.
PR (GETH ) GENENTECH INC.
FA Cheng J, Lasky LA;
PI WPI; 1998-018512/02.
XX N-PSDB; AAV15004.
DR Receptor protein tyrosine phosphatase lambda polypeptide - potentially
PT useful in treating paralytic diseases and preventing metastases.
XX Claim 6; Fig 1; 118pp; English.
XX This sequence represents the mouse receptor protein tyrosine phosphatase
CC (PTP) lambda polypeptide of the invention. PTP lambda is: (i) mainly
CC expressed in adult mammalian brain, lung and kidney; (ii) not expressed
CC in adult liver; and (iii) can dephosphorylate phosphorylated tyrosine
CC (pY) residues. The DNA sequence is used to express recombinant PTP
CC lambda, and also as a source of probes for screening DNA libraries. PTP
CC lambda is used to isolate the receptor's cognate ligand (potentially
CC useful for treating paralytic diseases), and for preventing metastatic
CC spread. PTP lambda is also used as a molecular marker for particular
CC tissues, as a reagent in an assay for identifying PTP (ant)agonists, and
CC as a molecular weight marker in protein gels. The Ab is used in
CC diagnosis, tissue-typing and purification of PTP lambda, also it may
CC crosslink the receptor, resulting in its upregulation. PTP lambda is a
CC mediator of cell adhesion and may be involved in development of
CC epithelial and neuronal structures (neuronal pathfinding)
XX
SQ Sequence 1436 AA;
Query Match 59.5%; Score 4586.5; DB 2; Length 1436;
Best Local Similarity 60.3%; Pred. No. 0;
Matches 854; Conservative 213; Mismatches 331; Indels 19; Gaps 9;
Qy 33 AGGCTFDDGPG---ACDYHODLYDDFEWVHVYSAQEPHYLPPEMPOGSMYVDSSDDHDPGE 89
Db 24 AAGCTFEASDFVVPFCFSQAQYDDFQEQVRIHPGTRTPEDLPHGAYLWMNASQHTPGQ 83
Qy 90 KARLQLPMTKENDTHCIDFSYLLYSQKLNPGTILNLRVKNKGPLANPINWVTGTGRDW 149
Db 84 RAHIIFQTLSENDTHCVQFSYFLYSRDHSFGLGVYRVNGGPGLSAVNMWMTSGHGRQW 143
Qy 150 LRALAVSTFWPNEYQVIFEAESVSGRSGYTAIDDIQVLSYPCDKSPHFLRLGDVEVNAG 209
Db 144 HQAELAVSTFWPNEQVLFALISPDHKGYIGLDDILLFSYPCAKAPHFSRLGDVEVNAG 203
Qy 210 QNATFOCIATGCDVAVHKNKLWLRNGEDIPIVAQTKNINHRFAASFRLOEYTKTDQDLYR 269
Db 204 QNASFQCMAGRAAEAEHFFLQROSGVLVPAAGVRHHSRRFLATFFPLASVGRSQDLYR 263
Qy 270 CVTQSERGSGVSNFAQLIVREPPRPIAPPQLLVGPTVLLIQLNANSIIGDGPILKEVE 329
Db 264 CVSQAPRGAGVSNFAELIVKEPPTPIAPPQLLRAGPTVLIQLNTNSIIGDGPVKEIE 323
Qy 330 YRMTSGSWTETHAVNAPTYKLWHLDPDTEYIRVLLTRPGSGGTGLPGPLITRTKCAEP 389
Db 324 YRMARGPWAHVAVNLXTYKLWHLDPDTEYISVLLTRPGDGTGRPGPLISRTKCAEP 383
Qy 390 MRTPKTLKIAEIOARRIADVHESLGYNITRCHTFNVTICYHYFRG--HNESKADCLDMDP 447
Db 384 TRAPKGLAFABIOARQLQWEPGLGVNTRCHTVAVSLCYRYTLGGSHNQITRECVKMER 443
Qy 448 KAPOHVVNHLPPYTNVSLKMLITNPEGRKESEETIIQTDDEDVPGVPVVKSLQGTGFENKI 507
Db 444 GASRYTIKNLLPFRNIHVRLITNPEGRKEGKEVTFTQDEDVPGGIAAESLTFTPLEMI 503
Qy 508 FLNWKPELDPNGIITQYEISYSSIRSDPAVPVAGPOTVSNLNMNSTHHVFMHLPGTTY 567
Db 504 FLKWEPEQEPNGLITQYEISYQSISSDPVAVNVPGRRTISKLRNETYHVSFNLHPGTTY 563
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:41:58 ; Search time 33.7887 Seconds
(without alignments)
3179.172 Million cell updates/sec

Title: US-09-887-669-2
Perfect score: 7709
Sequence: 1 MDTAAALPAFVALLLSP.....EAPQVRCYDVALEYLESS 1439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7692	99.8	1439	2	US-08-449-644-2
2	7692	99.8	1439	2	US-08-087-244A-2
3	7571	98.2	1457	2	US-08-652-971-3
4	7571	98.2	1457	2	US-08-449-644-1
5	7571	98.2	1457	2	US-08-087-244A-1
6	7571	98.2	1457	2	US-08-991-258A-3
7	7571	98.2	1457	2	US-08-769-399-3
8	7571	98.2	1457	3	US-08-931-953A-3
9	4807	62.4	1452	2	US-08-449-644-8
10	4807	62.4	1452	2	US-08-087-244A-8
11	4791	62.1	1452	2	US-08-652-971-4
12	4791	62.1	1452	2	US-08-991-258A-4
13	4791	62.1	1452	2	US-08-769-399-4
14	4791	62.1	1452	3	US-08-931-953A-4
15	4586.5	59.5	1436	2	US-08-652-971-2
16	4586.5	59.5	1436	2	US-08-991-258A-2
17	4586.5	59.5	1436	2	US-08-769-399-2
18	4586.5	59.5	1436	3	US-08-931-953A-2
19	4076.5	52.9	777	4	US-09-949-016-7158
20	3725.5	48.3	1075	4	US-09-949-016-8308
21	1529.5	19.8	1501	2	US-08-447-464-3
22	1529.5	19.8	1501	2	US-08-716-679-3
23	1487.5	19.3	1911	1	US-08-348-006B-5
24	1487.5	19.3	1911	1	US-08-800-825A-5
25	1487.5	19.3	1911	3	US-09-158-657-5
26	1487.5	19.3	1911	5	PCT-US94-10166-5
27	1187	15.4	793	1	US-08-015-985-3

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Sequence 7, Appli
Sequence 8, Appli
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Sequence 3, Appli
Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-449-644-2
; Sequence 2, Application US/08449644
; Patent No. 5856162
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-KAPPA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,644
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/087,244
; FILING DATE: 01-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1439 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-449-644-2

Query Match 99.8%; Score 7692; DB 2; Length 1439;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTTAAALPAFVALLILSPPLGSAQOQSAGSCTEDDGGACDHYQDLYDDFEWVHV 60
DB 1 MDTTAAALPAFVALLILSPPLGSAQOQSAGSCTEDDGGACDHYQDLYDDFEWVHV 60
QY 61 SAQEPHYLPPEPQSGSYMIVDSSDHDHDPGEKARLQLPWKENDTHCIDFSYLLYSQKGLNP 120
DB 61 SAQEPHYLPPEPQSGSYMIVDSSDHDHDPGEKARLQLPWKENDTHCIDFSYLLYSQKGLNP 120
QY 121 GTNLNLRVKNKGPLANPIWNTGTGTRDMLRAELAVSTFWPNEQVIFPEAEVSGRSYI 180
DB 121 GTNLNLRVKNKGPLANPIWNTGTGTRDMLRAELAVSTFWPNEQVIFPEAEVSGRSYI 180
QY 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVNKLWLRNGEDIPV 240
DB 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVNKLWLRNGEDIPV 240
QY 241 AQTKNINHRFAASPRLOEVTKTODLYRCVTSQSGSGSVNFAQLIVREPRPTAPPQL 300
DB 241 AQTKNINHRFAASPRLOEVTKTODLYRCVTSQSGSGSVNFAQLIVREPRPTAPPQL 300
QY 301 LGVGYTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
DB 301 LGVGYTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
QY 361 IRVLLTRPGEGETGLPGPPLIRTRTKCAEPMRPTKTKIAEQARRIAVDWESLGNITRC 420
DB 361 IRVLLTRPGEGETGLPGPPLIRTRTKCAEPMRPTKTKIAEQARRIAVDWESLGNITRC 420
QY 421 HTFNVTICVHYPRGHNESKADCLMDPKAPQHVNHLPPTYNVSLKMLTTPGKESSE 480
DB 421 HTFNVTICVHYPRGHNESKADCLMDPKAPQHVNHLPPTYNVSLKMLTTPGKESSE 480
QY 481 TTIOTDEDVPGVPVKSLQGTSGFENKI FLNWKEDLPNGIITQYBISYSSRSFDPAPV 540
DB 481 TTIOTDEDVPGVPVKSLQGTSGFENKI FLNWKEDLPNGIITQYBISYSSRSFDPAPV 540
QY 541 AGPPTQVNLNMTSHHVFMHLHPGTYQFFIRASTVKGFGPATANVTNISAPTLDPYE 600
DB 541 AGPPTQVNLNMTSHHVFMHLHPGTYQFFIRASTVKGFGPATANVTNISAPTLDPYE 600
QY 601 GVDASINETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTQY 660
DB 601 GVDASINETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTQY 660
QY 661 AMSGAPYFAELPGLNPEPAPFTVGNRTYQGFNPPPLAPRKGYNIFYQAMSSVEKE 720
DB 661 AMSGAPYFAELPGLNPEPAPFTVGNRTYQGFNPPPLAPRKGYNIFYQAMSSVEKE 720
QY 721 TKTQCVRIATKAATBEPEVIPDPAKQTRVVKIAGISAGILVFILLVILVIVKSKLA 780
DB 721 TKTQCVRIATKAATBEPEVIPDPAKQTRVVKIAGISAGILVFILLVILVIVKSKLA 780
QY 781 KKKDAMGNTRQEMTHVMNMDRSVADQSTLHAEDPLSTFMDQHNFPSPRYENHSATAES 840
DB 781 KKKDAMGNTRQEMTHVMNMDRSVADQSTLHAEDPLSTFMDQHNFPSPRYENHSATAES 840
QY 841 SRLLDVPRYLCGTSPYOTGQLHPAIRVADLLQHLNLMKTSDSYGFKEEYSPFEGOSA 900
DB 841 SRLLDVPRYLCGTSPYOTGQLHPAIRVADLLQHLNLMKTSDSYGFKEEYSPFEGOSA 900
QY 901 SMDVAKQONRAKNRGNIIAYDHSRVILQPVEDDPSSDYINANYIDGQRPESHYIATQG 960
DB 901 SMDVAKQONRAKNRGNIIAYDHSRVILQPVEDDPSSDYINANYIDGQRPESHYIATQG 960
QY 961 PVHETVDFWRMIWQEOSACIYVMTNLVEVGRVKCYKWPDDTEYVGFKVCVMEPLA 1020
DB 961 PVHETVDFWRMIWQEOSACIYVMTNLVEVGRVKCYKWPDDTEYVGFKVCVMEPLA 1020
QY 1021 EYVVRTFTLERRGYNEIRVKQFHFTGMPDGHGVPVHATGLLSFIRRVKLSNPPSAGPIV 1080
DB 1021 EYVVRTFTLERRGYNEIRVKQFHFTGMPDGHGVPVHATGLLSFIRRVKLSNPPSAGPIV 1080

QY 1081 HCSAGAGRTCYIVIDIMLDMABREGVVDIYNCVKALRRSRINNMVQTEEQYIFIHDAILE 1140
DB 1081 HCSAGAGRTCYIVIDIMLDMABREGVVDIYNCVKALRRSRINNMVQTEEQYIFIHDAILE 1140
QY 1141 ACLGETAIPVCEPKAAAFDMIRIDSQTNSSHLKXDEFQTLNSVTPRLOAEDCSIACLPRN 1200
DB 1141 ACLGETAIPVCEPKAAAFDMIRIDSQTNSSHLKXDEFQTLNSVTPRLOAEDCSIACLPRN 1200
QY 1201 HDKRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTOYPLPNTVKDFWR 1260
DB 1201 HDKRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTOYPLPNTVKDFWR 1260
QY 1261 LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNL 1320
DB 1261 LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNL 1320
QY 1321 TRPQEGYLMVQOQFQYLGWASHREVPVSGSKRSFLKILQVEKWQEBWKEGEGRTIIHCLNGG 1380
DB 1321 TRPQEGYLMVQOQFQYLGWASHREVPVSGSKRSFLKILQVEKWQEBWKEGEGRTIIHCLNGG 1380
QY 1381 GRSQMFCAIGIVEMVKRQNVVDVHFVAVKTLRNSKPNMVEAPEQYRFCYDVALEYLESS 1439
DB 1381 GRSQMFCAIGIVEMVKRQNVVDVHFVAVKTLRNSKPNMVEAPEQYRFCYDVALEYLESS 1439

RESULT 2

US-08-087-244A-2
; Sequence 2, Application US/08087244A
; Patent No. 5863755
; GENERAL INFORMATION:
; APPLICANT: Schlössinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-KAPPA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,244A
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1439 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-087-244A-2

Query Match 99.8%; Score 7692; DB 2; Length 1439;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTTAAALPAFVALLSPWPLLSAQGQFSAGGCTFDDGPGACDTHQDLYDDFEWVHV 60
DB 1 MDTTAAALPAFVALLSPWPLLSAQGQFSAGGCTFDDGPGACDTHQDLYDDFEWVHV 60

QY 61 SAQEPHYLPPEMPOGSMYVDSSDHPDGEKARLQPTMKENDTHCIDPSYLLYSQKGLNP 120
DB 61 SAQEPHYLPPEMPOGSMYVDSSDHPDGEKARLQPTMKENDTHCIDPSYLLYSQKGLNP 120

QY 121 GTLMILVRNKGPLANFIMVNTGTFGRDLRAELAVSTFWPNEQVTFEAEVSGRSGYI 180
DB 121 GTLMILVRNKGPLANFIMVNTGTFGRDLRAELAVSTFWPNEQVTFEAEVSGRSGYI 180

QY 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATPQCIATGRDAVHNKMLQRRNGEDIPV 240
DB 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATPQCIATGRDAVHNKMLQRRNGEDIPV 240

QY 241 AQTKNINHRFAASFRLOEYVTKTDQDLYRCVTOSERGSVSNFAQLIVRPPPIAPPOL 300
DB 241 AQTKNINHRFAASFRLOEYVTKTDQDLYRCVTOSERGSVSNFAQLIVRPPPIAPPOL 300

QY 301 LGVGPYLLQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYKLVHLDPDDEYE 360
DB 301 LGVGPYLLQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYKLVHLDPDDEYE 360

QY 361 IRVLLTRPGGGTGLPGPPLITRTKCAEPWRTPKTKIABIQARRIAVDWESLGYNITRC 420
DB 361 IRVLLTRPGGGTGLPGPPLITRTKCAEPWRTPKTKIABIQARRIAVDWESLGYNITRC 420

QY 421 HTFNVTICVYFPGHNSKADCLMDPKAPQHVNNHLPYTNVSLKMLTNPGREKSEE 480
DB 421 HTFNVTICVYFPGHNSKADCLMDPKAPQHVNNHLPYTNVSLKMLTNPGREKSEE 480

QY 481 TIQTDEDVPGPVKSLQSTFENKIFLNKPKPLDPNGIITOVEISYSGIRGFDPAVPV 540
DB 481 TIQTDEDVPGPVKSLQSTFENKIFLNKPKPLDPNGIITOVEISYSGIRGFDPAVPV 540

QY 541 AGPPQTVSNLWNSHHVFMHLPGTTQYFFIRASTVKGFPGPATINVTNISAPTLPDYE 600
DB 541 AGPPQTVSNLWNSHHVFMHLPGTTQYFFIRASTVKGFPGPATINVTNISAPTLPDYE 600

QY 601 GVDASINETAATITVLLRPAQAGAPISAYQIVVEELHPHRTKREAGAMECYQVPTYQN 660
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QY 661 AMGGGAPYYFAELPPGNLPEPAPFTVGDNRQYQGFNNPPLAPRKGNYIFQAMSSVEKE 720
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QY 721 TKTCQVRIATKAATEBEPIVDPKQTDVVKIAGISAGILVFILLVLLVILVVKSKLA 780
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QY 841 SRLLDVPRYLCEGTESPYQGLHPALRVADLLQHLNLMKTSYSGFKEEYEFEGQSA 900
DB 841 SRLLDVPRYLCEGTESPYQGLHPALRVADLLQHLNLMKTSYSGFKEEYEFEGQSA 900

QY 901 SWDVAKKQDNRAKNRYGNIITAYDHSRVILQVPEDDPSSDYINANYIDGYORPSHYIATQ 960
DB 901 SWDVAKKQDNRAKNRYGNIITAYDHSRVILQVPEDDPSSDYINANYIDGYORPSHYIATQ 960

QY 961 PVHETVYDFWRMIWQBSACIMVMTNLVGRVKCYKYPDDTEVYDGFVKVTCVMEPELA 1020
DB 961 PVHETVYDFWRMIWQBSACIMVMTNLVGRVKCYKYPDDTEVYDGFVKVTCVMEPELA 1020

QY 1021 EYVVRFTLLRRGYNEIREVKQHFCTGWPDPGVPYHATGLLSFIRRVKLSNPPSAGPIVV 1080
DB 1021 EYVVRFTLLRRGYNEIREVKQHFCTGWPDPGVPYHATGLLSFIRRVKLSNPPSAGPIVV 1080

QY 1081 HCSAGAGRTCYIVIDIMDMAEREGVVDIYNCVKALRSRRINNVQTEQYIFHDAILE 1140
DB 1081 HCSAGAGRTCYIVIDIMDMAEREGVVDIYNCVKALRSRRINNVQTEQYIFHDAILE 1140

QY 1141 ACLCGETAIPVCEFKAAFYDMIRDSQTSNLSHLKDEFQTLNSVTPRLOAEDCSACIAPRN 1200
DB 1141 ACLCGETAIPVCEFKAAFYDMIRDSQTSNLSHLKDEFQTLNSVTPRLOAEDCSACIAPRN 1200

QY 1201 HDKNRFDMLPPDRCLPFLITIDGESSNYINAAIMDSYROPAAFIQYPLPNTVKDFWR 1260
DB 1201 HDKNRFDMLPPDRCLPFLITIDGESSNYINAAIMDSYROPAAFIQYPLPNTVKDFWR 1260

QY 1261 LVTYDYGCTSIWMLNEVDLSQGCQYWPPEGMRLYGPQVTECMSCMDCDVINRIFRICNL 1320
DB 1261 LVTYDYGCTSIWMLNEVDLSQGCQYWPPEGMRLYGPQVTECMSCMDCDVINRIFRICNL 1320

QY 1321 TRPQEGYLMVQQOYQYLGMASHREVPGSKRSFLKLLQVEKWQEBEGEGRTIHCINGG 1380
DB 1321 TRPQEGYLMVQQOYQYLGMASHREVPGSKRSFLKLLQVEKWQEBEGEGRTIHCINGG 1380

QY 1381 GRSGMFCAGIVVEMVKRQNVVDVFHAVKTLRNSKPNWVEAPEQYRCYDVALEYLESS 1439
DB 1381 GRSGMFCAGIVVEMVKRQNVVDVFHAVKTLRNSKPNWVEAPEQYRCYDVALEYLESS 1439

RESULT 3

US-08-652-971-3
; Sequence 3, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-971-3

Query Match 98.2%; Score 7571; DB 2; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

MOLECULE TYPE: protein
US-08-449-644-1

Query Match 98.2%; Score 7571; DB 2; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

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DB 1 MD-VAAALPAFVALWLYEWPLLGSAQGFAGGCTFDDGPGACDTHQDLYDDFEWVHV 59

QY 61 SAQEPHYLPPEMPOGSMYVDSDDHDPGEKARQLPTMKENDTHCIDFSYLLYSOKGLNP 120
DB 60 SAQEPHYLPPEMPOGSMYVDSDDHDPGEKARQLPTMKENDTHCIDFSYLLYSOKGLNP 119

QY 121 GTNLILVRNKGPLANIPNVNFTGRDLWLAELAVSTFWPNEQVTFEAEVSGRSGYI 180
DB 120 GTNLILVRNKGPLANIPNVNFTGRDLWLAELAVSTFWPNEQVTFEAEVSGRSGYI 179

QY 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATPQCIATGRDAVHNKLMQRRNGEDIPV 240
DB 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATPQCIATGRDAVHNKLMQRRNGEDIPV 239

QY 241 AOTKNINHRPFAAFLRLOEVTKTDDLYRCVTSERGSYVNFQAQLIVRPPRIAPPOL 300
DB 240 AOTKNINHRPFAAFLRLOEVTKTDDLYRCVTSERGSYVNFQAQLIVRPPRIAPPOL 299

QY 301 LGVGPYLLQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
DB 300 LGVGPYLLQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359

QY 361 IRVLLTRPBGEGTGLPGPPLITRTKCAEPMRTPKTKIABIQARRIAVDWESLGYNITRC 420
DB 360 IRVLLTRPBGEGTGLPGPPLITRTKCAEPMRTPKTKIABIQARRIAVDWESLGYNITRC 419

QY 421 HTFNVTICVHYFCHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESEE 480
DB 420 HTFNVTICVHYFCHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESEE 479

QY 481 TIQTDEDVGPVPVKSLOQTSFENKIFLNKPKLPDNGIITQVEYSYSSIRSFDPAPV 540
DB 480 TIQTDEDVGPVPVKSLOQTSFENKIFLNKPKLPDNGIITQVEYSYSSIRSFDPAPV 539

QY 541 AGPPQTVSNLWNSHTHVFMLHPGTTTQFFIRASTVKFGFPATAINVTNISAPLPDYE 600
DB 540 AGPPQTVSNLWNSHTHVFMLHPGTTTQFFIRASTVKFGFPATAINVTNISAPLPDYE 599

QY 601 GVDASLNETATTTVLLRPAQAGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQN 660
DB 600 GVDASLNETATTTVLLRPAQAGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQN 659

QY 661 AMSGGAPYFAELPPGNLPEPAPFTVGDNRKTYQGFVWNPPLAPRKGNYIFQAMSSVEKE 720
DB 660 AMSGGAPYFAELPPGNLPEPAPFTVGDNRKTYQGFVWNPPLAPRKGNYIFQAMSSVEKE 719

QY 721 TKTCQVRIATK-AATEPEVIPPAPKQTRDVVKIAGISAGILVFILLVLLVILVKSKL 779
DB 720 TKTCQVRIATKAAATEPEVIPPAPKQTRDVVKIAGISAGILVFILLVLLVILVKSKL 779

QY 780 AKRKQAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSTFMDQHNPSRY----- 831
DB 780 AKRKQAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSTFMDQHNPSRY----- 839

QY 832 ----ENHSATAESRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHLNLMKTSYSGF 887
DB 840 AVLDENHSATAESRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHLNLMKTSYSGF 899

QY 888 KEYEYEFQCSQSWDAKQONRAKRYGNIAYDHSRVILQPVDEDDPSDDYINANYI- 946
DB 900 KEYEYEFQCSQSWDAKQONRAKRYGNIAYDHSRVILQPVDEDDPSDDYINANYI 959

QY 947 -----DGYQRPSPHYIATQGPVHETVDFWFMVWQESACIWMVTNLVEGVRKCYKWPD 1001
DB 947 -----DGYQRPSPHYIATQGPVHETVDFWFMVWQESACIWMVTNLVEGVRKCYKWPD 1001

Db 960 IWLRYDGYQRPSPHYIATQGPVHETVDFWFMVWQESACIWMVTNLVEGVRKCYKWPD 1019

QY 1002 DTEVYGDVKVTCVEMEPLEAAYVVRFTFLERRGYNEIREVKQFHTGPDHGPVPHATGLL 1061
DB 1020 DTEVYGDVKVTCVEMEPLEAAYVVRFTFLERRGYNEIREVKQFHTGPDHGPVPHATGLL 1079

QY 1062 SFTRRVKLSNPPSAGPIVIVHCSAGAGRTGCTYIVIDIMDMAEREGVVDIYNCVKALRSRR 1121
DB 1080 SFTRRVKLSNPPSAGPIVIVHCSAGAGRTGCTYIVIDIMDMAEREGVVDIYNCVKALRSRR 1139

QY 1122 INNVQTEEQYIFTHDAILEACLCGETAIPVCEFAAYFDMIRIDSDQSNSSHLKDEFOFLN 1181
DB 1140 INNVQTEEQYIFTHDAILEACLCGETAIPVCEFAAYFDMIRIDSDQSNSSHLKDEFOFLN 1199

QY 1182 SVTPRLQAECDSTACLPNRHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYROP 1241
DB 1200 SVTPRLQAECDSTACLPNRHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYROP 1259

QY 1242 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIYVNLNEVDLSQCGPQYWPBEGMLRYGPIQVEK 1301
DB 1260 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIYVNLNEVDLSQCGPQYWPBEGMLRYGPIQVEK 1319

QY 1302 MSCMDCDVNIRIFRINLTPQEGYLMVQOFOYLGWASHREVPGSKRSFLKLLOVEKW 1361
DB 1320 MSCMDCDVNIRIFRINLTPQEGYLMVQOFOYLGWASHREVPGSKRSFLKLLOVEKW 1379

QY 1362 QEEWKEGEGRTIHLCLNGGSGMFCAGIYVWVVKRQNVVDVFAVKTILNSKPNVVEA 1421
DB 1380 QEEWKEGEGRTIHLCLNGGSGMFCAGIYVWVVKRQNVVDVFAVKTILNSKPNVVEA 1439

QY 1422 PEQYRCYDVALEYLESS 1439
DB 1440 PEQYRCYDVALEYLESS 1457

RESULT 5
US-08-087-244A-1
; Sequence 1, Application US/08087244A
; Patent No. 5863755
; GENERAL INFORMATION:
; APPLICANT: Schliesinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-KAPPA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,244A
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:

TELEPHONE: (415) 781-1989
TELEX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1457 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-258A-3

Query Match 98.28; Score 7571; DB 2; Length 1457;
Best Local Similarity 97.33; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;
QY 1 MDTTAAALPAFVALLLSLPWLLGSAQOQFSAGGCTFDDGPGACDHYQDLYDDFEWVHV 60
DB 1 MD-VAAAALPAFVALWLLYPWLLGSLGQFSAGGCTFDDGPGACDHYQDLYDDFEWVHV 59
QY 61 SAQEPHYLPPEMPOGSGYMIWDSSDHPGEXKARLQLPMTKENDTHCIDFSYLLYSQKGLNP 120
DB 60 SAQEPHYLPPEMPOGSGYMIWDSSDHPGEXKARLQLPMTKENDTHCIDFSYLLYSQKGLNP 119
QY 121 GTNLILVRNKGPLANINWVTGTGRDWLRAELAVSTFWPNEVQVIFAEVSGRSGYI 180
DB 120 GTNLILVRNKGPLANINWVTGTGRDWLRAELAVSTFWPNEVQVIFAEVSGRSGYI 179
QY 181 AIDDIQVLSYPCDKSPHFLRGDVEVNAGQATFQCIATGRDAVHNMKWLQRRNGEDIPV 240
DB 180 AIDDIQVLSYPCDKSPHFLRGDVEVNAGQATFQCIATGRDAVHNMKWLQRRNGEDIPV 239
QY 241 AQTKNINHRFAASFRLEQVTKDQDLYRCVTOSESGSVNSFAQLIVREPPRIAPPOL 300
DB 240 AQTKNINHRFAASFRLEQVTKDQDLYRCVTOSESGSVNSFAQLIVREPPRIAPPOL 299
QY 301 LGVGPYVLLIQLNANSIIGDPIILKEVEYMTSGSWTETHAVNAPYKYLWHLDPDTEYE 360
DB 300 LGVGPYVLLIQLNANSIIGDPIILKEVEYMTSGSWTETHAVNAPYKYLWHLDPDTEYE 359
QY 361 IRVLLTRPGGGTGLPGPPLITRTKCAEPMRTPTKIAIEIQARRIAVDWESLYGYNITRC 420
DB 360 IRVLLTRPGGGTGLPGPPLITRTKCAEPMRTPTKIAIEIQARRIAVDWESLYGYNITRC 419
QY 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESEE 480
DB 420 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESEE 479
QY 481 TIIQTDDEVPVVKSLQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRGFDPAVPV 540
DB 480 TIIQTDDEVPVVKSLQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRGFDPAVPV 539
QY 541 AGPPQTVSNLWNSHTHVFHMLHPTQYFFIRASTVKFGPATAINVTNISAPLDPYE 600
DB 540 AGPPQTVSNLWNSHTHVFHMLHPTQYFFIRASTVKFGPATAINVTNISAPLDPYE 599
QY 601 GVDASLNETAITVILRPAQAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTVYQN 660
DB 600 GVDASLNETAITVILRPAQAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTVYQN 659
QY 661 AMSGGAPYFAELPPCNLPPEAPFTVGDNRQYOGFWNPPLAPRKGNYIFQAMSSVEKE 720
DB 660 AMSGGAPYFAELPPCNLPPEAPFTVGDNRQYOGFWNPPLAPRKGNYIFQAMSSVEKE 719
QY 721 TKTCQVRIATK-AATEPEVIPPDAKOTDRVVKIAGISAGILFVILLVLLVILVKKSKL 779
DB 720 TKTCQVRIATKAAATEPEVIPPDAKOTDRVVKIAGISAGILFVILLVLLVILVKKSKL 779
QY 780 AKKRKDMGNTROBMTWNVAMDRSYADQSTLHAEDPLSITFMDQHNFSRY----- 831
DB 780 AKKRKDMGNTROBMTWNVAMDRSYADQSTLHAEDPLSITFMDQHNFSRYLNDPLVPT 839
QY 832 ----ENHSATAESSRLDVPYLCEGTSPYQGLHPAIRVADLLQHLINLMKTSYGF 887

DB 840 AVLDENHSATAESSRLDVPYLCEGTSPYQGLHPAIRVADLLQHLINLMKTSYGF 899
QY 888 KEEYESFFEGQSASWDVAKKQNRKRYGNIITAYDHSRVILQVEDDPSDDYINANYI- 946
DB 900 KEEYESFFEGQSASWDVAKKQNRKRYGNIITAYDHSRVILQVEDDPSDDYINANYID 959
QY 947 -----DGYQRPISHYIATQGPVHETVDFWRMIWQEQSACIWMVTNLVEVGKVKYKWP 1001
DB 960 IWLRYDGYQRPISHYIATQGPVHETVDFWRMIWQEQSACIWMVTNLVEVGKVKYKWP 1019
QY 1002 DTEVYGDVKYTCVEMBPALAEYVVRTFTLERRGNEIREVKQFHTGPDGVPYHATGLL 1061
DB 1020 DTEVYGDVKYTCVEMBPALAEYVVRTFTLERRGNEIREVKQFHTGPDGVPYHATGLL 1079
QY 1062 SFIRRVKLSNPPSAGPIVHVCSAGAGRTGCIYVIDIMLMDAEREGVVDIYNCVKALRSRR 1121
DB 1080 SFIRRVKLSNPPSAGPIVHVCSAGAGRTGCIYVIDIMLMDAEREGVVDIYNCVKALRSRR 1139
QY 1122 INNVQTEEQYIFITHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEPOTLN 1181
DB 1140 INNVQTEEQYIFITHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEPOTLN 1199
QY 1182 SVTPRLOAEDCSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGESSNYINAAALMDSYROP 1241
DB 1200 SVTPRLOAEDCSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGESSNYINAAALMDSYROP 1259
QY 1242 AAFIVTQYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQCPQYWPBEGMLRYGPIOVEC 1301
DB 1260 AAFIVTQYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQCPQYWPBEGMLRYGPIOVEC 1319
QY 1302 MSCMDCDVINRIFRICNLTRPQEGYLMVQOYQYLGWASHREVPVSGKRSFLKLIQVEKW 1361
DB 1320 MSCMDCDVINRIFRICNLTRPQEGYLMVQOYQYLGWASHREVPVSGKRSFLKLIQVEKW 1379
QY 1362 QEEWKEGEGRTIITCLNGGSGRSMFCAIGIIVEMVKRONVVDVFAVKTILNSKPNMVEA 1421
DB 1380 QEEWKEGEGRTIITCLNGGSGRSMFCAIGIIVEMVKRONVVDVFAVKTILNSKPNMVEA 1439
QY 1422 PEQYRFDYVALRYLESS 1439
DB 1440 PEQYRFDYVALRYLESS 1457

RESULT 7

US-08-769-399-3
Sequence 3, Application US/08769399
Patent No. 597852
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Laaky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,399
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055

```
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-769-399-3

Query Match 98.2%; Score 7571; DB 2; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

QY 1 MDTTAAALPAFVALLSPPLLSAOGQFSAGGCTDDGPGACDHYHODLYDDPEWHV 60
DB 1 MD-VAALALPAFVALWLLYPPLLSALGQFSAGGCTDDGPGACDHYHODLYDDPEWHV 59
QY 61 SAQEPHYLPPEMPOQSGYIMVSSDHPDGEKARLQLPMTKENDTHCIDFSYLLYSQGLNP 120
DB 60 SAQEPHYLPPEMPOQSGYIMVSSDHPDGEKARLQLPMTKENDTHCIDFSYLLYSQGLNP 119
QY 121 GTNLILVRNKGPLANPINWVTGFTGRDLWRAELAVSTFWNEVOYIFEAESVSGRSGYI 180
DB 120 GTNLILVRNKGPLANPINWVTGFTGRDLWRAELAVSTFWNEVOYIFEAESVSGRSGYI 179
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DB 180 AIDDIQVLSYPCDKSPHFLRLGDLVEVNAQONATFOCIATGRDAVHKNLWLRNGEDIPV 239
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DB 240 AQTKNINRRFAASFLQEVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPPRIAPPOL 299
QY 301 LGVGPTYLLIQNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 360
DB 300 LGVGPTYLLIQNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 359
QY 361 IRVLLTRREGGTGLPGPLTRTKCAEPMRTPKLTKAEIOARIVADWESLGNITRC 420
DB 360 IRVLLTRREGGTGLPGPLTRTKCAEPMRTPKLTKAEIOARIVADWESLGNITRC 419
QY 421 HTFNVTICVHYPRGHNEKADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 480
DB 420 HTFNVTICVHYPRGHNEKADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 479
QY 481 TTIQTDVDPGVPVKSLQGTSEFNKIPLNWKPELDPNGIITQYBISYSSIRSFDPAPVP 540
DB 480 TTIQTDVDPGVPVKSLQGTSEFNKIPLNWKPELDPNGIITQYBISYSSIRSFDPAPVP 539
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DB 540 AGPPQTVSNLWNSTHHVFMLHPGTYQFFTRASTVKGFGPATAINVTTNISAPTLDPYE 599
QY 601 GVDASINETATTITVLLRPAQAKGAPISAYQIIVBELPHRTPKRAGAMECYQVPTVYQN 660
DB 600 GVDASINETATTITVLLRPAQAKGAPISAYQIIVBELPHRTPKRAGAMECYQVPTVYQN 659
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DB 660 ALSGAPYYFAAELPFGNLPEPAPPTVGDNRRTYQGFVWNPPLAPRKGYNIFYQAMSSVEKE 719
QY 721 TKTCQVRIATK-AAATEEPEVIPPDAKOTDRVVKIAGISAGILVFTLLLVLLVILVKKSL 779
DB 720 TKTCQVRIATKAAATEEPEVIPPDAKOTDRVVKIAGISAGILVFTLLLVILVILVKKSL 779
QY 780 AKKRDAMGNTQEMTHMVMNANDRSYADQSTLHAEDPLSLITFMDQHNFSPRY----- 831
DB 780 AKKRDAMGNTQEMTHMVMNANDRSYADQSTLHAEDPLSLITFMDQHNFSPRLPNDPLVPT 839
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QY 832 ----ENHSATAESSRLLDVPRYLCEGTESPYQTQOLHPAIRVADLLOHINLMKTSDSYGF 887
DB 840 AVLDENHSATAESSRLLDVPRYLCEGTESPYQTQOLHPAIRVADLLOHINLMKTSDSYGF 899
QY 888 KEEYESFFEGOSASWDVAKDONRAKNRYGNIIAYDHSRVILQPVEDDPSDDYINANYI- 946
DB 900 KEEYESFFEGOSASWDVAKDONRAKNRYGNIIAYDHSRVILQPVEDDPSDDYINANYI 959
QY 947 -----DGYQRPShYIATQGPVHETVYDFWRMIWQESACIWMVTNLVEVGKVCYKWPDP 1001
DB 960 IWLRYDGYQRPShYIATQGPVHETVYDFWRMVWQESACIWMVTNLVEVGKVCYKWPDP 1019
QY 1002 DTEYVYGFVKVTCVEMEPLEAEYVVRTFTLERRGYNEIREVKQFHTGPDHGVPHATGLL 1061
DB 1020 DTEYVYGFVKVTCVEMEPLEAEYVVRTFTLERRGYNEIREVKQFHTGPDHGVPHATGLL 1079
QY 1062 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRR 1121
DB 1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRR 1139
QY 1122 INMVQTEQYIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDSQTNSSHLKDFEOTLN 1181
DB 1140 INMVQTEQYIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDSQTNSSHLKDFEOTLN 1199
QY 1182 SVTPRLQAEDCSIACLPNHDKNRPFMDLPDRCLPLITIDGESSNYINAAALMDSYQRP 1241
DB 1200 SVTPRLQAEDCSIACLPNHDKNRPFMDLPDRCLPLITIDGESSNYINAAALMDSYQRP 1259
QY 1242 AAFIVTQVPLPNTVKDFWRLVVDYDCTSIWMLNEVDLSQGCPOQYWPBEGMLRYGPIQVEK 1301
DB 1260 AAFIVTQVPLPNTVKDFWRLVVDYDCTSIWMLNEVDLSQGCPOQYWPBEGMLRYGPIQVEK 1319
QY 1302 MSCSMDCDVINRIFRICNLTRPQEGYLMVQOQFYLGWASHREVPFGSKRSFLKLILQVEKW 1361
DB 1320 MSCSMDCDVINRIFRICNLTRPQEGYLMVQOQFYLGWASHREVPFGSKRSFLKLILQVEKW 1379
QY 1362 QEEWKEGEGRTIHLCLNGGSGMFCAGIIVEMVKQNVVDVHAVKTLRNSKPMVEA 1421
DB 1380 QEEWKEGEGRTIHLCLNGGSGMFCAGIIVEMVKQNVVDVHAVKTLRNSKPMVEA 1439
QY 1422 PEQYRFCYDVALEYLESS 1439
DB 1440 PEQYRFCYDVALEYLESS 1457

RESULT 8
US-08-991-953A-3
; Sequence 3, Application US/08991953A
; Patent No. 6083748
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,953A
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-991-953A-3

Query Match      98.2%; Score 7571; DB 3; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

QY 1 MDTAAALPAFVALLLLSPWLLGSAQGSAGGCTFDGPGACDYHODLYDDFEWVHV 60
DB 1 MD-VAAALPAFVALWLLYLPWLLGSAQGSAGGCTFDGPGACDYHODLYDDFEWVHV 59
QY 61 SAQEPHYLPPEMPOGYSYMIYDSSDHPGKARLQPTMKENDTHCIDFSYLLYSOKGLNP 120
DB 60 SAQEPHYLPPEMPOGYSYMIYDSSDHPGKARLQPTMKENDTHCIDFSYLLYSOKGLNP 119
QY 121 GTNLILVRNKGPLANIPINVTGTGRDMLRAELAVSTFWPNEYQVIFEAEEVSGRSYI 180
DB 120 GTNLILVRNKGPLANIPINVTGTGRDMLRAELAVSTFWPNEYQVIFEAEEVSGRSYI 179
QY 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQNAFQCIATGRDAVHNKMLQRRNGEDIPV 240
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QY 241 AQTKNINRRPAPAFRLQEVTKTDODLYRCVTOSESGVSNFAQLIVRPPPIAPPOL 300
DB 240 AQTKNINRRPAPAFRLQEVTKTDODLYRCVTOSESGVSNFAQLIVRPPPIAPPOL 299
QY 301 LGVPTVLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
DB 300 LGVPTVLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359
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DB 420 HTFNVTICYHYFRGHNSRADCLDMDPKAPQHVNVHLPPYTNVSLKMLTNPGRKESEE 479
QY 481 TIQTDEDDVPGVPVKSLQTSFENKIFLNKWEPLDPNGIITQVEISYSSIRSGFDPAVPV 540
DB 480 TIQTDEDDVPGVPVKSLQTSFENKIFLNKWEPLDPNGIITQVEISYSSIRSGFDPAVPV 539
QY 541 AGPPQTVSNLWNSTHVMHLHPGTTQFFIRASTVKGFGPATINVTNISAPTLPDYE 600
DB 540 AGPPQTVSNLWNSTHVMHLHPGTTQFFIRASTVKGFGPATINVTNISAPTLPDYE 599
QY 601 GVDAASLNETATTIVLARPAQAKAPISAYQIVVEELHPHRTKEEAGAMECYQVPVITYQ 660
DB 600 GVDAASLNETATTIVLARPAQAKAPISAYQIVVEELHPHRTKEEAGAMECYQVPVITYQ 659
QY 661 AMSGAPYFAAELPPGNLPEPAPFTVGNRTYQGFNWPPLAPRKGNINYFQAMSSVEKE 720
DB 660 ALSGAPYFAAELPPGNLPEPAPFTVGNRTYQGFNWPPLAPRKGNINYFQAMSSVEKE 719
QY 721 TKTCQVRIATK-AATEPEVIPPDAKQTDVWVIAGISAGILVPIILLVIVVIVKSKL 779
DB 720 TKTCQVRIATKAAATEPEVIPPDAKQTDVWVIAGISAGILVPIILLVIVVIVKSKL 779
QY 780 AKKRDAMGNTRQEMTHVMNAMDRSYADQSTLHAEDPLSITFMDQHNFSRY----- 831
DB 780 AKKRDAMGNTRQEMTHVMNAMDRSYADQSTLHAEDPLSITFMDQHNFSRPLPNDPLVPT 839
QY 832 ----ENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF 887
DB 840 AVLDENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF 899
QY 888 KEEVEFFEGQSASWDVAKKQNRKNRYNIIAYDHSRVILQPOVEDDPSDDYINANYI- 946
DB 900 KEEVEFFEGQSASWDVAKKQNRKNRYNIIAYDHSRVILQPOVEDDPSDDYINANYID 959
QY 947 ----DGYQRPISHYIATQGPVHETVDFWRMIWQESACIWMVTNLVEGVRKCYKWPD 1001
DB 960 IWLRYDGYQRPISHYIATQGPVHETVDFWRMIWQESACIWMVTNLVEGVRKCYKWPD 1019
QY 1002 DTEVYGDVFKVTCVEMEPPLAAYVVRTFTLERRGYNIREVKQFHTGMPDHGVPYHATGLL 1061
DB 1020 DTEVYGDVFKVTCVEMEPPLAAYVVRTFTLERRGYNIREVKQFHTGMPDHGVPYHATGLL 1079
QY 1062 SFIRRVKLSNPPSAGPIVHCSAGAGTGCYIVIDIMLMAEREGVVDIYNCVKALRSRR 1121
DB 1080 SFIRRVKLSNPPSAGPIVHCSAGAGTGCYIVIDIMLMAEREGVVDIYNCVKALRSRR 1139
QY 1122 INNVQTEEQYIFITHDAILEACLCGETAIPVCEFAAYFDMIRIDSTQNSSHLKDEFOTLN 1181
DB 1140 INNVQTEEQYIFITHDAILEACLCGETAIPVCEFAAYFDMIRIDSTQNSSHLKDEFOTLN 1199
QY 1182 SVTPRLOAEDCSITACLRNHDKNRFDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1241
DB 1200 SVTPRLOAEDCSITACLRNHDKNRFDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1259
QY 1242 AAFIVTQYPLPNTVKDFWRLVVDYDGTCTIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVE 1301
DB 1260 AAFIVTQYPLPNTVKDFWRLVVDYDGTCTIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVE 1319
QY 1302 MSCSMDCDVINRIFRINLTPQEGYLMVQOFOYLGWASHREVPFGSKRSLKLILQVEKW 1361
DB 1320 MSCSMDCDVINRIFRINLTPQEGYLMVQOFOYLGWASHREVPFGSKRSLKLILQVEKW 1379
QY 1362 QEEWKEGEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILNSKPNMVEA 1421
DB 1380 QEEWKEGEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILNSKPNMVEA 1439
QY 1422 PEQYRCYDVALEYLESS 1439
DB 1440 PEQYRCYDVALEYLESS 1457

RESULT 9
US-08-449-644-8
; Sequence 8, Application US/08449644
; Patent No. 5856162
; GENERAL INFORMATION:
; APPLICANT: Schlesinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```


ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/087,244A

FILING DATE: 01-JUL-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-042

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1452 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-087-244A-8

Query Match 62.4%; Score 4807; DB 2; Length 1452;
Best Local Similarity 60.8%; Pred. No. 0;
Matches 889; Conservative 206; Mismatches 326; Indels 42; Gaps 8;

QY 4 TAAALPAFVALLLLSPWLLGSAQGFSGAGCTFDDGPGACDYHQDLYDDFEWVHVAQ 63
DB 3 TLGTCLATLGLL-----TAAGTFSGCLFDFPSTCYGSGEGDDFNQVNTL 54
QY 64 EPHVLPPEMPOGSMIVDSDHDPGEKARLQLPMTKENDTHCIDFSYLLYSQKGLNGTL 123
DB 55 TKPTSDPWPSSGSLMUNASGRPPGQRAHLLLPOLKENDTHCIDFHYFVSKSNSPPGLL 114
QY 124 NILVRNKGPLANIPWVTFGRDMLRAELAVSTFWPNEYQVIFAEAVSGSGSYIAID 183
DB 115 NVVKNVNGPLNGPIWNISGDPTTNRAELAISTFWPNFQVIFEV-ITSGHQYLAI 173
QY 184 DIQVLSYPCDKSHFLRLGDVEVNAGQATFQCIATGRDAVHNKLMLORNGEDIPVAQT 243
DB 174 EVKVLGHPCRTTHFLRIQNVVNAGQFATFQCSAIGRTVAGDRLWLGIDVDRAPLKEI 233
QY 244 KNINHRFAAFRLQEVTKTDOLYRCVTOSESGSYNSAQLIVREPPPIAPPOLLGV 303
DB 234 KVTSSRRFIASFNVNTTKDAGKYRCMIRTEGGVGISNVAELVVKSPPIAPPOLASV 293
QY 304 GPTVLLQLNANSIIGDPIILKEVEVRMTSGSWTETHVNAPTYKLWHLDPDTEYIRV 363
DB 294 GATVWLQLNANSINGOPIVAREVEYCTASGWNDRQPDVSTSYKIGHLDPDTEYISV 353
QY 364 LLTRPGEGLPGPPLITRTKCAEMRTPTKLKIAIBIARRIAVDWESLGYNITRCHTF 423
DB 354 LLTRPGEGLPGPPLITRTKCAEMRTPTKLKIAIBIARRIAVDWESLGYNITRCHSY 413
QY 424 NVTCIHYFRGHNESKAD--CLMDPKAPQHVNVNHLPPYTNVSLKMLTTPBGRKSEET 481
DB 414 NLTVHYCYQVGGQEVQREVEVSWDTPENHPQHTITNLSPYTNVSVKLLMNPBGRKSEEL 473
QY 482 LIOTDEDPGVPVVKSLQGSFENKIFLNWKEPLDPNGIITQYVEISYSSIRSDPAVPA 541
DB 474 IVQDDELPQAVPTESIQGSTFEKIFLQWREPTQTYGVITLYEITTKAVSSDFPEIDL 533
QY 542 GPPQTVSNLWNSTHHVFMHLPGTQYOFFIRASTVKGFGPATAINVTNISAPTLPDYG 601

RESULT 11

US-08-652-971-4

; Sequence 4, Application US/08652971

; Patent No. 5814507

; GENERAL INFORMATION:

; APPLICANT: Cheng, Jill

; APPLICANT: Lasky, Laurence A.

; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE

; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA

534 NQGRVSKLGNETHFLFFGYPGTYSFTIRASTAKGFGPPATNQFTTKISAPSMPAYE- 592
QY 602 VDAISNETATTITVLLRPAOKAGAPISAYQVIVVEELHPHRTKREAGAMECYQVPTVYQNA 661
DB 593 LETPLAQTDNTVTVMLKPAHSGAPSVYQIVVEEERPRRTKKTTELKCYVPVPIHQNA 652
QY 662 MSGGAPYFAAELPPGNLPEPAPFTVGDNRTYQGFNPPPLAPRGYNYIYFOAMSSVBKET 721
DB 653 SLLNSQYFFAAEPADSLQAQPTIGDNKTYNGWNTPLLPYKSYRIYFOAASRANGET 712
QY 722 KTCVRIATKAATEEPEVIPPDAKQTDVVKIAGISAGILVFIILLVILVILVVKSLAK 781
DB 713 KIDCVQVATGAA--TPKPVPEPEKQTDHTVKIAGIAGILLFVIFLGVLMVKRKLAK 771
QY 782 KRKDMGNTRQEMTHVMNANDRSYADQSTLHAEDPLSITFMDQHNFSPPRY----- 831
DB 772 KRKETWSSITRQEMTHVMNANDRSYADQSTLHAEDPLSITFMDQHNFSPPRY----- 828
QY 832 -----ENHSATASSRLLDVPY-LCEGTSPYQOTQQLHPAIRVADLLQH 875
DB 829 TNLSTSPVNSYYPDETHTWASDTSLSVQSHYTKKREPADVPTQGLHPAIRVADLLQH 888
QY 876 INLMKTSDSYGFKEEYESPFEGOSASWDVAKDONRAKRYGNIITADHRSVILQVDEDD 935
DB 889 ITQMKCAEGYGFKEEYESPFEGOSAPWDSAKDENRMKNRYGNIITADHRSVILQVDEDD 948
QY 936 PSSDYNANYIDGQVORPSHYIATQGPVHTYVDFWPMIWOESACIWMVNLNVEGVKVC 995
DB 949 TNSDYINGNIIDGTHRNHYIATQGPQETIYDFWPMWHENTASIIWVNLNVEGVKVC 1008
QY 996 KYWPDDETEYIGDFKVTCEMEPLAEYVVRFTFLERRGYNEIREVKQFHTGTGWDHGVY 1055
DB 1009 CKYWPDDTEIYKIDKIVTLIETELAEVIRTFAVEKSGVHEIREIRQFHTGTGWDHGVY 1068
QY 1056 HATGLLSFTRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCKV 1115
DB 1069 HATGLLGFVRQVKSPPSAGPLVHCSAGAGRTGCFIVIDIMLDMAREGVVDIYNCKV 1128
QY 1116 ALRSRRNMVQTEQYIFIHDAILEACLGCETAIPTVCEPKAAVDFMIRIDSQTNSSHLKD 1175
DB 1129 ELRSRRNMVQTEQYIFIHDAILEACLGCETAIPTVCEPKAAVDFMIRIDSQTNSSHLKD 1188
QY 1176 EFOTLSNVTPLQAECDSIACLPRNHDKNRDMOMLPPDRCLPFLITIDGESSNYINAALM 1235
DB 1189 EFTLANVTPTLAVEDCSIALPRNHEKNCMDILPPDRCLPFLITIDGESSNYINAALM 1248
QY 1236 DSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCQYWPBEGMLRYG 1295
DB 1249 DSYKQPSAFIVTQYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCQYWPBEGMLRYG 1308
QY 1296 PIQVECMSCMDCDVINRIENLTPRQSGYLMVQOFOYLGWASHREVSGKRSFTKLI 1355
DB 1309 PIQVEFVSADLEEDISIRIFRIYNAARPDQYRMVQOQFGLGPMWYRTPVSKRSFKLI 1368
QY 1356 LQVEKQEEWKEGEGRTIIHCLNGGSGRGMFCAIGIVEMVXQNVVDVFAVKTLSK 1415
DB 1369 RQVWKQEEVNGEGPTVHCLNGGSGRGMFCAIGIVEMVXQNVVDVFAVKTLSK 1428
QY 1416 PNWVEAPEQYRFOVALEYLES 1438
DB 1429 PNWVLLDQYKFCYEVALEYLS 1451

Sequence 4, Application US/08769399
Patent No. 5976852
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,399
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-769-399-4

Query Match 62.1%; Score 4791; DB 2; Length 1452;
Best Local Similarity 61.3%; Pred. No. 0;
Matches 885; Conservative 205; Mismatches 320; Indels 34; Gaps 7;
QY 23 LIGSAGQGFAGGCTFDGPGACDYHQDLYDDFERVHVSQAQBPHYLPPMPQGSYMYDS 82
DB 14 LLLTAAGTFSGCLFDEPYSTCGYSQAQDEDDFNWEQVNTLTKTSDPMPSPGSMVNT 73
QY 83 SDHDPGEKARLQPTWKNDTHCIDFSYLLYSQKGLNPGTLNLRVKNKGPLANINVT 142
DB 74 SGKPEGQRAHLPLQLKENDTHCIDFHYFVSSKSNAAEGLLVYVKNVNGPLGNPINWIS 133
QY 143 GFTGDLWLAELAVSTFWNEQVIFAEVSGRSGYIAIDDIQVLSYPCDKSPHFLRLG 202
DB 134 GDTTTHRAELAISTFWNFVQVIFEV-VTSGHGYLAIDKVKVLGHPCTRTPTFLRIQ 192
QY 203 DVEVNAQGNATQCIATGRDAVHNKLWLQRRNGEDIPVAQTKNINRRHFAASFRLOEVTK 262
DB 193 NVEVNAQGFATQCSAIGRTVAGDRLLQIGIVDRAPLKEIKVTSRRFIASFNVNTTK 252
QY 263 TDQDLRYCVTQBSRGVSNFALIVREPPRIAPOLLGVGPTYLLQLNANSIIGDGP 322
DB 253 RDAGYRCMCTEGGVGISNAYELVVKPEPVPVAPPLASVATYLTQLNANSINGDGP 312
QY 323 IILKEVEYRMTSGSTETHAVNAPTYKMLWLPDDEYEIRVLLTRPGEGLGPGPLIT 382
DB 313 IVAREVEYTAGSNDRQPDVSTSYKIGLHPDDEYEISVLLTRPGEGLGSPGPAUT 372
QY 383 RTKCAEPMTPTKLIAEQARRIAVDWESLGNITRCHTFNVTICYHYFRGHNESKAD- 441
DB 373 RTKCADEMPGRKLEVEVVKSRQITIRWEPFGVNVTRCHSYNLTVHYGYQVGQGVRE 432

QY 442 -CLDMDPKAPOHVVNHLPPVYTNVSLKMLITNPEGRKESEETIIOTDEDPGVPVVKSLQG 500
DB 433 VSWDTNSHQHTITNLSPTYNVSVKULMPEGRKESQELTVQDEDPGAVPTESIQG 492
QY 501 TSPENKIFLWKEPLDPNGIITQYEISYSSIRDPDPVAVAGPPQTYSNLWNSTHHVPMH 560
DB 493 SAFEKIFLOWREPTQTVGVTLYEITYKAVSSFDPEIDLNSQSGRVSKLGNETHFLPFG 552
QY 561 LHPGTYOFFIRASTVKGFGPATVNTNISAPTLDPYEGVDASLNETATITVLLAPA 620
DB 553 LYPGTYSTIRASTAKGFGPATNQFTTKISAPSPAYE-FETPLNQTDNTVTVMKXA 611
QY 621 QAKGAPISAYQIVVEELHPHRTKREAGAMECYQPVTVYQAMSGGAPYFAELPPGNLP 680
DB 612 QSRGAPSVYQIVVEEERPRKTKTEILKICYPPIHFQNASIILNSYFFAAEPADSQ 671
QY 681 EPAPFTVGDNRITYQGFWNPPPLAPRGYNIYFQAMSSVEKETKTCVRIATKAATEEPEVI 740
DB 672 AAQFTIGDNKTYNGWNTPLPHKSYRIYQAAASRANGETKIDCVRVATKGAV-TPKPV 730
QY 741 PDPAKQTRVVKIAGISAGILVFIILLVVLIVKSKLAKRKDAMGNTQEMTHMNA 800
DB 731 PEPEKQTDHTVKIAGIAGILLFVIIFLGVVLVKKRKLAKRKETMSSTRQEMTVMS 790
QY 801 MDRSVADQSTLHAEDPLSITFMDQHFSPRY-----ENHS 835
DB 791 MDKSYAEQGTNCDE---AFSPWGTNNLNGRSVSPSSFTMTNTLSTSVPSNSYVPDETH 847
QY 836 ATABSSRLLDVPRY-LCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGFKEEYESF 894
DB 848 MASDTSSLAQHTYKKEAADVPYQTQLHPAIRVADLLOHITQMKCAEGYGFKEEYESF 907
QY 895 FEGQASNDVAKQONRAKNRYGNI IAYDHSRVLQPVDEDDPSDDYINANVYDGHQFSSH 954
DB 908 FEGQAPWDSAKDENRMKNRYGNI IAYDHSRVLQMLEGDNNSDYINGNYIDGHRFNH 967
QY 955 YIATQGPVHETVYDFWMIQEQSACIVMTNLVEGVRKCVKYPDDTEVVYDGFKVCV 1014
DB 968 YIATQGPVHETVYDFWMIQEQSACIVMTNLVEGVRKCVKYPDDTEVVYDGFKVCV 1027
QY 1015 EMEPLAEYVVRFTFLERRGYNEIREVKQFHTGWPDPHGVYHATGLLSFIRRVKLSNPPS 1074
DB 1028 DTELLAEVIRTFVAVKRGIEIREIQFHTGWPDPHGVYHATGLLGFRVQVKSPPN 1087
QY 1075 AGPIVHCSAGAGTGVIVIDIMDMAERGVVDIYNCVKALSRRRINMVQTEBOYIFI 1134
DB 1088 AGPLVHCSAGAGTGVIVIDIMDMAERGVVDIYNCVKALSRRRINMVQTEBOYIFI 1147
QY 1135 HDAILEACLCCGTAIPVCEPKAAVDFMIRIDSQTNSSHLKDBFOTLNSVTPRLOAEDCSI 1194
DB 1148 HDAILEACLCCGTSIPASQVRSLYDMNKLDPQTNSSQIKKEFRTLNMVTPTRVEDCSI 1207
QY 1195 ACLPRNHDKNRFDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQPLPNT 1254
DB 1208 ALLPRNHEKNCMDILPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQPLPNT 1267
QY 1255 VKDFWRLVYDGTSTIVMLNEVDLSQGPQVWPEGMRLRYGPIQVECMSCMDCDVIRI 1314
DB 1268 VKDFWRLVLDYHCTSVVMLNDVPAQLCPQVWPENGVRHGFQVFEVSADLEEDIISRI 1327
QY 1315 FRIENLTPORSGYLMVQOFOYLGWASHREVPGSKESFLKILIOVEKWOEAKWEGGRTII 1374
DB 1328 FRIYNASRPQDHRNVQFQFLGWPYRDTVPVSKKSFUKLIRQVKNQWEEYNGGPGTVV 1387
QY 1375 HCLNGGGRSGMFCATIGIVEMVVKRQNVVDVFAVKTLSNKPNNMVEAPEQYRFCYDVALE 1434
DB 1388 HCLNGGGRSGMFCATIGIVEMVVKRQNVVDVFAVKTLSNKPNNMVEAPEQYRFCYDVALE 1447
QY 1435 YLES 1438
DB 1448 YLNS 1451

QY 1435 YLES 1438
Db 1448 YLNS 1451

RESULT 15
US-08-652-971-2
; Sequence 2, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-971-2

Query Match 59.5%; Score 4586.5; DB 2; Length 1436;
Best Local Similarity 60.3%; Pred. No. 0;
Matches 854; Conservative 213; Mismatches 331; Indels 19; Gaps 9;

QY 33 AGGCTFDDGPG---ACDHYQDLYDDFWVHVAQBFHYLPPMPQGSYIMVDSDDHDFGE 89
Db 24 RAGCTFEASDPVFCFSQAQYDDFQWEQVRIHGTPTDPLPHGAYLMVNASQHTPGQ 83

QY 90 KARLQLPWKENDTHCIDPSYLLYSQKGLNPOTLNLVRNKGPLANPIVNWVTGTGRDW 149
Db 84 RAHIIFQTLSENDTHCVQFSYLSRDSGSPGLGVYVRVNGGPIGSAVWNNVTGSHGRQW 143

QY 150 LRAELAVSTFWNEQVIFEAESVGRSGYIAIDDIQVLVSXPCDKSPHFLRLGDEVVNAG 209
Db 144 HQAELAVSTFWNEQVIFEAESVGRSGYIAIDDIQVLVSXPCDKSPHFLRLGDEVVNAG 203

QY 210 QNATFQCIATGRDAVHNKMLWLRNGEDIPVAQTKNINHRHFAAFLRQEVTKTDQDLYR 269
Db 204 QNASFQMAAGRAAEAEHFFLQSGVLVPAAGVRHISHRRFLATFPLASVGRSQDLYR 263

QY 270 CVTQSGRGVSNFAQLIVREPPRIAPPQLLGVTPTLLIQLNANSIIGDPIILKEVE 329
Db 264 CVSQAPRGAGVSNFAELIVKEPPTIAPPQLLRAGPTVLIQLNTNSIIGDGPVIRKGEIE 323

QY 330 YMTSGSWTETHAVNAPTYKLWHLDPDTEYIRVLLTRPGEQGTGLPGPPLITRTKCAEP 389

Db 324 YRMARGPWAEEVHVNLYTKLWHLDPDTEYIEISVLLTRPGDGGTGRPGPPLISRTKCAEP 383

QY 390 MRTPKTLKIAEIQARRIADVWESLGYNIITRCHTFNVITICHHYFRG--HNESKADCLMDP 447
Db 384 TRAPKGLAFAEIQARQLTQWEPLGYNVTRCHTYAVSLCYRYTLGGSHQNTIRECVKMER 443

QY 448 KAPOHVVNHLPPYTNVSKMLITNPEGRKESEETIIOTDEDPVGPVPVKSLQGTSEFNKI 507
Db 444 GASRYTIKNLLPFNNIHVRILITNPEGRKEKEVTFQTDDEDPVGGIAAESLTFPLEDMI 503

QY 508 FLWKKEPLDPNGIITQYEISYSSIRSPDPAVPVAGPPQTVSNLWNSTHHVFMHLHPGTTY 567
Db 504 FLKWEPEQENGLITQYEISYQSIESSDPAVNVPGPRRTISKLRNETVHVFSNLHPGTTY 563

QY 568 QFFIRASTVVGFGPATVNTNISAPTLDPYEGVDASLNETATITVLLRPAQAKGAPI 627
Db 564 LFSVRARTSKGFGQAALTEITNISAPSF-DYADMPSPLGSESENTITVLLRPAQGRGAPI 622

QY 628 SAYOIVVEELHPHRTKREAGAMECYQVPVTVQNAMSGAPYFAAELPPGGLPAPPTV 687
Db 623 SVYQVVEERPRRLRREPQADCFSVLTFETALRGLVHYFGAELAAASLELAMPFTV 682

QY 688 GDNRTYQGFNPPPLAPRKGYNIYFQAMSSVEKETKTCQVRIATKAATEEPEVIPDPAKOT 747
Db 683 GDNQTYRGFNPPLEPKAYLIYFQAASHLKGTELRLNCIRIARKAACKESKRPLEVSQRS 742

QY 748 DRVVKIAGISA-GILVFILLVILVILVILVILVILVILVILVILVILVILVILVILVILV 806
Db 743 EEMGLILGICAGGLAVLILLGAILIIRKGPVNMTK-ATVNYROEKTHMMSAVDRSFT 801

QY 807 DOSTLHAEDPLSITFMDQHNFSPRYENHS--ATAESSRLLDVPRVLCBGTSPYQTGLH 864
Db 802 DOSTLQEDERLGLSFDAPGYSRQDQSGGVTEASSLLGSPRRPCGRKSPHYTGLH 861

QY 865 PAIRVADLLQHINLMKTSDSYGFKEYESPFEGOSASWDVAKQDNRAKNRYGNIAYDH 924
Db 862 PAVRVDLLQHINQMKTAEYGFKEYESPFEG---WDATKKDKLKGGRQEPVSAYDR 917

QY 925 SRVILQVEDDDPSDYNANVIGYQRPVSHVIATQGPVHETVYDFWRMIWQESACIWMV 984
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QY 985 TNLVEVGRVKCYKVPDDTEVYGFVKTCVMEPLAEVYVVTFTLERRGYNEIRVVKOFH 1044
Db 978 TKLVEVGRVKCSRYWPDSDMDGDKITLVKTETLAEYVVTFTLERRGYNSARHEVRQPH 1037

QY 1045 FTGWPDPHGPYHATGLLSFIRRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAR 1104
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QY 1165 DSQTNSSHLKDEFOTLNSVTPRLQAECSIACLPNHDKNFMMLPDRCLPFLITIDG 1224
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QY 1225 ESSNYINAALMDSYRQPAAFIVQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDLSQG--- 1281
Db 1218 DPNYINAALTDSYTRSAAFIYTLHLQSTTPDFWRLVYDYGCTSIIVMLNQLNQSNAWP 1277

QY 1282 CPQWPPEGMRLRYGPIQVECMSCSMDCVINRIPIICMLTPQBYLMVQQOYILGWASH 1341
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QY 1342 REVCSKESFLKLLQVEKQWQEWKEGGRITIIHCLNGGGRSGMFCATGIVVEMVKRONV 1401
Db 1338 RDTPSRKAFHLHLAEAVDKWQAE--SGDGRIVVHCLNGGGRSGTFCACATVLEMIRCHSL 1395

QY 1402 VDVHFAVTLNRNSKPNMVVEAPEQRYFCYDVDALEYLES 1438
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Job time : 39.7887 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:44:18 ; Search time 131.676 Seconds
(without alignments)
3777.694 Million cell updates/sec

Title: US-09-887-669-2
Perfect score: 7709
Sequence: 1 MDTTAAALPAFVALLLSP.....EAPQYRVCYDVALEYLESS 1439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum Match 0%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7709	100.0	1439	9	US-09-887-669-2
2	7688	99.7	1439	16	US-10-408-765A-284
3	7571	98.2	1457	9	US-09-887-669-1
4	4838	62.8	1452	9	US-09-887-669-8
5	4784	62.1	1452	16	US-10-408-765A-83
6	4602.5	59.7	1436	14	US-10-205-219-15
7	4564.5	59.2	1444	15	US-10-058-270A-98
8	4564	59.2	1463	14	US-10-176-847-22
9	4564	59.2	1463	14	US-10-205-823-343
10	4555	59.1	1499	15	US-10-296-115-1283
11	4374.5	56.7	1442	16	US-10-408-765A-805
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13	2493.5	32.3	623	15	US-10-296-115-1190

14	2210.5	28.7	815	15	US-10-296-115-1390	Sequence 1390, Ap
15	1534.5	19.9	1502	9	US-09-808-602-54	Sequence 54, Appl
16	1534.5	19.9	1502	10	US-09-800-198-44	Sequence 44, Appl
17	1509	19.6	1897	17	US-10-482-029-52	Sequence 52, Appl
18	1505.5	19.5	1907	15	US-10-291-265-250	Sequence 250, App
19	1505.5	19.5	1912	7	US-10-772-636-64	Sequence 64, Appl
20	1505	19.5	1948	9	US-09-808-602-55	Sequence 55, Appl
21	1505	19.5	1948	10	US-09-800-198-45	Sequence 45, Appl
22	1491	19.3	1495	15	US-10-258-666-12	Sequence 12, Appl
23	1460.5	18.9	2037	15	US-10-087-684-39	Sequence 39, Appl
24	1460.5	18.9	2037	15	US-10-218-779-39	Sequence 39, Appl
25	1457.5	18.9	2029	15	US-10-087-684-38	Sequence 38, Appl
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36	1170.5	15.2	807	15	US-10-366-547-65	Sequence 65, Appl
37	1138	14.8	699	15	US-10-087-192-1017	Sequence 1017, Ap
38	1138	14.8	774	13	US-10-366-547-63	Sequence 63, Appl
39	1132	14.7	700	15	US-10-444-795B-793	Sequence 793, App
40	1132	14.7	700	15	US-10-753-267-100	Sequence 100, App
41	1132	14.7	700	17	US-10-444-795B-795	Sequence 795, App
42	1115.5	14.5	642	15	US-09-788-626-9	Sequence 9, Appli
43	1109	14.4	305	9	US-10-366-547-67	Sequence 67, Appl
44	1107.5	14.4	569	13	US-10-087-192-1020	Sequence 1020, Ap
45	1085.5	14.1	560	13		

ALIGNMENTS

RESULT 1

US-09-887-669-2
; Sequence 2, Application US/09887669
; Publication No. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US/09/887,669
; PRIOR FILING DATE: 09/234,883
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-669-2

Query Match 100.0%; Score 7709; DB 9; Length 1439;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MDTTAAALPAFVALLLSPWLLGSAQGFSDGPGACDVHQDLYDDFEWHV 60

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Db 61 SAQEPHYLPPEMPOGSGYIMVDSDDHDPCEKARLQPTMKENDTHCIDFSYLLYSOKGLNP 120
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; Sequence 284, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Watson, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1439
; TYPE: PRT
; ORGANISM: Homo sapiens
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RESULT 3

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US-09-887-669-1
; Sequence 1, Application US/09887669
; Publication No. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1457
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-887-669-1
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Query Match 98.2%; Score 7571; DB 9; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;
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Qy 1 MDTAAALPAFVALLLLSPWLLGSAQGFAGGCTFDDGPGACDYHQDLYDDFWEVHV 60
Db 1 MD-VAAALPAFVALLLLYPWLLGSAQGFAGGCTFDDGPGACDYHQDLYDDFWEVHV 59
Qy 61 SAGEPHYLPPEMPOGSGYNIYVDSDDHPGEXKARLOLPTMKENDTHCIDFSYLLYSQKGLNP 120
Db 60 SAGEPHYLPPEMPOGSGYNIYVDSDDHPGEXKARLOLPTMKENDTHCIDFSYLLYSQKGLNP 119
Qy 121 GTNLILVRNKGPLANIPINVTGTGRDLRAELAVSTFWPNEYQVIFEAESGSRGYI 180
Db 120 GTNLILVRNKGPLANIPINVTGTGRDLRAELAVSTFWPNEYQVIFEAESGSRGYI 179
Qy 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNAFQCIATGRDAVHKLWLQRRNGEDIPV 240
Db 180 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNAFQCIATGRDAVHKLWLQRRNGEDIPV 239
Qy 241 AQTKNINHRPFAASFRLEQVTKTDQDLYRCVTSERGSVSNFAQLIVREPPPIAPPQL 300
Db 240 AQTKNINHRPFAASFRLEQVTKTDQDLYRCVTSERGSVSNFAQLIVREPPPIAPPQL 299
Qy 301 LGVGPYVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKULWHLDPDTEYE 360
Db 300 LGVGPYVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKULWHLDPDTEYE 359
Qy 361 IRVLLTRPGEQGTGLPGPPLITRTKCAEPMRTPKTLKIAETQARRIADVMSLGYNITRC 420
Db 360 IRVLLTRPGEQGTGLPGPPLITRTKCAEPMRTPKTLKIAETQARRIADVMSLGYNITRC 419
Qy 421 HTFNVTTCYHYFRGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESSE 480
Db 420 HTFNVTTCYHYFRGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESSE 479
Qy 481 TTIOTSDSDPGVPVKSLOQTSFENKIFLNKKEPLDPNGIITQYEISYSSIRSDPAVPV 540
Db 480 TTIOTSDSDPGVPVKSLOQTSFENKIFLNKKEPLDPNGIITQYEISYSSIRSDPAVPV 539
Qy 541 AGPQTVSNLWNSHHVFMHLHPCGTYQFFIRASTVKGFPGATATNTTINISAPLDYE 600
Db 540 AGPQTVSNLWNSHHVFMHLHPCGTYQFFIRASTVKGFPGATATNTTINISAPLDYE 599
Qy 601 GVDASLNETAATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQ 660
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Db	600	GVDSASLNETAATTITVLRPAQAAGAPISAYQIIVVEQLHPHRTKREAGAMECYQVPVYQN	659
Qy	661	AMSGGAPYYFAAEPLPGNLPEPAPFTVGDNRRTYQGFWNPPAPLPRKGYNIYFOAMSSVEKE	720
Db	660	ALSGGAPYYFAAEPLPGNLPEPAPFTVGDNRRTYKGFWNPPAPLPRKGYNIYFOAMSSVEKE	719
Qy	721	TKTQCVRATK-AATEEPEVIPDPAKQTDVRVVKIAGISAGILVFILLLLVILVKKSKL	779
Db	720	TKTQCVRATKAAATEEPEVIPDPAKQTDVRVVKIAGISAGILVFILLLLVILVKKSKL	779
Qy	780	AKKRKDANGTRQEMTHVMVAMDRSYADQSTLHAEDPLSTFMDOHNFSPRY-----	831
Db	780	AKKRKDANGTRQEMTHVMVAMDRSYADQSTLHAEDPLSTFMDOHNFSPRLPNDPLVPT	839
Qy	832	----ENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGF	887
Db	840	AVLDENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGF	899
Qy	888	KEBYESFFEQSASWDVAKKQDNRAKNRYGNIIAYDHSRVILQVPEDDPSSDIYANFYI-	946
Db	900	KEEYESFFEQSASWDVAKKQDNRAKNRYGNIIAYDHSRVILQVPEDDPSSDIYANFYID	959
Qy	947	-----DGYQBPESHYIATQGPVHETVDFWRMIWQEQSACIWMVTNLVEVGRVKCYKWPD	1001
Db	960	IWLRYDGYQBPESHYIATQGPVHETVDFWRMVWQEQSACIWMVTNLVEVGRVKCYKWPD	1019
Qy	1002	DTEVYGFQKTCVEMEPALAEVVRTPLERRGYNEIREVKQFHFTGWPDPDHGVPYHATGLL	1061
Db	1020	DTEVYGFQKTCVEMEPALAEVVRTPLERRGYNEIREVKQFHFTGWPDPDHGVPYHATGLL	1079
Qy	1062	SFIRRVKLSNPPSAGPIVHVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRR	1121
Db	1080	SFIRRVKLSNPPSAGPIVHVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRR	1139
Qy	1122	INMVQTEQYIFHDAILEACLQGETAI PVCEFKAAVYFDMIRIDTSQTNSSHLDKDEFQTLN	1181
Db	1140	INMVQTEQYIFHDAILEACLQGETAI PVCEFKAAVYFDMIRIDTSQTNSSHLDKDEFQTLN	1199
Qy	1182	SVTPRLQAEBCSIACLPRNDKPRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYROP	1241
Db	1200	SVTPRLQAEBCSIACLPRNDKPRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYROP	1259
Qy	1242	AAFTVQYPLPNTVKDFWRLVYDYGCTSIVMLENDLSQGCPCQYWPBEGMLRGPQIQCVC	1301
Db	1260	AAFTVQYPLPNTVKDFWRLVYDYGCTSIVMLENDLSQGCPCQYWPBEGMLRGPQIQCVC	1319
Qy	1302	MSCSMDCDVINRI FRI CNLTRPOBQGYLMVQOQFYLGWASHREVPGSKRSTFLKILQVEKW	1361
Db	1320	MSCSMDCDVINRI FRI CNLTRPOBQGYLMVQOQFYLGWASHREVPGSKRSTFLKILQVEKW	1379
Qy	1362	QEEWKEGEGRTIIHCLNGGGRSGMFCALIGIVEMVKQNVVDVPHAVKTLRNSKPNMVEA	1421
Db	1380	QEECEBEGRTIIHCLNGGGRSGMFCALIGIVEMVKQNVVDVPHAVKTLRNSKPNMVEA	1439
Qy	1422	PEQYRFCYDVALEYLESS 1439	
Db	1440	PEQYRFCYDVALEYLESS 1457	

RESULT 4

US-09-887-669-8
 ; Sequence 8, Application US/09887669
 ; Publication No. US20020082397A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCHLESSINGER, JOSEPH
 ; APPLICANT: SAP, JAN M.
 ; APPLICANT: ULRICH, AXEL
 ; APPLICANT: VOGEL, WOLFGANG
 ; APPLICANT: FUCHS, MIRIAM
 ; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE - KAPPA
 ; FILE REFERENCE: 038602/1246
 ; CURRENT APPLICATION NUMBER: US/09/887.669

Db 1009 CKYPPDDTEIYKIDKVTLIETELLAAYVIRTFVAVEKRGVHEIREIQPHFTGMPDHGVY 1068
Qy 1056 HATGLLSFIRRVKLSNPPSAGPIVHCSAGAGRTGCTYIVIMLMDAREGVDIYNCVK 1115
Db 1069 HATGLLGFVRQVKSPPSAGPLVVHCSAGAGRTGCTFIVIMLMDAREGVDIYNCVR 1128
Qy 1116 ALRSRINNVQTEEQYIFIHDAILEACLCGETAIVCFKAAYPDMIRIDQTNSSHLKD 1175
Db 1129 ELRSRVNVQTEEQYIFIHDAILEACLCGETSVPASQVRSLYYDMNKLDQTNSSQIKE 1188
Qy 1176 EFQTLNSVTPRLQABDCSIACLPRNHDKRRFMDMLPPDRCLPFLITIDGESSNYNAALM 1235
Db 1189 EFTLNMVTPTLRVEDCSIALPRNHEKRNCRWDILPPDRCLPFLITIDGESSNYNAALM 1248
Qy 1236 DSYRQPAFIVTQYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSGCGQYWPBEGMLRYG 1295
Db 1249 DSYQPSAFIVTQHPLPNTVKDFWRLVLDYHCTSVVMLNDVDPAQLCPQYWPBENGVRHG 1308
Qy 1296 PLOVECMSCSDCVINRIFRICNLTRPOEGVLMVQOQYGLGWASHREVPGSKSFLKLI 1355
Db 1309 PLOVEFVSADLEEDIISIRIFRYNARPDQGRHMVQOQYGLGWPMYRDTVPVSKSALLLI 1368
Qy 1356 LOVEKQWBEWKEGERTIHCINGGGRSGMFCAGIIVVMVKRQNVVDVFAVKTLRNSK 1415
Db 1369 QOVDKQWBEYNGEGPTVVHCLNGGGRSGTFCAISIVCEMLRHQRTVDVFAVKTLRNK 1428
Qy 1416 PNWEPAPQYRCYDVALEYLES 1438
Db 1429 PNWDLDDQYKFCYEVALEYLNS 1451

RESULT 6

US-10-205-219-15
; Sequence 15, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; PRIORITY FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1436
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Receptor protein tyrosine phosphatase-lambda
US-10-205-219-15
Query Match 59.7%; Score 4602.5; DB 14; Length 1436;
Best Local Similarity 60.3%; Pred. No. 0;
Matches 855; Conservative 214; Mismatches 329; Indels 19; Gaps 9;
Qy 33 AGCTFTDGGPG---ACDHYQDLYDDPEWVHVSQAQEPHYLPMPPOGSSYMYVDSSDHPGE 89
Db 24 AAGCTFEESDPVWPFCEFSQAQYDDFQWEQVRIHFGRTRTPEDLPHGAYLMVNASQHTFCQ 83
Qy 90 KARLQLPTMKENDTHCIDPSYLLYSQKGLNPGCTNLILVRNKGPLANPIVNWVTFGTGRDW 149
Db 84 RAHIIFQTLSENDDHCVQSFYFLYRSDHSPGTLGYVVRNKGPLGSAVNMWIGSHGRQW 143
Qy 150 LRAELAVSTFWPNEYQVIFAEVSGRSGYIAIDDIQVLSYPCDKSPFLRLGDVEVNAG 209
Db 144 HQAELAVSTFWPNEFQVLFALISPDHKGYIGLDDILLFSPYCAKAPHFSLRLGDVEVNAG 203

Qy 210 QNATFOCIATRDAVHNKMLWLQRNGEDIPVAOTKNINHRRFAASFRLEQVTKTDQDIYR 269
Db 204 QNASFQCAAGRAAEASHFFLQSQGVLPVPAAGVYRHSRRFLATFPLASVGRSEQDIYR 263
Qy 270 CVTQSGRGVSNPAQLIVREPPPIAPPQLLGVPYVLLIQLNANSIIGDGPILKEVE 329
Db 264 CVSQAPRGAGVSNPAELIVKEPPTPIAPPQLLRAGTYLIIQLNTNSIIGDGPVIRKEIE 323
Qy 330 YRMTSGSWTETHAVNATYKMLHLDPDTEYFIRVLLTRPGEGCTGLCPPLITITKCAEP 389
Db 324 YRMARGPMAEVAHNLQYKMLHLDPDTEYFISVLLTRPGDGGTGRGPPLISRTKCAEP 383
Qy 390 MRPTEKTIKIAEIOARRTAVDWESLGYNITRCHTFNVATICVHYFRG--HNESKADCLMDMP 447
Db 384 TRAPKGLAFPAEIOARQTLQWEPGLCYNVTRCHTYAVSLCYRYTLGGSHNOTIRECVKMER 443
Qy 448 KAPOHVVNHLPPYTNVSLKMLTNPEGRKSEBETIIQTDDEDVPGVPVFKSLOGTSFENKI 507
Db 444 GASRYTIKNLLPPRNHVRILITNPEGRKEKEVTFQTDDEDVPGIAAESLTFPTPLEDMI 503
Qy 508 FLANKPELDPNGIITQYEISYSSIRSDPPAVPVAGPQTUSNLNNSHTHVMHLPGTTY 567
Db 504 FLKWEPEQEPNGLITQYEISYQSIESSDPVNVPGPRTTISKLRNETYHVFNSLHPGTTY 563
Qy 568 QFFTRASTVKGFGPATAINVTNINISAPLTPDYEGVDASLNETATTITVLLRPAQAKGAPI 627
Db 564 LFSVRARTSGFGQAALTEITNINISAPF--DYADMPSPLGSESENTITVLLRPAQGRGAPI 622
Qy 628 SAYQIVVEELHPHRTKREAGAMECYQVPVTVYQNASMGAPYFAAELPPGNLPBPAPPTV 687
Db 623 SVYQVWVEERPRLRREPQAQDCFSVPLTETALARGLVHFGAELAAASLLEAMPPTV 682
Qy 688 GDNRTYQGFNPPPLAPRKGNYIYFOAMSSVEKETQCVRIATKAAATEPEEVIDPPAKQT 747
Db 683 GDNQTYRGFWNPPLPRKAVLIYFQAASHLKGRTLCIRIARAKAACKESKRPLEVSQRS 742
Qy 748 DRVVKIAGISA-GILVFLILLVLIVLIVKSKLAKRKADMGNTROEMTHVMVNMADRSYA 806
Db 743 EEMGLIIGICAGGLAVLILLGAILIIRKQKPVNMTK-ATVNYRQEKTHMSAVDRSFT 801
Qy 807 DQSTLHAEDPLSITFMDQHNFSPRYENHS--ATAESSRLLDVPRYLCBGTSPYOTGQLH 864
Db 802 DQSTLQEDERLGLSFMADAPGYSPRGDSQSGVTEASSLLGSGPRPCRGKSGPYHTGQLH 861
Qy 865 PAIRVADLLQHINLMKTSDSYGFKEEYBSPFEGQSASWDVAKQONRAKNRYGNIIAYDH 924
Db 862 PAVRVADLLQHINQMKTAEYGFQYEVSEFFEG----WDATKKDKDKLKGGRQEPVSAYDR 917
Qy 925 SRVILQPVEDDDPSDDYNANYIDGVRPSHYIATQGPVHETVYDFWRMIWQESACIVMV 984
Db 918 HHVKLHPMLADPDADYISANYIDGVRHSNHFATQGPXPEMIYDFWRMVWQEQACSIWMI 977
Qy 985 TNLVEVGRVKCYKWPDDTEYVGDVKVTCVMEPLAEYVVRFTTLEREGYNEIREVKQFH 1044
Db 978 TKLVEVGRVKCSYWPEDSDMYGDIKITLVKTETLAEYVVRFTFALEREGYSARHEVRQFH 1037
Qy 1045 FTGHPDHGVPHATGLLSFIRRVKLSNPPSAGPIVHCSAGAGRTGCTYIVIMLMDARE 1104
Db 1038 FTAWPEHGVPHATGLLAFIRRVKASTPPDAGPIVHCSAGTGTGCTYIVLDVMDLMAEC 1097
Qy 1105 EGVVDIYNCVKALRSRRINMVQTEEQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRI 1164
Db 1098 EGVVDIYNCVKTLCSRRVNMIIQTEBEQYIFIHDAILEACLCGETTIPVNEFRATYEMIRI 1157
Qy 1165 DSQTNSSHLKDEFOTLNSVTPRLQABDCSIACLPRNHDKRNFMMLPPDRCLPFLITIDG 1224
Db 1158 DPQSNSSQLREEFQTLNSVTPPLDVEECSIALPRNDRKNRSMVDVLPDRCLPFLISSDG 1217
Qy 1225 ESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQG--- 1281
Db 1218 DPNNYINAAALDSYRSAAFIVTQLPQSTTTPDFWRLVYDYGCTSIYMLNQLNQNSAMP 1277
Qy 1282 CPQYWPBEGMLRYGPIQVECMSCSDCVINRIFRICNLTRPOEGVLMVQOQYGLGWASH 1341

Db 1278 CLQWPFGRQOGLMEVFSGTANEDLSRFRVQNSRKLQGHLLVHFQELRSAY 1337
Qy 1342 REVPGSKRSFLKLLOVEKQEWKEGEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNV 1401
Db 1338 RDTPDSCRKAFHLHLAEVDKQAB--SGDGRVTVHCLNGGGRSGTFCACATVLEMIRCHSL 1395
Qy 1402 VDFPHAVKTLRNKPNMVEAPEQVRFCDYVALEYLE 1438
Db 1396 VDVFFAAKTLRNKPNMVEVTDQYHFCYDVALEYLEA 1432

RESULT 7
US-10-058-270A-98
; Sequence 98, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-005210US
; CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 1444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-270A-98

Query Match 59.2%; Score 4564.5; DB 15; Length 1444;
Best Local Similarity 58.0%; Pred. No. 0;
Matches 844; Conservative 239; Mismatches 343; Indels 29; Gaps 8;

Qy 1 MDTAAALPAFVALLLSFWLLGSAQGFSGGCTFDDGPGACDYHQDL-YDDFEWVH 59
Db 1 MASLAALAL---SLLLRLQLPLPGARAQAFGCSFDEHYSNCGYSVALGTNGFTWEQ 56
Qy 60 VSAQEPHYLPPEMQSGYIMVSDSDHDHGEKARLQLPTMKENTHCTIDFSLYLSQKGLN 119
Db 57 INTTEKPMLOQAVPTGSFMMVNSGRASGQKALHLLPTLKENDTHCIDFHYFSSRRSS 116
Qy 120 PGTNLILVRNKGPLANPINNVGTGRDMLRAELAVSTFWPNEYQVIFEAESVGGSGY 179
Db 117 PGALNVTVKNGGFGQGNPWNVSGVTEGWVKAELAISTFWPHFYQVIFESVSLKGGHPY 176
Qy 180 IAIIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKMLQRRNGEDIP 239
Db 177 IANDEVRLAHPEKAPHFRLQNVENVNQNATFOCIAGCKWSQHDKMLQWQNGRDTA 236
Qy 240 VAOTKINHRPFAASFRLOEVTKTDQDLXRCVTSQSERGSGVSNFAQLIVREPPRPPIAPQ 299
Db 237 LMWTVVNVHRRFSATVSADTAQRSVSKYRCVIRSDGSGSVNAELIVKEPTPIAPPE 296
Qy 300 LLGVGPTLLIQLNANSIIGDPIILKEVEYRTSGSWTETHAVNAPTYKLWHLDDPTEY 359
Db 297 LLAVGATYLWIKPNANSIIGDPIILKEVEYRTTGTGTAETHIVDSNPNYKLWHLDPVEY 356

Qy 360 EIRVLLTRPGEQGTGPPPLIIRTKCABPMRTPTKLKIAEIQARRIAVDWESIGYNITR 419
Db 357 EIRVLLTRPGEQGTGPPGAPLITRTKCADPVHGPQNVEIVDIRARQLTLQWEPFGYAVTR 416
Qy 420 CHTFNVTICVHYFRGHNESKADCLDMDPKAPQHVHNLPPVTVNSLAKMLTNPGRKESE 479
Db 417 CHSYNLTVQYV--FNQOQYBAEVIQTSHTSLRGLRPFMTIRLLLSNPGRWESE 474
Qy 480 ETIIQTDDEVPGPVVKSLQGSTFENKIFLNWKEPLDPNGIITQYEISYSIRSIRDFPAPV 539
Db 475 ELVVQTEEDVPGAVPLESIQGGPFEEKIYIQWPPNETNGVITLIEINXKAVGSLDPSAD 534
Qy 540 VAGPPQTVSNLWNSHTHVFMHLHPGTYQFFIIRASTVKGFGDATAINVTNINISAPTPDY 599
Db 535 LSSQRGKVFKLNRNETHHLFVGLYPGTYTSTIKASTAKGFGPPVTTRITAKISAPMPEY 594
Qy 600 EGVDAFINETATTITVLLRPAQAKGAPISAYQIVVEELHPRHTKREAGAMECVQVPTYQ 659
Db 595 D-TDTPLNETDTITVNLKPAQKRGAPSVQIVLVEERLQKRRADIIIECSVPVSYR 653
Qy 660 NAMSGGAPYYFAAEPLPPGNLPEPAPFTVGNRTYQGFNPPPLAPRGYNIYFOAMSVK 719
Db 654 NASLSLHYFAAEKXANLPVTQPTVGNKTYGWNPPPLSPLKSYISYFQALSXANG 713
Qy 720 ETKTQCVRIATKAATBEPEVIPPAKQTDREVKIAGISAGILFILLVLLVILVK-- 776
Db 714 ETKINCVRLLATTGASTQNSNTVEPEKQVNDNTVMAGVIAGLLMFIILLGVMLTIKRRN 773
Qy 777 -----SKLAKKRDAMNGTROETHVNMVAMDRSYADQSLHAEDPLSTFTFMDQHN 826
Db 774 AYSYSYLSQRLAKKQKQKQTSQAQREMGPVASA-DKPTTKLSASRNDEGFSSSQVNG 832
Qy 827 FSPRYENHSATBSSRLLDV---PRYLCEGTSPYQTGQLHPAIRVADLLOHINLMKTS 883
Db 833 FT----DGRGELSQTTLITQTHPYRTCDPVMSYPRDQFQLAIRVADLLOHITOMKRG 888
Qy 884 SYGFKSEYSFFEQSGASMDVAKQDNRAKRYGNIAYDHSRVILQFVDEDDPSSDYNA 943
Db 889 GYGFKSEYALPEGQTASMDTAKEDENRNKNRYGNIISYDHSRVRLVLDGDPHSDYNA 948
Qy 944 NYIDGYQRSHYIATQGPVHETVYDFWRMTWQOSACIWMVTLNVEGRVKCYWPD 1003
Db 949 NYIDGYHRPHYIATQGPQOETVDFWRMTWQENSASIVMVTNLVEGRVKCYWPD 1008
Qy 1004 EYVGDFTVCTVEMEPLAEYVVRFTLLERGYNIREVKQFHTGWPDPHGPYHATGLLSF 1063
Db 1009 EYVGDIKVLIETEPLEAYVIRFTVQKGYHIRELRLEHFTSWPDHGPVCTATGLGF 1068
Qy 1064 IREVKLSNPPSAGPIVVHCSAGAGRTGCTIVIDIMLDMAREGVVDIYNCKALRSRIN 1123
Db 1069 VRQVKFLNPPEAGPIVVHCSAGAGRTGCTAIDTMDMAENEGVVDI-FNCVRELRAQRVN 1128
Qy 1124 MVQTEQYIFIHDAIIEACLCGETAIPVCEPKAAYFDMIRIDQTSNSSHUKDFQTLNSV 1183
Db 1129 LVQTEQYVFWHDAIIEACLCGNTAIPVCEFRSLYINISRLDPQTNSSQIKDFQTLNIV 1188
Qy 1184 TPQLQEDCSIALPNHDKNRFMDMLPDRCLPELITIDGESSNYINAAIMDSYRQPA 1243
Db 1189 TPRVRDEDCSGLLPRNHNKNSMDVLPDRCLPELISVDGESSNYINAAIMDSHQPAA 1248
Qy 1244 FIVTYPLNPTVKDFWRLVYDCTSIIVMLNEVDLSQGCQPYWPPEGMRLRYGIQVBCMS 1303
Db 1249 FVYTHPLNPTVADFRLVFDYNCSSVMLNENDTAQFCMQYWPKEKTSYCGYIQVFEVS 1308
Qy 1304 CSMDCVINIRIFRICNLTRPQEGYLMVQFQYLGWASHREVPGSKSFLKILQVEKQ 1363
Db 1309 ADIDEDIHRIFRICNWARPDGYRIVQHLQYIGWPAYRDTPPSKSLLKVVARLEKQ 1368
Qy 1364 EWKEGEGRTIICLNGGGRSGMFCAGIIVEMVKRQNVDFHAKTLRNSKPNWEAPE 1423
Db 1369 QYDREGRTVHCLNGGGRSGTFCALICVCEMIQQQNIIDVPHIVKTLRNKNMVTLE 1428

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Qy 1424 QYRCYDVALEYLES 1438
Db 1429 QYKFVYVALEYLS 1443

RESULT 8
US-10-176-847-22
; Sequence 22, Application US/10176847
; Publication No. US20030068636A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petteer Ole
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/10/176.847
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-176-847-22

Query Match 59.2%; Score 4564; DB 14; Length 1463;
Best Local Similarity 57.5%; Pred. No. 0;
Matches 847; Conservative 238; Mismatches 341; Indels 48; Gaps 9;

Qy 1 MDTTAAALPAFVALLLLSPPLGSAQOFSAGGCTFDGPGACDYHDL- YDDFEVWH 59
Db 1 MASLAALAL-----SULLRLQLPPLCARAQAPGCGSDEHYNSGYSVALGTNGFTWEQ 56

Qy 60 VSAQEPHYLPPEMPOGSMYVDSDDHPGEXKARLQLPMTKENDTHCIDFSYLLXSQKLN 119
Db 57 INTTEKPLMDQAVPTGSPFMVNSSGRASQXAHLLLPCLKENDTHCIDFHYFSSDRSS 116

Qy 120 PGTNLIVRVNKGPIANPINWVTGTGRDWLRPAELAVSTFWPNEYQVIFBAEVSNGRGY 179
Db 117 PGALNVYKVGPOGPNVNVSGVVTGFWKAEALAISTFWPHEFYQVIFESVSLKHPGY 176

Qy 180 TAIDDIQVLSYPCDKSPHFLRGDVRVAGQATFQCIATGRDAVHKLWLQRRNGEDIP 239
Db 177 JAVDEVRVLAHPCRKAPHLRQNVENVNGQATFQCIAGKWSQHDKLMLQOMNGRDTA 236

Qy 240 VAQTKNINHRPFAASFRLOQVTKTDQDLYRCVCTQSERGSGVSNFAQLIVREPPPIAPPQ 299
Db 237 LMVTRVNVNHRFSATVSVADTAQRSVSKYRCVIRSDGGSGVSNYAEILVKEPPTPIAPPE 296

Qy 300 LLVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSTETHAVNAPYKLMHLPDPTXY 359
Db 297 LLAVGATVLMWIKPNANSIIGDGPILKEVEYRMTTGTWAEITHIVDSPNYKLMHLPDVEY 356

Qy 360 EIRVLLTRPGEGGTGLPGPLTRTKCAEPMTKTKIAETQARRIADVMSLGYNITR 419
Db 357 EIRVLLTRPGEGGTGPPGAPLTRTKADPVHGPQNVIEVDIRAQTLQWEPFGYAVTR 416

Qy 420 CHTFNVTICYHYFRGHNSKADCLDMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESE 479
Db 417 CHSYNLTVQYQV--FNQOQYEAEEVITQSSHYTLRGLRPFMTIRULLNSNPEGRMSE 474

Qy 480 ETIIQTDDEVPVGVKSLQGTSGFNKFLPNKPELDPNGIITQYIEISYSIRSDPAVP 539
Db 475 ELVQTEEDVPVGAVPLESIQGGPFBEKIYIQWKPNETNGVITLYEINYKAVGSLDPSAD 534

Qy 540 VAGPQTVSNLWNSHHVFMHLPGTYQFFTRASTVKGFGPATAINVTNTISAPTLDPY 599
Db 535 LSSQKQKPKLRNETHHFLVGLYPGTYSTFTKASTAKGFGPPVTRTATKIASPSMPEY 594

Qy 600 EGVDAASLNATATTITVLLRPAQAKAPIISAYQIVVVEELHPHRTKREAGAMECYQVPTVYQ 659
Db 595 D-TDTPNLNEDTITITVWLKPAQSRGAPVSVYQLVKEERLQKSRRAADIIECFSPVSVYR 653
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Qy 660 NAMSGGAPYYFAAELPPGNLPEPAPFTVGDNRNITVQGFNPPPLAPRKGYNIYFOAMSSVEK 719
Db 654 NASLSLHVFAAELKPANLPVTPQFTVGNKTYGYNPNPLSLKSYIYFQALSANG 713

Qy 720 ETKTCVRIATKAATEBEVIP
Db 714 ETKINCURLATKAPMGSAQVTPGTPCLLTGASTQNSNTVEPEKQVDNTVKMAGVIAGL 773

Qy 761 LVFILLVLLVILVK-
Db 774 LMFIIILLGYMLTIKRRNAYSYSYLSQRKLAKKQKETSQGAQREMGPVASA-DKPTTK 832

Qy 808 QSTLHAEDPLSITFMDQHNFSRYENHSATAESRLLDV---PRYLCEGTESPTQTGLH 864
Db 833 LSASRNDGESSSSQDVNGFT----DGSRGELSQPTITIQTHPYRTCDPVMSYPRDQFQ 888

Qy 865 PAIRVADLLQHLINLMKTSDSYGFKEEYESFPFEGOSAWDVAKDONRAKNRYGNIAYDH 924
Db 889 LAIRVADLLQHIITQMKRGQGYGFKEEYALPEGQTASWDTAKEDENRNKNRYGNIISYDH 948

Qy 925 SRVILQPVEDDPSDDYINANYIDGYQRPVSHYIATQGPVHETVYDFWMIWQESACIMV 984
Db 949 SRVELLVLDGPHSDYINANYIDGYHPRHYIATQGPQMOETVKDFWMIWQENSASIMV 1008

Qy 985 TNLVEGRVKCYKWPDDTEVYGFKVTCEMEPLAEVVRFTTLERRGYNEIREVKQFH 1044
Db 1009 TNLVEGRVKCVRWPDTEVYGDIKVLTETEPLAEYVIRFTVQKKGHEIRELRLFH 1068

Qy 1045 FTGWPDHGVPHATGLLSFIRRVKLSNPPSAGPIVWHCSAGAGRTGCYIVIDIMLDMABR 1104
Db 1069 FTSWPDHGVPCYATGLLGFVRQVKFLNPPEAGPIVWHCSAGAGRTGCFIADTMDMAEN 1128

Qy 1105 EGVVDIYNCKVALBSRRINMVQTEEQIFHDAILEACLGETAIPVCEFAAYFDMIRI 1164
Db 1129 EGVVDIENCVELRAQRVNLVQTEEQVVFVHDAILEACLGCNTAIPVCEPESLYNIRL 1188

Qy 1165 DSQTNSSHLKDEFOTLNSVTPRLOAEDCSIACTLRNHDKNRFDMLPPDRCLPFLITIDG 1224
Db 1189 DPQTNSSQIKDEFOTLNVTPRVRPEDCIGLLPRNHDKNRSDVLPDLRCLPFLISVDG 1248

Qy 1225 ESSNYINAAALMDSYRQPAAFITVQPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQGCQ 1284
Db 1249 ESSNYINAAALMDSHKQPAAFVVTQHPLENTVADFWRLVFDYNCSSVVMLEMDTAQFCWQ 1308

Qy 1285 YWPBEGMLRGPVIOVECMSCMCDVINRIPRINLTPQEGYLMVQFQYLGHASHREV 1344
Db 1309 YWPEKTSYCYGFIQVEFVSADIDEDIIHRIFRICNMAPQDGYRIVQHLQYIGNPAYRDT 1368

Qy 1345 PGSKRSFLKLILOVEKQOEWEKGEGRTHIHLNGGGRSGMFCAGIIVVMVKRONVVDV 1404
Db 1369 PPSKRSLLKVVRRLEKQOEQYDGRGRTVTVHCLNGGGRSGTFCALCSVCEMIQQQNIIDV 1428

Qy 1405 FHAVKTLRNSKPNVPEAPEQYRFCYDVVALEYLS 1438
Db 1429 PHIVKTLRNNKSNVTELEQYKFVYVALEYLS 1462

RESULT 9
US-10-205-823-343
; Sequence 343, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastien
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Duetin
```

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
 ; FILE REFERENCE: MRI-044
 ; CURRENT APPLICATION NUMBER: US/10/205,823
 ; CURRENT FILING DATE: 2002-07-25
 ; PRIOR APPLICATION NUMBER: 60/307,982
 ; PRIOR FILING DATE: 2001-07-25
 ; PRIOR APPLICATION NUMBER: 60/314,356
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/325,020
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: 60/341,746
 ; PRIOR FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: 60/362,158
 ; PRIOR FILING DATE: 2002-03-05
 ; NUMBER OF SEQ ID NOS: 455
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 343
 ; LENGTH: 1463
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-205-823-343

Query Match 59.28; Score 4564; DB 14; Length 1463;
 Best Local Similarity 57.5%; Pred. No. 0;
 Matches 847; Conservative 238; Mismatches 341; Indels 48; Gaps 9;

QY 1 MDTTAAALPAFVALLLLSPWLLGSAQGSAGCTFDGPGACDQHDL-YDDFEWVH 59
 DB 1 MASLALAL-----SLLRLQLPPLGARAQAGCGCSFDEHYSNCGSVLALGNGFTWEQ 56
 QY 60 VSAQEPHYLPMPQGSYIMVDSDDHPGEBKARLQLPTMKENDTHCHIDFSLYLSQKGLN 119
 DB 57 INTTEKPMLOQAVPTGSFWMVNSSGRASGQKAHLLLPFLKENDTHCHIDFHYSSRRDSS 116
 QY 120 PGTNLILVRNKGPLANPINWVTGTRDMLRAELAVSTWPNNEYQVIFAEVSGGRSGY 179
 DB 117 PGLNVVYKVGNGPQGNFVNVSGVTEGWKAEALSTFWPFYQVIFESVSLKHGPGY 176
 QY 180 IATDDIQVLSYPCDSPHFRLGDEVNAGONATFOCIATGRDAVNKLQRRNGEDIP 239
 DB 177 IADVEVRVLAHPCRKAPHFRLQNVNVNQNATFOCIAGKWSQDKMLQWNGRDTA 236
 QY 240 VAOTKMINHRRFAASFLQEVTKTDQBLRYCVTQSERGSGVSNPAOLIVREPPRPIAPPQ 299
 DB 237 LMVTRVNHRRFSATVSADTAQRSVSKYRCVIRSDGSGVSNVAELIVKEPTPIAPPE 296
 QY 300 LLGVGPTYLILQNLANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEY 359
 DB 297 LLAVGATYLIWKPNSIIGDGPILKEVEYRTTGTWAEITHIVDSPNYKLMHLDPDVEY 356
 QY 360 EIRVLLTRPGEGGTGLPGPLITRTKCAEPMRTPKTLKIAEQARRIANDWESLGNITR 419
 DB 357 EIRVLLTRPGEGGTGPGAPLITRTKCADPVHGPQNVEIVDIRARQLTLQWEPFGAVTR 416
 QY 420 CHTFNVITCYHFRGHNESKADCLMDPKAPQHVHNLPPVTNVLSKMLITNPEGRKESE 479
 DB 417 CHSYNLTVQYV--FNQOYEAEEVLOTSSHTYLRGLRFPMTIRLLLSNPEGRMESE 474
 QY 480 ETIITQDEDDVGPVPVKSLQGTGFENKIFLNWKEPLDPNGIITQYIYSISIRSFPDPAVP 539
 DB 475 ELVVQTEEDVEGAVPLESIQGGPFEEKIYIQWPPNETNGVITLYEINYKAVGSLDPSAD 534
 QY 540 VAGPPQTVSNLWNSHTHVFHLPHTTYQFFIRASTVKGPGPATAINVTNINISAPTLDPY 599
 DB 535 LSSQKRGVFKRLRNETHFLVGLYFGTYSYTIKASTAKGFGPPVTTTIATKISAPSMPEY 594
 QY 600 EGYDASLNETAATTITVLLRPAQAKGAPISAYQIVWEELHPHRTKREAGAMECYQVPVYQ 659
 DB 595 D-TDTPLNETDITITVLMKPAQGRGAPSVIQLVKEERLOKRRRAADIIECFSPVPSYR 653
 QY 660 NAMSGGAPYYFAAELPGLNLPAPFTVGNDRVTQGFNPNPLAPRKGNYNYFOAMGSVEK 719

DB 654 NASSLDLHRYFAAELKPAANLPVTPFTVGNKTYGWNPLSPKSYISYFQALSXANG 713
 QY 720 ETKTQCVRITAKAATEPEVIP-----DPAKOTDRVVKIAGISAGI 760
 DB 714 ETKINCVRITAKAPMSAQVTPGTPLCLLTGTASTQNSNTVEPEKQVNDTVKMGAVTAGL 773
 QY 761 LVFILLLVVILIVK-----SKLAKKRKADAMGNTRQEMTHMVNAMDRSYAD 807
 DB 774 LMFITILLGVMLTIKRRRNAYSYSYLSQRKLAKKQKETSQGAQREMGPVASA-DKPTTK 832
 QY 808 QSTLHAEDPLSIIFMDQHNPSRYENHSATAESRLDV---PRYLCEGTESPTQGLH 864
 DB 833 LSASRNDEGFSSSQDVNGFT---DGSRGELSOPTLTITQHPYRTCDPEMSYPRDQFQ 888
 QY 865 PAIRVADLLQHINLMKTSDSYGFKEEYESFEGOSASWDVAKKDONAKRNYGNIAYDH 924
 DB 889 LAIRVADLLQHIQMKRGQGYGKEEYEALEPEGQTASWDTAKEDENKRYGNIISVDH 948
 QY 925 SRVILQPVEDDPSDDYINANYIDGYQRPSHYIATQGPVHETVYDFWRMIWQEQSACIVM 984
 DB 949 SRVRLVLVDGPHSDYINANYIDGYHRPRHYIATQGPVQETVKDFWRMIWQENSASIVM 1008
 QY 985 TNLVEGRVKCYKWPDDTEVYGFVTCVEMPELABYVVRTFTLLRRGNEIREVQKPH 1044
 DB 1009 TNLVEGRVKCVRYWPDDETVYGDIVKTLIETEPLEAEYVIRFTVQKGYHIRELRFLH 1068
 QY 1045 FTGWPDPHGVPYHATGLLSFIRRVKLSNPPSAGPIVHVHCSAGAGTGCIVIVIDIMLDMAE 1104
 DB 1069 FTSWPDHGVPCYATGLLGFVRKFLNPPBAGPIVHVHCSAGAGTGCIFAIDTMDMAEN 1128
 QY 1105 EGVVDIYNCVICALRRRINMVQTEEQYIFITHDAILEACLGCTAIPVCEPKAAAFDMIRI 1164
 DB 1129 EGVVDIFNCVRELRAQRVNLVQTEEQYVVDHDAILEACLGCTAIPVCEFRSLYNNISRL 1188
 QY 1165 DSQTNASHLKDEFTQTLNSVTPRLOAEDCSIACTPRNHDKRKFMDMLPPDCLPLIITDG 1224
 DB 1189 DPQTNSSQIKDEFTQTLNIVTPRVRPEDCSIGLLPRNHDKRSMVLPDLRCLPLISVDG 1248
 QY 1225 ESSNYINAAALMDSVROPAAFIYQYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQGPCQ 1284
 DB 1249 ESSNYINAAALMDSHKOPAAFPVVTQHPLFNTVADFWRLVFDYNCSSVVNLMNEMDTAQFCMQ 1308
 QY 1285 YWPEEGMLRYGPTQVECMSCMDVINRIFRINLTPRQEGYLMVQOQFOYVLGWASHREV 1344
 DB 1309 YWPEKTSQCYGPIQVEFVSADIDEDIIHFRICNWARPDQGYRIVQHLQYIGWPAYRT 1368
 QY 1345 PGSKRFLKLIQVKEWKEWKEGEGRTIIHCLNGGSGRGMFCAIGIVVEMVKRQNVVDV 1404
 DB 1369 PPSKRSLIKVRRLEKWEQYDQREGRTVVHCLNGGSGRSGTFCALCSVCBIMIQOQNIIDV 1428
 QY 1405 FHAVKTLRNSKPNMVEAPEQYRCYDVALEYLS 1438
 DB 1429 FHIVKTLRNNKSNMVTLEQYKPYVEVALEYLS 1462

RESULT 10

US-10-296-115-1283
 ; Sequence 1283, Application US/10296115
 ; Publication No. US20040053248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq Inc
 ; TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 784PCT
 ; CURRENT APPLICATION NUMBER: US/10/296,115
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: US09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 1478
 ; SEQ ID NO 1283
 ; LENGTH: 1499

QY 212 ATFOCIATGRDAVHKLWLORENGEDIPVAQTKNINHRPAAFRLOEVTKTDODLYRCV 271
Db 206 ASFOCMAAGR-AEAERFLLQSGALVAGVRHISHRSFLATPTPLAAVSAEQDLYRCV 264
QY 272 TQSERGSGVS-NFAQLIVRPPRIAPQLIGVGTPLLIOLNANSIIGDGPILKEVEY 330
Db 265 SQAPRGRGTSINFAEFVWKEPPTIAPQLLRAGTPLYLIQNTNSIIGDGPVIRKEIEY 324
QY 331 RMTSGSTETHAVNAPYIKLWHLDPDTEYEIRVLLTRPGEGLGPGPLLTRKCAEPM 390
Db 325 RMARGPWAHVAESLOTYKWLWHLDPDTEYEISVLLTRPGDGTGRLGPPPTISRKCAEPM 384
QY 391 RTPKTLIAEIOARRIADVESLGYNTTRCHTENTVTCYHYFRG--HN-----ESKAD 441
Db 385 RAPKGLFAEIOARQLTOLEPLNGVNTIRCHTYTVSLCYHTLSSNQITIPRVCEDRAR 444
QY 442 CLMDPKAPQVNVNHLPPYNTVNSLKMILTNPGEKKESEETIIQDDEVPVGPVVKISQGT 501
Db 445 CQPLHHEEPAAL-----SERSREVLTNPGEKKEGKVTFTQDDEVPSCIAESLTFT 497
QY 502 SFENKIFLNKKEPLDPNGIITQYBEISYSSIRSPDPVAPVAGPQTQVSNLWNSTHVFMLH 561
Db 498 PLEDMIPLKWEEOPEQENGLITQYBEISYOSIESSDPAVNVQA-TSTISKLRNETVHVSNL 556
QY 562 HPGCTYOFFIRASTVKGFGATAINVTNISAPLTPDYEGVDASLNTATITVLLRPAQ 621
Db 557 HPGTTLFSVGARTKGFGQAALTEITTYISAPSL-DYADMPSPLGSENNITVLLRPAQ 615
QY 622 AKGAPISAYOIVVBEHL- PHRTKREAGAMECYQVPTVQNAMSGAPYFAAELPPGNLP 680
Db 616 GRGAPISVQVIVVEEEOGSRRLRREPQGCQCFVPLTFEALARGLVDFGAELAAASLP 675
QY 681 EPAPFTVGDNRTOGFWNPPLAPRGKYNIFYQAMSSVEKETKTCQVRIATKAATEEPEVI 740
Db 676 EAMPFTVGDNKTGFWNPPLPRKAYLIYFOASHLKGTRCLNCIRIARAKACKESKRP 735
QY 741 PDKAQTDVRVKTAGISA-GILVPIILLVILLIVKSK-----LAKRKDA 786
Db 736 LEVSQSEENGILGICAGGLAVLILLGAIIVIRKGRDHYAYVYKPVNMTK----A 791
QY 787 MGNTRQSMTHVAMDRSVADQSTLHAEDPLSTIFMDHNPSPRYNHS--ATAESSRL 844
Db 792 TVNVRQKTHMGSAVDRSFTDQSTL---QPPGUSFMDTHGSTRGEORSGGVTEASLLG 848
QY 845 DVPRYLCEGTESPYQTQLHPAIRVADLQHLNLMKTSDSYGFKEEYESFFEGOSASWDV 904
Db 849 GSPPRCGRKGSPTHTVQLHPAVRVDLQHLNLMKTAEGYFKQEVESFFEG---WDA 904
QY 905 AKDQNRKAKRYGNI IAYDHSRVILQVEDDPSDDYINANYIDGYQRPSPHYIATQGPVHE 964
Db 905 TKKDKYKGSQBPMAYDRHRVKLHPMLGDPNADYINANYIDGYHRSNHFATQGPKE 964
QY 965 TVYDFWRMIWQEOSACIVMTNLVEGRVKCYKYPDDTEVYGDPKVTCVMEPLAEYV 1024
Db 965 MVYDFWRMVMQEHCSLVMITKLVEVAGCKSRYPEDSDTYGDKIMLVKTETLAEYV 1024
QY 1025 RTFTLERRGNEIREVQKQFHTGPDHGVPHATGLLSFIRRVKLSNPPSAGPIVHVCSA 1084
Db 1025 RTALERRGYSARVEVQKQFHTGPDHGVPHATGLLSFIRRVKLSNPPSAGPIVHVCSA 1084
QY 1085 GAGRTGCIYVIDIMLMAEREGVVDIYCNVKALESRRINNVQTEEQYIFIHDAILEACLC 1144
Db 1085 GTGRTGCIYVLDVMDLMAEREGVVDIYCNVKALESRRINNVQTEEQYIFIHDAILEACLC 1144
QY 1145 GETAIPCEKAAFYDMIRIDSQNSHLKDEQTLNSVTPRLOAECDSIACILPRNHDKN 1204
Db 1145 GETTIPVSEFKATYKEMIRIDPOSNSQLREEFQTLNSVTPPLDVEEYSIALLPRNHDKN 1204
QY 1205 RFMDMLPPDRCLPLITIDGESSNYINAALMDSYRQAPAFIVTOYPLPNTVKDPFWRLYVD 1264
Db 1205 RSMVLPDRCLPLITIDGESSNYINAALMDSYRQAPAFIVTOYPLPNTVKDPFWRLYVD 1264
QY 1265 YGCTSIIVMLNEVDLSQG---CPQYWPBEGMLRGP IQVECMSCMDCDVINRIFCNLT 1321

Db 1265 YGCTSIIVMLNQLNOSNANPCLOYPBEPGRQYQYGLMEVEFMSTADEDLVARVFRVQNIS 1324
QY 1322 RPOEGYLMVQOFOYVLGWASHREVPGRSKRSFLKLQLOVEKWEKGEGRTHIICLNGGG 1381
Db 1325 RLQEGHLLVRHFQFLRWSAYRDPDSEKAFHLHLLAEVDKQAB--SGDGRTHVCLNGGG 1382
QY 1382 RSGMFCAGIVEMVKRQNVVDVPHAVKTRNSKPNVVEAPEQYRCPYDVVALEYLES 1438
Db 1383 RRGTSALRTVLEMRCHNLVDVSAFAKTLRNKPNVETMDQYHFCYDVVALEYLEA 1439
RESULT 12
US-10-087-993-34
; Sequence 34, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Navlor, Oliver
; Kharitonov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
; AND SIRP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Qy 1008 DFKVTCVEMPELAEEVVRFTFLERRGYNEIREVQFHTGPHDGHGVPYHATGLLSFIRRV 1067
Db 192 DIKVTLETELAEYVINTFAVERKGVHEIREIQFHTGPHDGHGVPYHATGLLGFVRQV 251
Qy 1068 KLSNPPSAGPTVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRRNMVQT 1127
Db 252 KSKSPSAGPLVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRRNMVQT 311
Qy 1128 BEQYFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOQLNSVTPLR 1187
Db 312 BEQYFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOQLNSVTPLR 371
Qy 1188 QAEDCSIACLPRNHDKNRPFMDLPPDRCLPLIITIDGESSNYINAALMDSYRQAAFIIVT 1247
Db 372 RVEDCSIALPRNHEKRCMDILPPDRCLPLIITIDGESSNYINAALMDSYRQAAFIIVT 431
Qy 1248 QYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQYWPPEGMLRGVPIQVECMSCMD 1307
Db 432 QHPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQYWPPEGMLRGVPIQVECMSCMD 491
Qy 1308 CDVINRIFRICNLTRPOEGYLMVQFQYLGWASHREVPGSRKSLKLILQVEKQEEWKE 1367
Db 492 EDIISRIFRINYAARPQDGYRMVQFQYLGWASHREVPGSRKSLKLILQVEKQEEWKE 551
Qy 1368 GEBRTIHLNGGSGRMCAIGIVEMVRQNVVDVFAVKTILRNSKPNMVEAPEQYRF 1427
Db 552 GEBRTVHCLNGGSGRTFCAISIVCEMLRQRTVDVFAVKTILRNNKPNMVDLLDQYKF 611
Qy 1428 CYDVALEYLES 1438
Db 612 CYEVALEYLNS 622

RESULT 14

US-10-296-115-1390
; Sequence 1390, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1390
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1390

Query Match 28.7%; Score 2210.5; DB 15; Length 815;
Best Local Similarity 53.2%; Pred. No. 3.2e-154;
Matches 412; Conservative 123; Mismatches 227; Indels 13; Gaps 5;
Qy 4 TAAALPAFVALLLLSPWLLGSAQGFAGGCTFFDGGACDYHQDYDDFEWVHSAQ 63
Db 3 TLGTCLATLALL-----TAAGETFGGCLFDEPYSTCGYSQSGDDFNWEQNTL 54
Qy 64 EPHYLPPEMPOGSMYVDSDDHDPGEKARLQLPMTKENDTHCIDFSYLLYSOKGLNPGTL 123
Db 55 TKPTSDPWFMSGSPMLVNASRPGQRAHLLLPOLKENDTHCIDFHFVSKSNSPPGLL 114
Qy 124 NILVRNKGPLANPIWVTGTRDWLAELAVSTFWPNEYQVIFAEVSGSGSYIAID 183
Db 115 NVYKVNGLPLNPIWISGDPTRWNAELAISTFWNFYQVIFEV-ITSGHQYLAID 173
Qy 184 DIQVLSYPCDKSFLRLGDEVNAGQATFQCIATORDAVHKNLWLRORNGEDIPVAQT 243
Db 174 EVKVLGHPCRTTHFLRIQNVENAGOFATFQCSAIGRTVAGDRLWLQGLDVRDAPLKEI 233

Qy 244 KNINHRFAASFRLOEVTKTDQDLYRCVTOBSRGSGVSNFAQLIVREPRPIAPPQLGV 303
Db 234 KVTSSRFIASFNVVNTTKRDAGKYRCMIRTEGGVGISNYAELVVKPEVPPIAPPQLASV 293
Qy 304 GPTVLLIQLNANSIIGDGPILKDEVEVMTSGSWTETHAVNAPYTKLWHLPDPTDEYIRV 363
Db 294 GATYLLIQLNANSINGDGPVAREVEYCTASGWNDRQPVDSYTKIGHLPDPTDEYISV 353
Qy 364 LLTRPGGGTGLPDPPLITRTKCAEPMRTPKTLKIAEIOARRIAVDWESLGVNTRCHTF 423
Db 354 LLTRPGGGTGSFGPALTRTKCADPMRGPKLEVEVKSQIIRWEPFGYNVTRCHSY 413
Qy 424 NVTCYHYFRGHNESKAD--CLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEET 481
Db 414 NLTVHYCYQVGQGVQREVEVSWDENGHPQHTINLSFYTNVSVKILMLNPEGRKESQEL 473
Qy 482 IIQTDDEVPGRVPKSLQGTSEFNKIPLNWKPELDPNGIITQYEISVSSRSRFPAPVPA 541
Db 474 IVQTDDELPGAVPTESIQGSTFEKIFLOWREPTQTYGVITLYEITYKAVSSFPDEIDL 533
Qy 542 GPPTQVSNLWNSHTHVFHMLHPGTYQFFIRASTVKGFGPATAINVTNINISAPTLPDYEG 601
Db 534 NQSRVSKUGNETHFLFGYPGTYFTIRASTAKFGFPATNQFTTKISAPSMPAYE- 592
Qy 602 VDAISNETATTITVLLRPAQAKAPISAYQIVVVEELHPHRTKREAGAMECYQVPVYQNA 661
Db 593 LETPLAQNTDNTVTVMLKPAHSGAPVSYQIVVEEERPRRTKKTTEILKCYVPPIHQNA 652
Qy 662 MSGGAPYFAAELPPGNLPEPAPPTVGDNRTYQGFVWNPPLAPRKGYNIIYFOAMSVEKET 721
Db 653 SLLNSQYFAAEFFADSLQAAPFTIGDNKTYNGYNTPLLPYKSYRIYFOAASRANGET 712
Qy 722 KTCVRIATKAATEEPEVIPPDAKOTDRVVKIAGISAGILVFIILLVWILLVKK 776
Db 713 KIDCVQATKGA--TPKPVPEPEKQTDHTVKIAGIAGILLVFIILVGLVLMKK 766

RESULT 15

US-09-808-602-54
; Sequence 54, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Heirman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-54

Query Match 19.9%; Score 1534.5; DB 9; Length 1502;
Best Local Similarity 30.7%; Pred. No. 8.1e-104;
Matches 422; Conservative 213; Mismatches 480; Indels 259; Gaps 46;
Qy 205 EVNAGQATFQCIATGRDAVHKNLWLRORNG-----EDIPVAQTKNINHRFAASFRLOEV 260

Dd	242	EIMPGGNVITCVAAGSPMPYVK-WMOGAEDLTPDDMPVG---RNV-----LELTUV	290
Qy	261	TkTDODLYRCVTOSERGSGVNSFAQLIVREPPRPPIAPPOLLGVGPYLLIQLNANSIIIGD	320
Dd	291	-KDSANYHPCVAMSSLG-V-TEAVAQITVKSPLKAPGTFMVNTATSIITWDSGN---P	345
Qy	321	GPIILKEVEYRMVS--GSWTETHAVNAPTYKLWHLPDPTBYEYBIRVLTLTRPGEGTGLPGP	378
Dd	346	DPVSYYVIEYKSKSDQFYKEDIKTTRYISIGGLSPNSEYEIWV--SAVNSIQGPPSE	403
Qy	379	PLITRTKCAEBMRTPKLKTAETQARRIAVDMS-----LGYNI-----	417
Dd	404	SVVTRTGEQAPPRPNVQARMLSATMIWOMEEPVEPNGLIRGYRVYTYMEPEHPVGNW	463
Qy	418	-----T	418
Dd	464	KQHNVDSLTTVGSLLDETTYVRVLAFITSVGDGPLSDPIQVKTQOGVPQGPMNLRAEA	523
Qy	419	RCHTFNVITCVH-----YFRGHNESKADCLMDMDPKAQHVNHLPYTIVNSLJK	466
Dd	524	RSET-SITLSWSPPROESSIIKYELLFREGDHREVGRTPDP-TTSVVVEDLKNTEYAFR	581
Qy	467	MILTNPBG-----RKESERTIODEDVDPGPVPVKSLQGTSPFNKFIPLWKKEPLDPN	518
Dd	582	LAARSPOGLAFTPVVRQRTLQS-----SPKNFKVMTKMTS-----VLLSWEPF-DNY	630
Qy	519	GIITQYBEISYSIRSFPDPAVPAGPQTGVSNLMNSTHVFHMLHPGTTVOFFT--RASTV	576
Dd	631	NSPTPYKIQNGL-----TLDVDG-----RTYKKLIHLKPHTFYNFVLNRGSSL	676
Qy	577	KGFGEPA---TAINVTT-NISAPTLPDYEGVDASLNETAATTITVLLRPAQAAGAPISAYQ	631
Dd	677	GGLOQTVTAWTAFNLNGKPSVAPKPADGPF-----IMVLPDGQSP-VPQSYF	725
Qy	632	IvVEELHPHR-----TKREAGAMECVQ-----VPVTVONMSGGAPYIFA-AE	673
Dd	726	IVMVPLARKSGGQFLTPLGPSMDLEELIQDISRLQRSLRSRQLEVPRPYIAARFSV	785
Qy	674	LPCGNLPEPAPFTVGDNRTYOGFWNNPPLAPRGKGNVIYFOAMSSVEKETKTQCVRATKAA	733
Dd	786	LPP-----TFHPGDKQYGFDNRRGLEPGRHYLVLFVLAV--LQKSEPT-----FAASP	831
Qy	734	TEEPEVI--PDPAKQTRDVVKIAGISAGIILVIFILLLVWI-LIVKKSCLKAKKRCDAMGNT	790
Dd	832	FSDFFOLDNDPDPQFIVDGEGLIWIIVGPVLAVFIICIVIAILLXKNKPKSRKSDSEPT	891
Qy	791	ROEMTHMVNAMDRYAQOSTLHAEDPLSITFTMDOHNFSPRYENHSATAESSRLLDVRYL	850
Dd	892	KCLINN-----ADLAPHHPKDYPE--MRRINF-----	916
Qy	851	CEGTESPQTCQL-HPAIRVADLLQHLNMKTSDSYGFEKEYESFFEGQASMDVAKDQ	909
Dd	917	----QTP---GMLSHPPIPADMAEHETERLKANDSLKSQEYSISIDPGOQFTWEHNSLEV	969
Qy	910	NRAKNRYGNITAYDHSRVILQPVEDDDPSSDIYNANYIDGYCRPSHYTIATQGVHETYDYF	969
Dd	970	NKPKNRYANVIAYDHSRVILQPIEGISGSDVINANYVDGYRRQNAYIATQGLPETGDF	1029
Qy	970	WRMTWQEOSACIVMVTNLVEVGRVKCYKYPDP-DTEYVGDYKFTCTVEMEPLAEYVRTFT	1028
Dd	1030	WRMWYEQRSATIVMMTRLERKSRIKCQDYPNRRGTETYGTFTVLTLLDTIELATFCVTRFS	1089
Qy	1029	LERGYNIREFKVOPHTGCPHDHGVPYHATGLSFIRVKLSNPSPSAGPIVHVCSAGAGR	1088
Dd	1090	LHKNGSSKREVRQFQFTAWPDHGVPEYPTFLAFLRRVTKCNPDAGPIVHVCSAGVGR	1149
Qy	1089	TGCYIVIDIMLDMAEREQVDVINCYNCVALARSRRINMVOTBEQYIFIHDAILEACLQCEA	1148
Dd	1150	TGCFIVIDLAMLERIKPEKTVDVYGHVTLMRSORNYVMVQTEDQYSFIEALLLEAVGCNTE	1209
Qy	1149	IPVCEFKAADFMTRIDSQTNSSHUKDEFQTLNSTRVTPRLOADCISIACLPRNHDKNRFMD	1208
Dd	1210	VPAKSLYAIYIOKLAQAGEHEVHTGMELEFKEL--ANSKAHTSRFISANLCKKFKORLVN	1267

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:40:58 ; Search time 38.2607 Seconds
(without alignments)
3618.750 Million cell updates/sec

Title: US-09-887-669-2
Perfect score: 7709
Sequence: 1 MDTTAAALPAFVALLLSP.....EAPQVRFYVDVALEYLESS 1439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7595.5	98.5	1440	2 JC6312	protein-tyrosine-p
2	7571	98.2	1457	1 A48066	protein-tyrosine-p
3	4807	62.4	1452	1 S17659	protein-tyrosine-p
4	4791	62.1	1452	1 S17670	protein-tyrosine-p
5	4632	60.1	1436	2 JC5290	protein-tyrosine-p
6	4374.5	56.7	1442	2 S72441	protein-tyrosine-p
7	1529.5	19.8	1501	2 I58148	protein-tyrosine-p
8	1517.5	19.7	1898	2 S46216	leukocyte antigen-
9	1509	19.6	1897	1 TDHULK	leukocyte antigen-
10	1508.5	19.6	1499	2 I50212	protein-tyrosine-p
11	1505.5	19.5	1912	2 A56178	protein-tyrosine-p
12	1490.5	19.3	1496	1 A48758	protein-tyrosine-p
13	1483	19.2	1691	1 D54689	protein-tyrosine-p
14	1483	19.2	1894	2 C54689	protein-tyrosine-p
15	1470.5	19.1	1290	2 A56493	leukocyte common a
16	1462.5	19.0	1863	2 S46217	protein-tyrosine-p
17	1457.5	18.9	2029	1 TDFFLK	protein-tyrosine-p
18	1446	18.8	1907	2 S50893	protein-tyrosine-p
19	1426	18.5	1231	2 S53089	protein-tyrosine-p
20	1366	17.7	1437	2 T31093	probable protein-t
21	1349.5	17.5	1585	2 T19421	probable protein-t
22	1324	17.2	2051	2 T30938	receptor tyrosine
23	1255	16.3	582	2 A57068	protein-tyrosine-p
24	1196	15.5	796	1 JC1285	protein-tyrosine-p
25	1172.5	15.2	802	1 A36065	protein-tyrosine-p
26	1164.5	15.1	832	2 JC8051	protein tyrosine p
27	1153	15.0	829	1 A47373	protein-tyrosine-p
28	1143	14.8	699	2 JC6132	protein-tyrosine-p
29	1132	14.7	700	1 S12053	protein-tyrosine-p

30	1106	14.3	1262	1 B48758	protein-tyrosine-p
31	1071	13.9	680	2 JC8052	protein tyrosine p
32	1023.5	13.3	2314	1 A46151	protein-tyrosine-p
33	1017.5	13.2	1442	1 B48148	protein-tyrosine-p
34	996.5	12.9	1445	1 A48148	protein-tyrosine-p
35	979.5	12.7	1422	2 T42636	protein-tyrosine-p
36	953	12.4	1301	1 A41622	protein-tyrosine-p
37	952.5	12.4	1462	1 B36182	protein-tyrosine-p
38	940.5	12.2	1273	1 TDRTLT	leukocyte common a
39	940	12.2	1291	1 A28334	protein-tyrosine-p
40	931.5	12.1	1304	1 A46546	leukocyte common a
41	908	11.8	1200	2 T43148	probable protein-t
42	882.5	11.4	1409	2 T42522	protein-tyrosine-p
43	875.5	11.4	1237	2 A54080	protein-tyrosine-p
44	866	11.2	1422	2 T30111	hypothetical prote
45	765	9.9	711	2 T23738	probable protein-t

ALIGNMENTS

RESULT 1
JC6312

protein-tyrosine-phosphatase (EC 3.1.3.48) receptor-type - human

C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000

C;Accession: JC6312

R;Yang, Y.; Gil, M.C.; Choi, E.Y.; Park, S.H.; Pyun, K.H.; Ha, H.

Gene 186, 77-82, 1997

A;Title: Molecular cloning and chromosomal localization of a human gene homologous to th

A;Reference number: JC6312; MUID:97199372; PMID:9047348

A;Accession: JC6312

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1440 <YAN>

A;Cross-references: GB:L77886

C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe

-tyrosine-phosphatase homology

C;Keywords: phosphoric monoester hydrolase

F;31-194/Domain: MAM homology <MAM>

F;209-272/Domain: immunoglobulin homology <IMM>

F;294-372/Domain: fibronectin type III repeat homology <3PR>

F;911-1131/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 98.5%; Score 7595.5; DB 2; Length 1440;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1421; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

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Db 1 MDTTAAALPAFVALLLSPWLLGSAQQGFSAGGCTFDDPGACDYHQDLYDDFEWVHV 60

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Db 61 SAQEPHYLPPEMPOGQSYMIVDSSDHPGEXARLQPTMKENDTHCIDFSVLLYSQKGLNP 120

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Db 121 GTLNILVRVKNKGLPANIWNVTGCTGRDMLRAELAVSTFWPNEYQVITFEAEVSGRSGYI 180

Qy 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAGQATFQCIATGRDAVHNKMLQRRNGEDIPV 240

Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAGQATFQCIATGRDAVHNKMLQRRNGEDIPV 240

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Qy 301 LGVGPYLLIQLNANSIIGDPIILKEVEVRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 360

Db 301 LGVGPYLLIQLNANSIIGDPIILKEVEVRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 360

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Db 361 IRVLLTRRGGGTGLPGPLLTIRTKCAEPMRTKTLKIAEQARRIADVMSLGNLTRC 420
Qy 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLITNPEGRKSE 480
Db 421 HSFNVTICYHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLITNPEGRKSE 480
Qy 481 TTIOTDEVPVPGVVKSLQGTSFENKIFLNKKEPLDNGIITQVEISYSSRSRSDPAVPV 540
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Db 721 TKTQCVRIATKAAATEEPEVIPPDAKQTDVVVKIAGISAGILVFTLLLLVWILIVKSKL 780
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Db 781 AKKRKDMGNTRQEMTHVMNMDRSYADQSTLHAEDPLSITFMDQHNFSPRYENHSATAE 840
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Db 901 ASWDVAKKDONRAKNRYGHI IAYDSRVLQVVEDDPSDDYINANYIDGQRP SHYIATQ 960
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Qy 1020 ABYVVRTFTLERRGNEIREVKQFHFTGWPDHGVPHYATGLLSFTRVKLSNPPSAGPIV 1079
Db 1021 ABYVVRTFTLERRGNEIREVKQFHFTGWPDHGVPHYATGLLSFTRVKLSNPPSAGPIV 1080
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Db 1081 VHCASAGRTGCYIVIDIMLMAEREGVVDIYNCKALRSRRINNMVQTEEQYIFTHDAIL 1140
Qy 1140 EACLGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAECDSCIAPLR 1199
Db 1141 EACLGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAECDSCIAPLR 1200
Qy 1200 NHDKNRFMDLPPDRCLPLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLNTVVKDFW 1259
Db 1201 NHDKNRFMDLPPDRCLPLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLNTVVKDFW 1260
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Db 1261 RLAVDYGCTSIWMLNEVDLSQCPQYWPBEGMLRYGPIQVECMSCMDCDVNIRIFCN 1320
Qy 1320 LTRPQEGYLMVQOFOYLGWASHREVPFGSKRSFLKLIQVEKQWEEKGEGRITIIHCLNG 1379
Db 1321 LTRPQEGYLMVQOFOYLGWASHREVPFGSKRSFLKLIQVEKQWEEKGEGRITIIHCLNG 1380
Qy 1380 GRSCHMFCAGIIVEMVKRQNVVDFHAKVTIRNSKPNMVEAPEQVRFICYDVALSYLESS 1439
Db 1381 GRSCHMFCAGIIVEMVKRQNVVDFHAKVTIRNSKPNMVEAPEQVRFICYDVALSYLESS 1440

A48066
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type kappa precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: A48066
C:Jiang, Y.P.; Wang, H.; D'Eustachio, P.; Musacchio, J.M.; Schlessinger, J.; Sap, J.
Mol. Cell. Biol. 13, 2942-2951, 1993
A:Title: Cloning and characterization of R-PTP-kappa, a new member of the receptor prote
ion.
A:Reference number: A48066; MUID:93233655; PMID:8474452
A:Accession: A48066
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1457 <JIA>
A:Cross-references: UNIPROT:P35822; GB:L10106; NID:G2937771; PIDN:AAA40021.1; PID:G2937772
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBI:129880)
C:Complex: after cleavage by a furin-like endopeptidase, the two chains remain associate
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe
tyrosine-phosphatase homology
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran
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F:29-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, uncleaved #status
F:29-641/Product: protein-tyrosine-phosphatase, receptor type kappa, chain 1 #status pre
F:29-641,644-755/Domain: extracellular #status predicted <EXT>
F:30-193/Domain: MAM homology <MAM>
F:208-271/Domain: immunoglobulin homology <IMM>
F:293-371/Domain: fibronectin type III repeat homology <FN3A>
F:388-477/Domain: fibronectin type III repeat homology <FN3B>
F:489-581/Domain: fibronectin type III repeat homology <FN3C>
F:593-682/Domain: fibronectin type III repeat homology <FN3D>
F:644-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, chain 2 #status
F:756-772/Domain: transmembrane #status predicted <TMN>
F:773-1457/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:841-1457/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:922-1148/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:100,139,210,415,423,435,461,551,585,589,606,689/Binding site: carbohydrate (Asn) (cova
F:215-269/Dissulfide bonds: #status predicted
F:643-644/Cleavage site: Arg-Glu (furin-like endopeptidase) #status experimental
F:1100/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1106/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1394/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1400/Binding site: substrate phosphate (Arg) #status predicted

Query Match 98.2%; Score 7571; DB 1; Length 1457;
Best Local Similarity 97.3%; Pred. NO. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy 1 MDTTAAALPAFVALLLLSPWPLLSAQOQSAGGCTFDDGPGACDYHQDLYDDFEWVHV 60
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Db 120 GTLNILVRNKGPLANPIWNVGTGTRDMLRAELAVSTFWPNQYQVIFEAESVSGRSGYI 179
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Db 180 AIDDIQVLSYPCDKSPHFLRLGDVEVNAQONATFCIATGRDAVNKLQORNGEDIPV 239
Qy 241 AQTKNINHRRFAASFRLEQVTKDQDLYRCVTSRSGSVSNFAQLIVREPPRPPIAPPOL 300
Db 240 AQTKNINHRRFAASFRLEQVTKDQDLYRCVTSRSGSVSNFAQLIVREPPRPPIAPPOL 299
Qy 301 LGVGFTYLLIQLNANSIIGDGPILKVEYRMTSGSWTETHAVNAPTYYKLMLHLDPDTEYE 360
Db 300 LGVGFTYLLIQLNANSIIGDGPILKVEYRMTSGSWTETHAVNAPTYYKLMLHLDPDTEYE 359


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QY 383 RTKCAEPMRTPKTLKIAEIQARRIADVWESLGYNIITRCHTFNVTICHYFRGHNESKAD- 441
Db 373 RTKCADPMRGPKLEVVVEVSRQITIRWEPFGYNVTRCHSYNLTVHYGYQVGQGVRRSE 432
QY 442 -CLDMDPKAQHVNVHLPPTVNSLKMILNPEGRKESEETIOTDSDVPVPVKSLQG 500
Db 433 VSWDTDNHSHQHTITNLSPYTVNSVKLILNMPGRKESQELTVQTDSDLPNAVPTESIQG 492
QY 501 TSPENKILFNWKEPLDNGIITQVEISYSIRSPPDPAVPVAGPQPTVNSLNWSTHHVFMH 560
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QY 561 LHPGTTVQFIRASTVKGFGPATVNTNISAPTLDPYEGVDASLNENATITTLVLRPA 620
Db 553 LYFGTITTSFIRASTAKGFGPATNQFTTKISAPSPAYE-FETPLNQTDNTVTVMLKPA 611
QY 621 QAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVYQAMSGAPYFAAEALPPGNLP 680
Db 612 QSRGAPSVVQIVVEEERPRTKTTEILKCPVPPIHFQNASILNSQYFAAEFPADSLQ 671
QY 681 EPAPFTVGDNRITYOGFWNPPLAPRKGNIYIFQAMSSVEKETQCVRIATKAATEBEPIV 740
Db 672 AAQPFTIGDNKTYNGVWNTPLPHKSYRIYVQAASRANGETKIDCVRVATKGAV-TKPKV 730
QY 741 PDPAKQTDVVKIAGISAGILVFLILLVILVVKSLAKKRDAMGNTROETHWVNA 800
Db 731 PEPEKQTDHTVKIAGVITAGILLFVIFLVGLVVMKGRKLAKRKETMSSRQENTVMVNS 790
QY 801 MDRSYAQDQSLHAEDPLSITFMDOHNSPRY-----ENHS 835
Db 791 MDKSYAEQGTNCDE---AFSGMTHNLNGRSVSPSFTWKTNTLSTSVNSYVPDETHI 847
QY 836 ATAESSLRLDVPYR-LCEGTESPYQTQLPAIRVADLLQHILNMLKTSDSYGFKEEYESF 894
Db 848 MASDTSLSLAQPHYTKREAADVPQTQLPAIRVADLLQHIQMKCAEYGFKEEYESF 907
QY 895 FEGQSASVDVAKQDNRAKRYGNIITAYDHSRVLQVPEDDPSDYINANYIDGYQRPSPH 954
Db 908 FEGQSAPWDSAKDENRMKRYGNIITAYDHSRVLQVLEGNDSYINGYIDGYRPNH 967
QY 955 YIATQGVPHVTVDVFWEMIWQESACIVMTVNLVEGRVKCYKVPDDETVYGFKVTVCV 1014
Db 968 YIATQGVPMQETIYDFWHRWHEHTASLIIMTVNLVEGRVKCCYKVPDDETVYIDKIKVTLI 1027
QY 1015 EMPELAEYVYVTRTLERRGYNEIREVKQFHTGPDHGVPHYHATGLISFIRRVKLSNPPS 1074
Db 1028 DTELLAEYVIRTAVERKGIHEIREIQFHTGPDHGVPHYHATGLLGFVRQVKSPPN 1087
QY 1075 AGPIVHCSAGAGRTGCIYVIDIMLMAEREGVVDIYNCVKALRSRRINNVQTEEQYIFI 1134
Db 1088 AGPLVHCSAGAGRTGCFIYVIDIMLMAEREGVVDIYNCVRELRSRRINNVQTEEQYVI 1147
QY 1135 HDAILEACLCGETAIPVCEPKAAFYFDMIRIDSTQNSSHLKDEFQTLNVTPLRQAECSI 1194
Db 1148 HDAILEACLCGDSIPSASQVRSYIYDMNKLDPQNTSSQIKEEFTLMNVTPLRVEDCSI 1207
QY 1195 ACLPRNHKXRFMDMLPPDCLPELITIDGESSNYINAAIMDSYROPAAFIIVQYPLPNT 1254
Db 1208 ALPLPRNHKXRCMDLPPDCLPELITIDGESSNYINAAIMDSYKQPSAIFIVQHPLPNT 1267
QY 1255 VKDFWRLIYDYGCTSIYVLMNEVLSQSCQCPQYWPBGMRLYGPQIQCWMSCMDVINRI 1314
Db 1268 VKDFWRLIYDHYCTSVVLMNDVDPALCPQYWPBGMVHRGPIQVFPVSADLEEDIISRI 1327
QY 1315 FRICNLTRPQEGYLMVQOFOYLGWASHREVPGSKRSPFLKILQVEKQWBEWKEGEGHTII 1374
Db 1328 FRIYNASRPQDGRHWVQOQFGLGPMYWRDTPVSKRSPFLKILRQVQWKEEYNGEGEPTVV 1387
QY 1375 HCLNGGGRSGWFCAGIYVBMVKRONVVDVFAVKTLRNSKPNVPEAPQYRFCYDVALE 1434
Db 1388 HCLNGGGRSGTFCISIVCEMLRHQRITVDVFAVKTLRNNKPNVLLDQYKFCYEALE 1447
QY 1435 YLES 1438
```

Db 1448 YLNS 1451

RESULT 5

JC5290

protein-tyrosine-phosphatase (EC 3.1.3.48) - human
N/Alternate names: Phosphotyrosine phosphatase

C/Species: Homo sapiens (man)

C/Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C/Accession: JC5290

R/Wang, B.; Kishihara, K.; Zhang, D.; Hara, H.; Nomoto, K.

Biochem. Biophys. Res. Commun. 231, 77-81, 1997

A/Title: Molecular cloning and characterization of a novel human receptor protein tyrosi-
ma cells.

A/Reference number: JC5290; MUID:97223402; PMID:9070223

A/Accession: JC5290

A/Molecule type: mRNA

A/Residues: 1-1436 <MAN>

A/Cross-references: UNIPROT:O00197; GB:U73727; NID:g1923222; PIDN:AA51343.1; PID:g192323
C/Comment: This enzyme belongs to type II receptor protein tyrosine phosphatase which me
and an immunoglobulin-like domains.

C/Genetics:

A/Gene: htrp-J

C/Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe
-tyrosine-phosphatase homology
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F/22-188/Domain: MAM homology <MAM>

F/203-266/Domain: immunoglobulin homology <IMM>

F/288-366/Domain: fibronectin type III repeat homology <3PR>

F/826-1436/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F/903-1123/Domain: protein-tyrosine-phosphatase homology <PTP1>

F/1193-1418/Domain: protein-tyrosine-phosphatase homology <PTP2>

F/1075/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1081/Binding site: substrate phosphate (Arg) #status predicted

F/1370/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1376/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 60.1%; Score 4632; DB 2; Length 1436;

Matches 867; Conservative 211; Mismatches 339; Indels 26; Gaps 10;

QY 6 AAALPAFVALLLSPLILGSAQGSAGGCTFD---DGFACDYHQDLVDFEWHVSA 62

Db 4 AQALVALATFQLCAP-----ETETPAAGCTFEASDPAVPCEYSQAQYDDFQWEQVRI 56

QY 63 QEHYLPPEMQSGYMLVDSSDHDHGEKARLQLPTMKENDTHCIDSYLLYSQKLNPGT 122

Db 57 HPGTRAPDLLPHGSYLWNTVSQAPGQRAHVIFQSISENDTHCQVFSYFLYSRDGHSPT 116

QY 123 LNTILVRNKGPLANPIWNVTFGRDWLRAELAVSTFWPNEYQVIFPAEYSGRSGYIAI 182

Db 117 LGYVVRVNGGPGLSAVWNTGSHGRWQHAEALAVSTFWPNEYQVIFALLSPDRGYMGL 176

QY 183 DDIQVLSYPCDKSPHFLRLGDEVNAGQNAFTFCIATGRDAVHNKMLQRRNGEDIPVAQ 242

Db 177 DDILLSPYCAKAPHFSRLGDEVNAGQNASFCMAAGRAAEERFLQSQGALVPAAG 236

QY 243 TKNINIRRAAASFLRLEVTKDQDLVRCVTSQSRGSGVSNFAQLIVREPPRPAPPOLLG 302

Db 237 VRHISRRFLATPPLAAVSRAEQDLYRVCVSAQPRGAGVSNFABLIKVKEPPTAPPOLLR 296

QY 303 VGPYLLIOLNANSIIGDGPILIKVEYRMTSGSWTETHAVNAPTLYKLWHLDDPDEYR 362

Db 297 AGPTYLIILQNTNSIIGDGPVIRKEIYRMARGPWAIEVHVAISLQTYKLWHLDDPDEYR 356

QY 363 VLLTRPEGGTGLPGPLITRTKCAEPMRTPKTLKIAEQARRIADVWESLGYNITRCHT 422

Db 357 VLLTRPEGGTGRPGPLISRTKCAEPMRAPKGLAFAEIQARQLTLQWEPLGNVTRCHT 416

QY 423 FNTVICYHVRG--HNESKADCLMDPKAPQHVNVHLPPTVNSLKMILNPEGRKESEE 480

Db 417 YTVSLCYHYTLGSSHNQITRECVKTEQGVSRYSYIKNLLPYRNVHVRVLTNPGRKEGKE 476

Qy	481	TLIQTDENVGPVPVKSLQGTSPFNKIFLNKKEPLDPNGIITQYEISYSSSTRSDPAVPV	540
Db	477	VTQTDENVGSGIAAESLFTPLEDMIFLKEEPEQENGLITQYEISYQSLESSDPAVV	536
Qy	541	AGPQTVSNLWNSTHHVMHLHPGTYGFFIRASTVKGFGPATAINVTTNISAPLDPYE	600
Db	537	PGPRTISKLNETYHVSNLHPGTYLFSVARTGKGFGQAALTEITTNISASFSF-DYA	595
Qy	601	GVDASLNETAATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTVQN	660
Db	596	DMPSPLGSESENTITVLLRPAQGRGAPISVYQIVVEEERARLRREPQGGQCFVPPLTPEA	655
Qy	661	AMSGAPYFPAELPPGNLPPAPPTVGDNRTYQGFWNPPLAPRKGYNIIYQAMSSVEKE	720
Db	656	ALARGLVHYFGAELAASSLPEAMPPTVGDNQTIRGFWNPPLPRKAYLIIFYQAASHLKGD	715
Qy	721	TKTCVRIATKAATEPEVIPPDAKQTDVRVKIAGISA-GILVFTLLALLVLLVVKSKL	779
Db	716	TRLNCIRIARKAACKESKRPLEVRSQRSEMGILLICAGGLAVLILLGALIIIVIRKGP	775
Qy	780	AKIKRDAMGNTRQEMTHMNVANDRSYDQSTLHAEDPLSITFMDOHNFSPRYENHS--AT	837
Db	776	VNMTK-ATVNVYRQEKTHMNSAVDRSFDTQSTLOEDERLGLSFMDSYTRGDSQSGVT	834
Qy	838	AESSRLLDVPRYLCGTSPTQYTGOLHPAIRVADLLQHINLWKTSDSYGFKEEYSPFEG	897
Db	835	EASSLLGSGPRPCRGKSPVHTGOLHPAVRVADLLQHINQMKTAEGYGFKEEYSPFEG	894
Qy	898	QSASDVAKKQNRAKNRYGNIIAVDHSRVILQPVEDDPSDIYNANVIDYQRPESHVIA	957
Db	895	----WDATKKDKKVGSKQEPMPAVDRHRVKLHPLMGDPNADYINANVIDYGHRSNHPFA	950
Qy	958	TQGPVHETVYDFWRMIWQESACIYVMVTNLVEVGRVKCYKYMPDDTEYVYGDFKTCVEME	1017
Db	951	TQGPKEWYDFWRVWQEHCSIIWMIKLVGVGRVKSRYWPEDSDTYGDIKMLVKTE	1010
Qy	1018	PLAEVYVTFTLRRGYNEIREVKQFHTGWPDPHGVPYHATGLLSFIRRVKLSNPPSAGP	1077
Db	1011	TLAEVYVTFALERRGYSARHEVRQFHTAWPEHGVPYHATGLLAFIRRVKASTPPDAGP	1070
Qy	1078	IIVHCSAGAGRTGCYIVIDIMLDMARERGVVDIYNCVKALSRRLNMVOTBEQYIFHDA	1137
Db	1071	IIVHCSAGTGTGCYIVLDVMLDMAECGVDIYNCVKTLCRRVNMVOTBEQYIFHDA	1130
Qy	1138	ILEACLGETAIPVCEFAAYPDMIRIDSQTNSSHLKDEFOFLNSVTPRLQAEDCSIACL	1197
Db	1131	ILEACLGETTIPVSEFKATYKEMIRIDPQSNSSQLREEFQTLNSVTPRLDVEBCSIALL	1190
Qy	1198	PRNHDKNRMDLPPDRCLPFLITIDGSSNNYINAALMDSYRQPAAFIVTOYPLPNTVKD	1257
Db	1191	PNRDNKRSMDVLPDRCLPFLISTDGSNNYINAALTSYTRSAAFIIVTLHPLOSTTPD	1250
Qy	1258	FWRLYVDYGCYSIVMLNEVDLSQG---CFQYWPBEGMLRYGPIQVECHSCSMDCDVINRI	1314
Db	1251	FWRLYVDYGCYSIVMLNOLNOSNAWPCLQYWPBEGQOYGLMEVFEVMSGTAEDLVARV	1310
Qy	1315	FRICNLTRPQEGYLMVQOYFQYLGWASHREVPGSKSFLKLILQVEKWQEBEKEGGRITII	1374
Db	1311	FRVQNISRLQEGHLLVRHFQFLRWASAYRDTPSKAFLLHLLAEVDKQAE--SGDGRITV	1368
Qy	1375	HCLNGGSGRMFCAIGIVVMYKRVQNVVDVFHAVKTLRNSKNPMVEAPEQYRFCYDVALE	1434
Db	1369	HCLNGGSGSGTCACATVLEMIRCHNLVDVFFAAKTLRNYKENMVTMDQYHFCYDVALE	1428
Qy	1435	YLE 1437	
Db	1429	YLE 1431	

RESULT 6
S72441

protein-tyrosine-phosphatase (EC 3.1.3.48) pi - human

N:Alternate names: FMI protein; receptor-like protein tyrosine phosphatase pi
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S72441
R:Crossland, S.; Smith, P.D.; Crompton, M.R.
Biochem. J. 319, 249-254, 1996
A:Title: Molecular cloning and characterization of PTP-psi, a novel receptor-like protein
A:Reference number: S72441; MUID:97024447; PMID:8870675
A:Accession: S72441
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1442 <CRO>
A:Cross-references: UNIPROT:Q92735; EMBL:X95712; NID:gi666422; PIDN:CAA65016.1; PID:gi666422
A:Experimental source: mammary; cell line MCF-7
C:Genetics:
A:Gene: fmi
C:Function:

A:Description: regulates cellular function by dephosphorylating phosphotyrosine residues
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat
-tyrosine-phosphatase homology
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:29-188/Domain: NAM homology <MAM>
F:288-366/Domain: fibronectin type III repeat homology <3PR>
F:910-1130/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 56.7%, Score 4374.5; DB 2; Length 1442;
Best Local Similarity 58.5%; Pred. No. 4.7e-289;
Matches 840; Conservative 202; Mismatches 332; Indels 63; Gaps 18;

Qy	35	GCTDDGPG--ACDYLHQDLYDDFEWVHVSAQEAPHYLPEMPQGSYMIVDSSDHPDGSKA	91
Db	33	GCTPEESDDPAVPCPEYSAQYDDDFQWDPGS-----PADLPHGSLYLMVNTSQHAPGORA	85
Qy	92	RLQPLTKWKENDDHICIDSYLLYSQKLNPGFTNLILVRNKGPLANIPINWVTGFTGRDWLR	151
Db	86	HVIFQSLSENDTHCVQSYFLYSRDGHSPTGLGVVVRVNGGFLGSAAVNMVMTGSHGROWHQ	145
Qy	152	AELAVSTFWPNEYQVIFEAEEVSGRSGYAIIDDIQVLSYPCDKSPHFURLGDVEVNAQON	211
Db	146	AELAVSTFWPNEYQVLFALISPDRLGYMGDDICILSYPCAKAPHFHSRLGDVEVNAQON	205
Qy	212	ATFOCIATGRDAVHVKLWLRNGEDIPVAQTKNINHRFAASPRLOQVTKTDQDLYRCV	271
Db	206	ASFQCMAGR-AEAERFLQSQSALVPAAGVRHISHRSFLATPPLAAVSRAEQDLYRCV	264
Qy	272	TQSRGSGVS-NFAQLIVREPPRIAPPQLLGVPPTYLLIQLNANSIIGDGPILKVEY	330
Db	265	SQAPRGRGTSLSNFAEFWKEPPTPIAPPQLLRAGPTYLLIQNTNSIIGDGPVIRKEIEY	324
Qy	331	RMTSGSWTETHAVNAPYVKLWHLDPDTEYEIRVLLTRPEGGGTGLPPLTRTKCAEPM	390
Db	325	RMARGPMAEVHAVSLQTYVKLWHLDPDTEYEISVLLTRFEGDGTGRGPPFISRTKCAEPM	384
Qy	391	RTPTKLTAETQARRIADVWESLGVNTRCHTENVITCYHYFRG--HN-----ESKAD	441
Db	385	RAPKGLFABIQAQQLTLQWEPLGTVNTRCHTYTVSLCYHYTLGSSHQTTTPRVCEDDR	444
Qy	442	CLDMDKPAQVNVNHLPPYTNVSLKMLITNPEGRKESEETIIQTDEDVPGVPVVKSLQGT	501
Db	445	COPLHHEEPAL-----SERSREVLTNPEGRKEGKEVTFQTDVPSGIAAESLFTT	497
Qy	502	SFENKIFLNWKEPLDPNGIITQYEISYSSISKSFDPVAVAGPQPTQVSNLWNSTHVFMHL	561
Db	498	PLEDMIFLKWEEPOBPNGLITQYEISYQSIIESSDPANVQA--TSTISKLNRNETYHVSNL	556
Qy	562	HPGTYGFFIRASTVKGFGPATAINVTTNISAPLTPDVEGDVASINETATITVLLRPAQ	621
Db	557	HPGTYLFSVGARTKGFGQAALTEITYIISAPSL-DYADMPSPLGESENNITVLLRPAQ	615
Qy	622	AKGAPISAYQIVVBEHLH--PHRTKREAGAMECYQVPVTVQNAMSGAPYFPAELPPGNLP	680
Db	616	GRGAPISVYQIVVEEQSGRRRLRREPQGGQCFVPPLTPEAALARGLVDFYFGAELAASSLP	675

Qy	681	EPAPFTVGDNR	TYQF	GNPPLAPK	RGYNIYPQ	AMSSVEKE	TKTQCVRI	AKAATERPEVI	740
Db	676	EAMFPTVGDN	KTYGFW	GNPPLPR	KALVYIPQ	AAHLKGT	RLNCIRI	AKAACKESKRP	735
Qy	741	PDPAKOTDRV	VVKIAGIA	-GILVFIL	LLLVILV	LKKS-	-----	-LAKKERDA	786
Db	736	LEVQRSEEM	GLIIGI	CAGHUV	LLLLGAIL	VIIRKGR	DHAYVY	PKPVNMTK	791
Qy	787	MGNTRQEM	THMVNADR	SYAQD	SLHAED	PLSIIT	FMDQHN	PSPRYENHS	844
Db	792	TNVYRQEK	THMWSADR	SFTD	OSTL	---QPGL	SFMDTH	GYSYTRGE	848
Qy	845	DVPRYLCE	GTPSYQT	GOLHPA	IRVADL	LQHINL	MKTS	DSYGVGFEE	904
Db	849	GSPRRPCR	KSGPYHT	VLQHPA	VRVADL	LQHINQ	MKTAEG	YGFQRYES	904
Qy	905	AKQONRAK	NRYGNII	AYDHSR	VILQPV	EDDPS	SDIYNAN	YIDQYQPS	964
Db	905	TKKXDKV	KSGQBP	MPAYDR	HRVKLH	PMLGDP	NADYIN	ANVIDGTH	964
Qy	965	TVYDFWRM	IWOBSAC	IYMTNL	VEVGRV	KCYKYW	PDDEYV	GYGDFKVC	1024
Db	965	MVYDFWRM	VQEHCS	IVMITKL	VEVACK	CSRYP	EDSDTY	GDIKIMLVK	1024
Qy	1025	RTFTLRRG	YNEIRE	VQFHTG	PHDP	HGVPHAT	GLLSF	RRVKLSN	1084
Db	1025	RTFALERG	YSARYE	VRQFHT	PAWPEG	VPYHTT	GLLAF	IRRVKAST	1084
Qy	1085	GAGRTGCY	VIVIDML	DMAER	GVVDIY	NCVKAL	SRINNV	OTEEOYIF	1144
Db	1085	GTGRITGC	YVLVDV	MLDMAE	CEGVVDI	YNCVKL	CSRNM	IQTEBQYIF	1144
Qy	1145	GETAIPVCE	FAAYFDM	IRID	SOQNS	SHLKDE	FOTLNS	VTPLRQAE	1204
Db	1145	GETTIPVSE	FATYKEM	IRIDPQ	SNSQLR	EEFOTL	NSVTPL	PDVEYSIAL	1204
Qy	1205	RFMDMLP	PDRLCP	PLIITID	ESSNYI	NAALM	DSYTRQ	PAAFITVQ	1264
Db	1205	RSMDLV	PDRLCP	PLISITD	GSNNYI	NAALTD	SYTRS	AAFIIVTL	1264
Qy	1265	YGCTSI	YVLMNE	VDLSQ	---CPQY	WPEGM	LRVGP	IOVCGM	1321
Db	1265	YGCTSI	YVLMQL	QNSNAW	PCLQY	WPBFG	QQYGLM	VEFM	1324
Qy	1322	RPQBGYLM	VOQFYL	GHWASH	REVPG	SRFLKL	IQVEK	QWEEK	1381
Db	1325	RLQEGHLL	VRHFQ	FLRSAY	EDT	PDSEK	AFHL	LLAEV	1382
Qy	1382	RSGMFCAI	GIVIVEM	VKQNV	VDVPH	AVKTL	RNSKPN	NVAP	1438
Db	1383	RRGTSCAL	RTVLEM	IRCHNL	VDVS	FAAKTL	RNYKPN	NVET	1439

RESULT 7

I58148
protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form IAR - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58148; S46218
R:Walton, K.M.; Wartell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
Neuron 11, 387-400, 1993
A>Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
A:Reference number: I58148; MUID:93357030; PMID:8352946
A:Accession: I58148
A:Status: preliminary;
A:Molecule type: translated from GB/EMBL/DBDJ
A:Residues: 1-1501 <WAL>
A:Cross-references: UNIPROT:Q64605; GB:I19333; NID:G310242; PIDN:AAA42309.1; PID:G310243
A:Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus n
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A>Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phos

Db 165 ITWF--KDFLPVDPST-----NGRIKQLRSGGLQIESSEETDQKQECVASNS 211
Qy 196 -----PHFLRIG-DVEYNAGQATFOCIATGRDAVHNKMLQRRNG 235
Db 212 AGVRYSSPANLYVRVRVAPRFSILPVSGHEIMPGGNNVITCVAVGSPMPYK-WMOGAED 270
Qy 236 ----EDIPVAQTKNINHRFPAASFLQEVTKTDQDLYRCVQSGSVSNFAQLIVREP 291
Db 271 LTPBDDMPVG--RNV-----LELTDVKDSANYTCVAMSSLGV-IEAVAQITVKS 317
Qy 292 PRPIAPPOLLGVPTYLILQNLANSIIGDGPIILKEVEYRMTS--GSMTEHAVNAPYK 349
Db 318 PKAETPVVTTATISITWDSGN--PDVSYVVIYKSKSQDGPQIUKEDITITRYS 374
Qy 350 LWHLDPTTEYIRVLLTRPGGGTGLPGPPIILITRKCABPMTPTKTLKIAEIOARRIAD 409
Db 375 IGLSPNSEYIHW--SAVNSIGQPPSESVVTRTGEQAPASAPRNVQGRMLSTMIQ 432
Qy 410 WES-----LGYNITFCHTFNVTICVHYFRGHNESKADCLMDPKAP-----OHVNH 456
Db 433 WEBPVEPNQIRGYRV-----YY-----TMEPDQPVSNWQKHND- 467
Qy 457 LPPYTNVSLKMLNPEGRKESEETIQT-----DEDVPGVPVKSLOG----- 500
Db 468 -----DSLLTVGSLLEDEYTVRVLAFTSVGGDPLSDPIQVTKQQGPGQPNFR 518
Qy 501 --TSFENKIFLNWKEPLDPNGIITQYEISYSS-----IRSFDPAPVAVGPPQTVSNLW 551
Db 519 AEAKTETSIVLSWSPRQE--IIVKYELLFKEGDHGREVPNFPF----- 561
Qy 552 NSTHHVFMHLHPGTYOFFPRASTVKGFGPAT-----AINVTT----- 589
Db 562 --TTSFTVEGLKPENYEVFLRAARSGALGAPTPBVRTLOSILPKNFVKVTKTSVLL 620
Qy 590 ----NISAPTLR--DYEG--VDASINETATIT----- 614
Db 621 SWEPENYNSPT-PYKIQYINGLNVVDGRTTKLITNLKPHFTFYFVLMNRGNSMGGLQQ 679
Qy 615 -----VLLRPAQAKGAPISAYQIVW-----BELH 638
Db 680 NVAATAANMLSRKPEVTHKPDADGNVVIILPDVKSSVAVQAVYIVVPLKSRGGQFLN 739
Qy 639 PHRTKREAGMECYQ-----VPVTYQNAMSGAPYFFAAELPGNLPPEPAPFTVGDNR 691
Db 740 PLGSPDEMLEELTDIARLRRSLRHSRQLDFPKP-YIARF--RSLPN--HFLVGDMLK 794
Qy 692 TYQGFWNPPLAPRGYNYIFQAMSSVEKETQCVRIATKATPEPEVI-----PDPAKQT 747
Db 795 HYDNFENRALEPGQRYVIFILAVIQ-BPE-----ATFAASPFPDPIQLNDPDPPII 845
Qy 748 DRVVKIAGISAGILVIFILLVVI-LIVKKSKLAKKRDAMGNTRQBMTHMVNAMDRSYA 806
Db 846 DGEGLIHWIGPVLAVFIICIVAILLYKNKPSKRDSEPRTKCLNN-----A 896
Qy 807 DQSTLHAEDPLSITFMDQHNPSRYENHSATAESSRLLDVPRYLCEGTESPYQTGL-HP 865
Db 897 EITPHPKDPE--MRRINF-----QTP--GMLSHP 923
Qy 866 AIRVADILLOHNLNMTSDSYGFEKEYESFPFGQSASWDVAKQONRAKNRYGNIAYDHS 925
Db 924 PIPVSELAETHHLKANDNLKLSQEYESIDFGQOFTWEHSNLEYNKPNRYANIAYDHS 983
Qy 926 RVILQPVDEDDPSDIYINANYIDGQRPESHYIATQGVHETVYDFPWRMWPQOSACIYVMT 985
Db 984 RVILLPIEGIVGSDIYINANYIDGRKQNAVYATQGLPFTGDFWRVWQORSATIVYMT 1043
Qy 986 NLVEGVRKCYKYPD-DTEYIGDFKVTCTVEMEPLAEYVVRFTFLERRGYNEIREVQFH 1044
Db 1044 KLEEKSRICKQDQWPGRGTDYGMIVQLTDLTIELATFCVTFSLHKNKSGSEKEVQFQ 1103
Qy 1045 FTGWPDHGVPHATGLLSFTRVRKLSNPPSAGPIVHVCSAGAGTGCYVIVIDIMLMAER 1104
Db 1104 FTAMPDGHVPEYPTFFLAFLRRVKTCPDPDAGPIVHVCSAGVGTGCFVIDAMLERIKH 1163

Qy 1105 EGVVDIYNCVKALRRRINMVQTEBEQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRI 1164
Db 1164 EKTVDIYGHVTLMESSQRYMVQTEQYFSFIHDALEAVACGNTEVPARNLYTIQKLAQI 1223
Qy 1165 DSQTNSSHLKDEFQFOTINSVTPRLQAECSIACLRNDHDKRPMOMLPPDRCLPFLIITDG 1224
Db 1224 EVGSHVTGMELFEKRL--ANSKAHTRFISANLPCNFKPNLNVIMPYETTRVCLOPIRG 1281
Qy 1225 -ESSNYINAALMDSYROPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDL--SQG 1281
Db 1282 VEGSDYINASFIDYGRQOKAYIATQGLAETTEDFWRLWENNSTIVVMLTKLBEMGREK 1341
Qy 1282 CPQYWPEGLMRYGPIQVECHSCSMDCDVINRIFRICNLTRPQEGY-LMWQOFOYLGWAS 1340
Db 1342 CHQYWPAAERSARYQYFVVDPMMA--EYNMPQYILREBFKVTARDGQSRVRFQFTDW-P 1397
Qy 1341 HREVPGSKRSFLKILLQVEKQWEEKSEGEETIHLCLNGGORSQMFCAIGHVWEMVRQN 1400
Db 1398 EQGPKSGEGFIDFIGVHKTKQFGQ-DGPISVHCSAGVGTGVFTLSIVLERMYEG 1456
Qy 1401 VVDVFHAVKTLRNSKPNWAEPEQYRFCYDVALEYLES 1438
Db 1457 VDIQTVKMLR-TQPMVQTEDEYQCYQALSYLGS 1493

RESULT 11

A56178

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
N/Alternate names: protein-tyrosine-phosphatase BPTP-2
C/Species: Homo sapiens (man)
C/Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C/Accession: A56178; S12052; B44929
R/Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995
A/Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.
A/Reference number: A56178; UID:95204468; PMID:7896816
A/Accession: A56178
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1912 <PUL>
A/Cross-references: UNIPROT:P23468; GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653
R/Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A/Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases
A/Reference number: S12049; UID:9106018; PMID:2170109
A/Accession: S12052
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 390-1912 <KRU>
A/Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790
A/Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T
R/Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yac
Cancer Res. 52, 737-740, 1992
A/Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A/Reference number: A44929; UID:92119637; PMID:1370651
A/Accession: B44929

A/Molecule type: mRNA

A/Residues: 1756-1804, 'C', 1806-1845 <ADA>

A/Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546

A/Experimental source: pre-B cell NALM-6

A/Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBI:P:78087)

A/Note: the authors did not report the entire codon for residue 90

C/Genetics:

A/Gene: GDB:PTPRD

A/Cross-references: GDB:131384; OMIM:601598

A/Map position: 9p24-9p24

C/Supfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; cgy

C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F;38-100/Domain: immunoglobulin homology <IMM1>

F;140-209/Domain: immunoglobulin homology <IMM2>

F:250-304/Domain: immunoglobulin homology <IMM3>
F:711-811/Domain: fibronectin type III repeat homology <3RP>
F:1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1653/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1559/Binding site: substrate phosphate (Arg) #status predicted
F:1844/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.5%; Score 1505.5; DB 2; Length 1912;
Best Local Similarity 29.3%; Pred. No. 1.6e-93;
Matches 421; Conservative 204; Mismatches 462; Indels 349; Gaps 42;

QY 254 SPRLQEVTKTDOOLYRCVTCQSERGSGVNSFAQLIVRE--PPRIAPQLLVG---GPTVLL 309
DB 569 SYRLQGLKPNLSLYFLAARSQGLGAST-ABISARTQSPKSPAPPDISCTSPSSTSL 627
QY 310 IQLNANSIIGDPIILK-EVEYRMTSGSWTEHAV-----NAPTYKLWHLDPDTEYERV 363
DB 628 VSMQPPPEKQNGIITEYSIKYTAVDGDDPKHEILGIPSDTYKLLQLEKWTIEY--RI 685
QY 364 LLTRFEGEGTGLPGPLIRTKCABPMPTPKTKIAEIQARRIADVDES-----L 413
DB 686 TVTAHTDVGPGESLSLIRTNEDVSPGPRKVEAVNSTSVKVSRSPPVKNQHGQIR 745
QY 414 GYNITRCHTFNVTICVHYFRGHN-----ESBETIIQTD----- 436
DB 746 GYQV-----HYVRMENGEPKQOPMLKDVMLADAQWEDDTTEHDMIIISGLQPE 793
QY 437 -----ESKADCLMDPK-----APOHVNHLPPTNYSLSMLITNPE--- 473
DB 794 TSYSLTVTAYTKGDGASKPKLVSTTGAVPKPLVINH-----TQMNTALIQWPPVD 849
QY 474 -----GRK-----ESBETIIQTD----- 486
DB 850 FGPLQGYRLKFKRQKMEPLTLLEFSEKEDHFTATDIHKGASVYFRLSARNKVGFEEMVK 909
QY 487 -----EDVPGPVVKSQGTSENKIFLNWKEPL--DPNGIITQYEISYSSRSRDPAPV 539
DB 910 EISIEEVPPTGPNQLHSEGTSTSVQLSQWPPVLAERNGIITKTYLLYRDINI--PLLP 967
QY 540 VAG-----PPTVSNLWNSHHVFMHLHGTYTFFIRASTVKFGFPATAINVTNISAPTL 596
DB 968 MEQLVPADTTWTLG-----LKPDTYDVKVRATSKGPG-----YSPSVQFRLL 1014
QY 597 PYDEGVDAASLNATATIT-VLLR---PAQAKGAPISAYOI-----VVEELHPHRTKR-- 644
DB 1015 PVDQVFAKNFHVKAVMKTSVLLSWEIPENYNSA--MPFKILYDDGKMVEVDGRATQKLI 1072
QY 645 -EAGAMECYQVPTVQNAMSGAPYFAELPPG-----NLPE-- 681
DB 1073 VNLKPEKSYSFVLTNRGNSAGLQHRVTAKTAPDVLRTKPAFIGKTNLDGMTVQLPEVP 1132
QY 682 ----- 681
DB 1133 ANENIKGYIIIVPLKSRGKFIKPWESPDMEDELLEKISKRBSRYRGREVLKPYI 1192
QY 682 -----PAPFTVGNDRYTGFWNPPLAPRKGYNIYFQAMSVBEKTKTCQVRIATKAT 734
DB 1193 AAHFVDPVLPTEFTLGGDKHYGFTNKQLSQGQEV-VFFVLAVMEHAESK-----MYATSPY 1246
QY 735 EPEVPI--DPAKQTRVRVKIAGISAGIL--VFILLVILVILVVKSKL-AKKRKDAMGN 789
DB 1247 SDPVSMOLDPQFITDEEGLIWWGVLAVVFIICIVAILLYKRRKRAESDSRSKSSIPN 1306
QY 790 TQEMTHMVNMDRSVADQSTLHAEDPLSITFMDQHNPSRYENHSATAESSRLLDVPRY 849
DB 1307 NKEIPSH-----HPTDPVELRLN----- 1325
QY 850 LCEGTESPYQTQGL--HPAIRVADLLQHLNLMKTSYSGFKBEYESFFEQSASMDVAKK 907
DB 1326 -----FQTPGMASHPIPIELADHTLERLKANDNLKFSQYESIDPQOFTWEHNSL 1377

QY 908 DONRAKNRYGNI IAYDHSRVILQVEDDPSSDIYANVYIDGYQRPSPHYIATQGPVHETVY 967
DB 1378 EVNPKRYANV IAYDHSRVLLSIEGIPGSDYVYANVYIDGYRKQNIATQGSIPETFG 1437
QY 968 DFWRMIWQESACIVMVTNLVEGRVKCYKYPD-DTEVYGDGFKVTCVEMEPLEAYVVRT 1026
DB 1438 DFWRMIWQESATVVMVTNKLERSRVKCDQWPSRGTEHGLVQVTLDTVELATYCVRT 1497
QY 1027 FTLERRGYNEIREVKQFHTGWPDPHGVYHATGLLSPIRRVKLSNPPSAGPIVHCSAGA 1086
DB 1498 FALYKNGSSEKREVRQFQTAMPDHPGVEHPTFLAFLRRVKTNCNPPDAGPMVHCSAGV 1557
QY 1087 GRTCYIVIDIMLWASREGVVDIYNCVKALRSRINNVQTEEOYIFIHDAILEACLCGE 1146
DB 1558 GRTCCFVIDMLERIKEKTVDIYGHVTLNRAQRNVAVQTEDQYIFIHDALEAVTCGN 1617
QY 1147 TAIPVCFKAAYPDMIRIDSQTNSSHLKDEPQTLNSVTPRLOAEDCSACIPLRNHDKNRF 1206
DB 1618 TEVPARNLYAIOKLTQIETGENTVGMELFKLAS--SKAHTSRFISANLPCNFKFNRL 1675
QY 1207 MDMLPPDRCLPFLITIDG-ESSNYINAALMDSYRQPAFIVTOYPLPNTVKDWRVLVDY 1265
DB 1676 VNIMPEYESTRYCLQPIRGVEGSDYINASFIDGYRQKAYIATQGPLAETTFDFWRMLWEH 1735
QY 1266 GCTSIMVLEVDL--SOGCPOYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNLTRP 1323
DB 1736 NSTIVMLTKLRENGREKCHOYWAERSARYQYFVDPMA---EYNMPOYILREEKVTDA 1792
QY 1324 QEGY-LMVQOQYQLGWASHREVPGSKRSFLKLILQVEKMQBWEKEGERTIHCINGGGR 1382
DB 1793 RDGSRTRVROFQFTDW-PEQGVPKSGEGFIDFIGVHKTEQFGQ-DGPISVHCSAGVGR 1850
QY 1383 SCMECATGIVEMVKRQNVVDVFAVKTLSKNKPMWAEAPQYRCYDVALEYLELS 1438
DB 1851 TGVFITLSILVMRYEGVWDIFQTVKMLRTQRPAMVQTEQYQFSYRAALEYLG 1906

RESULT 12
A:8758
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form P1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48758
R:Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.
J. Biol. Chem. 268, 19284-19291, 1993
A:Title: Cloning and expression of two structurally distinct receptor-linked protein-ty
A:Reference number: A48758; MUID:93374907; PMID:8396131
A:Accession: A48758
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1496 <PAN>
A:Cross-references: GB:L19180
A:Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as Gl
as Phe
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
Oxy
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; transmem
F:149-209/Domain: immunoglobulin homology <IMM1>
F:246-300/Domain: immunoglobulin homology <IMM2>
F:318-405/Domain: fibronectin type III repeat homology <FN3A>
F:411-504/Domain: fibronectin type III repeat homology <FN3B>
F:509-599/Domain: fibronectin type III repeat homology <FN3C>
F:600-684/Domain: fibronectin type III repeat homology <FN3H>
F:880-1496/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1256-1477/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1146/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1146/Binding site: substrate phosphate (Arg) #status predicted
F:1429/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1435/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.3%; Score 1490.5; DB 1; Length 1496;
Best Local Similarity 29.9%; Pred. No. 1.1e-92;
Matches 414; Conservative 204; Mismatches 472; Indels 296; Gaps 46;

Db 420 SWQPPPVKQNGIITEYSLKVAADVGDYKPEHEIIGNSSDTTKYLLEQLEKWTEY--RIT 477
Qy 365 LTRPGEGETGLPGPLIIRTRTCAEPMRTPKTLKIAEIOARRIADWES-----LG 414
Db 478 VTAHTDVGPWPESLSVLRTDEDPSPGPRKVEEAVNATAVKVSWRSPVFNKQHGQIRG 537
Qy 415 YNITRCHTFNVTICVHYPRGHN--ESK-----ADCLDM----- 445
Db 538 YQV-----HYVKMENGEPKSAMLKDVMADADAQDMIIISGLQPETSYSLTAYT 585
Qy 446 -----DPAQOHVAVHLLPYTNVSLKMLITWPE-----G 474
Db 586 TKGDGARSKPLVSTGSPGKPLRVINH-----TQMTALIQMHPVDVTFGLQGVRLKFG 641
Qy 475 RK-----ESEETIIQTD-----EDVPQPV 493
Db 642 RKDMPLTLTFSEKEDHFTATDIHKGASYVPRLSARNKVGGBEMVKEISVPEEIPGF 701
Qy 494 PVKSLOGTSFENKIFLNKWEPL--DPNGIITQYEISYSIRSFDPAVPVAG---PPQTVS 548
Db 702 PQNLHSEGTSTSVQSLWSPQVPLAERNGVITKYITLLYRDINV--PLLPMEHLIIVPADTSM 759
Qy 549 NLWNSTHVFVHLLHGTYYQFIRASTVKGCPATAINVTNINISAPTLDPYEGVDASL-- 606
Db 760 TLTG-----LKSDDTTYDVKVRATSKRRG-----YSPSPQRTLP-----VDQSMFA 802
Qy 607 ----NETATTITVLIR--PAQAKAPISAVOI-----VBEELHPHRTKR---EAGAMEC 651
Db 803 KNFHVKANVKTSVLLSWEIPENYNPAILSKFPMMDGKWEVEVDGRTAQKLVNLPKPKS 862
Qy 652 YQVPVTVQNMGGGAPYFAAELPPG-----NLPE----- 681
Db 863 YSFVLTRNGNSAGGLQHRVTAKTADVLRTKPAFTGKTNLDGMTVQLPDPVANENIKGY 922
Qy 682 -----HPTDPELRLN----- 1107
Db 923 YIIIVPLKKSROKFKIPWESPDEMBELDLKEISKRKRSIRYGREVELKPYIAAHFDVLP 982
Qy 683 APFTVGDNRITYQFNPPPLAPKGYNIYVQAMSSVEKETKTQCVRIATKAATEEPEVIP- 741
Db 983 TEFTLGDDKHVGFTNKQLSQOEY-VFVLAVMDHAESK-----MYATSPYSDPVVMD 1036
Qy 742 -DPAQOTDRVVKIAGISAGIL--VFILLVVLIVKSKL-AKKRQDAMGNTRQEMTH 797
Db 1037 LDPQPTTDEEGLIIVGVVLAVVFIICIVIAILLYKKRAESRKSLSPLNSKEVPSH- 1095
Qy 798 VNAMDRSVADQSTLHAEDPLSITFMDQHNFSRYENHSATAESSRLLDVPRVLCBGTSP 857
Db 1096 -----HPTDPELRLN----- 1107
Qy 858 YQTGOL--HPAIRVADLLQHINLMKTSDSYGFKBEVSEPFQEQSASWDVAKKQDNRAKNR 915
Db 1108 FOTPGWASHPPPIELADHIELKANDNLKESQYESIDPCQQTWEHSLNVLNPKNR 1167
Qy 916 YGNIIAYDHSRVILQVEDDPSDYINANYIDGQRPSHYIATQGVNETHVYDFWRMLWQ 975
Db 1168 YANVIAYDHSRVLLSAIEGIPGSDYVYANYIDGVRKQNAVYATQGLSPETFGDFWRMIW- 1226
Qy 976 EQSACTVMVNLVEGRVKCYKXWPD-DTEVYGDFKVTCTVEMEPLAEYVVRFTLERRGY 1034
Db 1227 EQEATVMMTKLEERSRVKCDQVWPSRGTFTHGLVQVTLDDTVELT-YCVRTFALYNNGS 1285
Qy 1035 NEIREVKQFHFTGWPDPHGVPHYHATGLLSFIRVKLSNPPSAGPIVHVCSAGAGRTGCYIV 1094
Db 1286 SEKKVRQOFTANPDHGVPEHPTFLAFLRRVKTCPNPDAGPMVHVCSAGVGRGCFIV 1345
Qy 1095 IDIMLDMAEREGVDVINYCNVKAALRSRRINNVQTEBOYIFIHDAILEACLCGSTAIPVCEH 1154
Db 1346 IDAMLERIKHEKTVDIYGHVTLMAQRNVNVQTEBOYIFIHDAILEAVTCGNTEVPARNL 1405
Qy 1155 KAAVFMIDISQTNSSHLKDESFOTLNSVTPRLOAEDCSIACLPRNHDKNRPMDLPPDR 1214

Db 1406 YAYIOKLTQIETGNTVGMELFKRLAS--SKAHTSRFISANLPCNFKNRLNVIMPYES 1463
Qy 1215 CLPLITIDG-ESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVVDYDGTCTSIWML 1273
Db 1464 GRVCLQPIRGVEGSDYINASFLOGYRQOKKAYIATQGPLAETTEDFWRLMWEHNSITVWML 1523
Qy 1274 NEVDL--SQSCPQVWPEEGLRYGPIQVECMSCSDCVINRIFRICNLTRPQSGYLMVQ 1331
Db 1524 TKUREMGREKCHQWPAERSARYQYFVVDPMW---EYNMPOYILUREFKVTDARQDSRTVR 1580
Qy 1332 QFOYLGWASHREVPGSKRSFLKILQVEKWQOEKKEGERTIIHCLNGGSGRMFCFCAIGI 1391
Db 1581 QFQPTDM-PRQGVPKSGEGFIDFQGVHKTKEQFGQ-DGPISVHCSAGVGRGTGVFITLSI 1638
Qy 1392 VVEMKQNVVDVPHAVKTLRNKSPKNVPEAPQYRQPCYDVVALEYLES 1438
Db 1639 VLERNRYEGVVDIFQTVKMLRTQRPAMVQTEQYQFCVRAALEYLG 1685

RESULT 14
C54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor
N;Alternate names: MTP delta type B/C
N;Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C;Accession: C54689; B54689
R;Misuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A;Title: MTP delta, a putative murine homolog of HTP delta, is expressed in specialize
A;Reference number: A54689; MUID:93360986; PMID:8355697
A;Accession: C54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1894 <MI2>
A;Cross-references: UNIPROT:Q64487
A;Experimental source: brain; splice form B
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:137487)
A;Accession: B54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MI2>
A;Experimental source: brain; splice form C
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBI:136530)
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F;45-107/Domain: immunoglobulin homology <IMM1>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;317-399/Domain: fibronectin type III repeat homology <FN3A>
F;1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1536/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1542/Binding site: substrate phosphate (Arg) #status predicted
F;1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.2%; Score 1483; DB 2; Length 1894;
Best Local Similarity 29.3%; Pred. No. 5.2e-92;
Matches 418; Conservative 205; Mismatches 460; Indels 344; Gaps 43;

Qy 254 SFRLEQVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPFRPIAPQLLGV---GPTYLLI 310
Db 564 SYRLOGLKPNLSLYFRLSATSPQGLGAST-AEISARTWQKPSAPPQDISCTSPSSITLV 622
Qy 311 QLNANSITGDGPIILK-EVEYRMTSGSWTETHAV-----NAPTYKLWHLDPDTEYIRVL 364
Db 623 SWQPPPVKQNGIITEYSLKVAADVGDYKPEHEIIGNSSDTTKYLLEQLEKWTEY--RIT 680
Qy 365 LTRPGEGETGLPGPLIIRTRTCAEPMRTPKTLKIAEIOARRIADWES-----LG 414

Db 681 VTAHTDVGWPESLSVLRTDDEDVPSGPPRKVEVEAVNATAVKVSWSRSPVKNKHQGIQ 740
QY 415 YNTRCHTFNVTICYHYFRGHN-ESK-----ADCLDM----- 445
Db 741 YQV-----HYVKMENGEPKSAMLKDVMLADAQDMIISGLQPETSYSLTVAYT 788
QY 446 -----DPKAPQHVNVHLPPVTNVSLKMLTNPE-----G 474
Db 789 TKGDGARKPKLVSTTGSVPGKFLVNH-----TQMTALIQHPPPVDTFGLQYRLKFG 844
QY 475 RK-----ESETIIQTQD-----EDVPGPV 493
Db 845 RKQMEPLTLTLEFSEKEDHETATDIHKGASVYFRLSARNKVGFGEMVKEISVPEEIPGF 904
QY 494 PVKSQGTSTENKIFLNKLEPL--DPNGIITQVEISYSSIRSDPDPAVPVAG--PPQTVS 548
Db 905 PQNLHSEGTSTSVQLSQWPQVFLAERNGVITKTYLTYRDINV--PLLPMELHLVPADTSM 962
QY 549 NLWNSTHVPMLHLPHTTYQFFIRASTVKGFGATAINVTNISAPLDPYEGVDASL-- 606
Db 963 TLTG-----LKSDTTYDVKRAHTSKRRGP-----YSPSQOFRTP--VDQSMFA 1005
QY 607 ----NETATTITVLLR---PAQAKGAPISAYOI-----VVEELHPHRTKR---EAGAMEC 651
Db 1006 KNFHVRAVMKTSVLLSWEIENYNPALSKFFMMMDGKVEVDGRATQKLIYNLAPKES 1065
QY 652 YQVPVTVQNMAGCAPYFAELPPG-----NLPE----- 681
Db 1066 YSFVLNTRGNSAGGLQHRVTAKTAPDLVTRKPAFIGKTNLDGMITVQLPDVPANENIKGY 1125
QY 682 -----P 682
Db 1126 YIIIVPLKSRGFIKPWESPDMEDELDELKEISRKRSTRYGREVELKPYIAHFDPVLP 1185
QY 683 APFTVGDNRTYQGFWMPLAPRGYNIYFOAMSVKEKTKTQCVRATKAATREPEVIP- 741
Db 1186 TEFTLGDGRHYGFTKQLOSGQGY-VFFVLAVMDHAEK-----MYATSPYSDPVVSM 1239
QY 742 -DPAKOTDRVVKIAGISAGIL--VFILLALLVILI VKSKL-AKRKRDMAGNTRQEMTHM 797
Db 1240 LDPQPTDEEGLIWWGVLAVVFIICVIAILLKRAESESRRKSLSPNSKEVPSH- 1298
QY 798 VNAMDRSYADOSTLHAEPLSITFMDOHNSPRYENHISATAESRLLDVPRYLCEGTESP 857
Db 1299 -----HPTDPELRLN----- 1310
QY 858 YQTGQL--HPAIRVADLLQHINLMKTSDSYGKKEEYESFEGOSASNDVAKDONRAKOR 915
Db 1311 FQTPGHASHPPPILELAHIERLKANDNLKFSQYESIDPGQOFTWESHNLBNKPKNR 1370
QY 916 YGNIIAYDHSRVILQPVEDDPSSDIYNANYIDGYQRPISHYIATQGPVHETVYDFWRMIQ 975
Db 1371 YANVIAVDSHRSVLSSALEGIPGSDYNNVANYIDYRKQNAVIAATQGSIPETFGFWMIW- 1429
QY 976 EQSACIYVMNVLVEGRVKCYKWPD-DTEYVGDVKVTCVMEPLABYVVRFTFLBERRY 1034
Db 1430 EQEATVVMTKLEERSRVKCDQWPSRGTEHGLVQVTLDTVELT-YCVRTFALYNGS 1488
QY 1035 NEIREVKQHEFTGCPDHPGYHATGLLSFTRRVKLSNPPSAGPIVHCSAGARTCCYIV 1094
Db 1489 SEKKVRQOFTAMPDHPGHEHTPTFLAFLRRVKT CNPPDAGPMVHCSAGVGTCCFIV 1548
QY 1095 IDIMLMAEREGVVDIYNCKALRSRINNVOEEQVIFTHDAILEACLCGETAIPVCEF 1154
Db 1549 IDAMLERIKHEKTVDIYGHVTLNRAQRYNVQTEDQYIFHIDALLAEVATCGNTEVPARNL 1608
QY 1155 KAAFYDMIRIDSGTNSHLKDEFTQLNSVTPRLQAECDSCIALPRNHDKNRMFMDLPDR 1214
Db 1609 YAYIQKLTQIETGENTVGMELFEPKRLAS--SKAHTSRFISANLPCNFKNRLNINPYES 1666
QY 1215 CUPFLITIDG-ESSNVIINALMDSYQPAAFIVQYPLNVTXKDFWRLVYDYCTSIYML 1273
Db 1667 GRVCLQPIRGVEGSDYINASFLDGYQKAYIATQGLAETTEDFWRLMWEHNSSTIVVML 1726

QY 1274 NEVDL--SQCCPOYWPBEGMLRYGPIQVECMSCMDCDVINRIFRINLNRPOBGLMWQ 1331
Db 1727 TKLREMGREKCHQYWPASRARYQYFVVDPM---EYNMPOYLILREFKVTDAQDSRTVR 1783
QY 1332 QFOYLGWASHREVPKSRKSLKILLOVEKQWKEGEGRTIILCLNGGSGSNFCAIGI 1391
Db 1784 QFOFTDW-PEQGVKSGEGFIDFIGQVHKTKQFGQ-DGPISVHCSAGVGTGVTITLSI 1841
QY 1392 VVMVXRQNVVDVYFHAVKTLRLSKPNVVEAPEQVRCFYCDVALEYLES 1438
Db 1842 VLERMRYGVVDIFQIVTKMLRTQRPAMVQTEDQYQFCYRAALEYLG 1888

RESULT 15

A56493

leucocyte common antigen-related protein (LAR) - rat (fragment)

N;Alternate names: LAR receptor-linked tyrosine phosphatase

N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: A56493; I55393

R;Zhang, J.S.; Longo, P.M.

J. Cell Biol. 128, 415-431, 1995

A;Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the

A;Reference number: A56493; MUID:95146548; PMID:7844155

A;Accession: A56493

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1290 <RES>

A;Cross-references: UNIPROT:Q62917; EMBL:X83505; NID:g732918; PIDN:CAAS8495.1; PID:g7329

J. Longo, P.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.

J. Biol. Chem. 268, 26503-26511, 1993

A;Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulati

A;Reference number: I55393; MUID:94075340; PMID:8253779

A;Accession: I55393

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 831-1290 <RE2>

A;Cross-references: EMBL:U00477; NID:g392565; PIDN:AAC04306.1; PID:g392566

C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F;80-166/Domain: fibronectin type III repeat homology <3PR>

F;667-1290/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F;1047-1270/Domain: protein-tyrosine-phosphatase homology <PTP2>

F;931/Active site: Cys (phosphocysteine intermediate) #status predicted

F;937/Binding site: substrate phosphate (Arg) #status predicted

F;1222/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1228/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 19.1%; Score 1470.5; DB 2; Length 1290;

Matches 402; Conservative 221; Mismatches 465; Indels 247; Gaps 42;

QY 230 LQRRNGEDIPVATKININRRFAASFRLOEVTRTDQDLYRCVTSQSRGSGVSNFAQLIVR 289

Db 71 VRATGEQAPSSPPRRVQARMLSASTLVQWEPPE-----EPNGLVRGVRYVYP 120

QY 290 EPPRIAP-----PQLLGVTPTYLIIOLNANSIIGDGP----- 322

Db 121 DSRRLPSAHKHTDAGLLTTLVGSLL-PGITYSL-RVLAFTAVGDGPPSPTIQVKTQGV 178

QY 323 -----IILKEVERMTSGSWTETHAVNAPT--YKLWH 352

Db 179 PAQAPDFQAKASDTRIQLSWLLPPQERIIVKELVYVAAADEGQGHKVTDFPTSSYTL 238

QY 353 LQPDTEYERVLLTRPGEQGLPGPPLITRTKCAEPMRTPKTKIAEQARRIADVW-- 410

Db 239 LKPDITLHFQ--LAASDLGVGVFTTVEARTAAQSNPSGPPRKVEPLNSTAVHWSKL 296

QY 411 -----BSLGVNITRCHTFNVTICYHYFRGHN-ESKADCLDM-----PKAPQH 452

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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:32:43 ; Search time 166.956 Seconds
(without alignments)
4413.635 Million cell updates/sec

Title: US-09-887-669-2
Perfect score: 7709
Sequence: 1 MDTTAAALPAFVALLLLSP.....EAPQYRFCDVALEYLESS 1439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	7688	99.7	1439	1	PTPK_HUMAN	Q15262 homo sapien
2	7673.5	99.5	1440	2	Q86WJ2	Q86WJ2 homo sapien
3	7670.5	99.5	1440	2	Q68DT8	Q68dt8 homo sapien
4	7571	98.2	1457	1	PTPK_MOUSE	P35822 mus musculu
5	4807	62.4	1452	1	PTPW_HUMAN	P28827 homo sapien
6	4791	62.1	1452	1	PTPW_MOUSE	P28828 mus musculu
7	4784	62.1	1486	2	Q68FM4	Q68fm4 mus musculu
8	4726	61.3	1390	2	Q86V60	Q86v60 homo sapien
9	4697.5	60.9	1434	2	Q6YI48	Q6yi48 gallus gall
10	4632	60.1	1436	2	Q00197	Q00197 homo sapien
11	4623	60.0	1436	2	Q92850	Q92850 homo sapien
12	4608.5	59.8	1436	2	Q35564	Q35564 mus musculu
13	4602.5	59.7	1436	2	P70125	P70125 mus musculu
14	4588.5	59.5	1454	1	PTPT_MOUSE	Q99m80 mus musculu
15	4581.5	59.4	1439	2	P78399	P78399 homo sapien
16	4564	59.2	1463	1	PTPT_HUMAN	O14522 homo sapien
17	4520	58.6	1434	2	Q6E5N7	Q6e5n7 brachydanio
18	4374.5	56.7	1442	2	Q92735	Q92735 homo sapien
19	4352	56.5	1430	1	PTPU_HUMAN	Q92729 homo sapien
20	4343	56.3	844	2	Q8C462	Q8c462 mus musculu
21	3481	45.2	1195	2	Q9PUM2	Q9pum2 xenopus lae
22	2651	34.4	492	2	Q8IV94	Q8iv94 homo sapien
23	2615	33.9	990	2	Q6PDN0	Q6pdn0 mus musculu
24	2518.5	32.7	502	2	Q9WUL3	Q9wul3 rattus norv
25	2255	29.3	465	2	Q9IB99	Q9ib99 potamotrygo
26	1913	24.8	617	2	Q66JV9	Q66jv9 mus musculu
27	1706	22.1	542	2	P70643	P70643 rattus norv
28	1539	20.0	1788	2	Q9IAJ0	Q9iaj0 xenopus lae
29	1534.5	19.9	1502	2	Q9UM81	Q9um81 homo sapien
30	1533.5	19.9	1529	2	Q6PG86	Q6pg86 mus musculu
31	1529.5	19.8	1501	2	Q9QW00	Q9qw00 rattus sp.

32	1527.5	19.8	1501	2	Q7TTI7	Q7tti7 mus musculu
33	1526.5	19.8	1887	2	Q9QW67	Q9qw67 rattus sp.
34	1519.5	19.7	1898	2	Q9EQ17	Q9eq17 mus musculu
35	1517.5	19.7	1898	2	Q64604	Q64604 x protein-t
36	1513	19.6	1254	2	Q8VBV0	Q8vbv0 mus musculu
37	1509	19.6	1897	1	PTPF_HUMAN	P10586 homo sapien
38	1508.5	19.6	1499	2	Q908I5	Q908i5 gallus gall
39	1505.5	19.5	1912	1	PTPD_HUMAN	P23468 homo sapien
40	1498	19.4	1948	1	PTNS_HUMAN	Q13332 homo sapien
41	1497	19.4	1898	2	Q86W50	Q86w50 homo sapien
42	1494.5	19.4	1191	2	Q723X4	Q723x4 homo sapien
43	1485	19.3	278	2	Q8C819	Q8c819 mus musculu
44	1476.5	19.2	1889	2	Q7QXK2	Q7qxk2 anopheles g
45	1476	19.1	1896	2	Q9IAJ1	Q9iaj1 xenopus lae

ALIGNMENTS

RESULT 1
ID PTPK_HUMAN STANDARD; PRT; 1439 AA.
AC Q15262; Q14763;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase kappa precursor
DE (EC 3.1.3.48) (R-PTP-kappa).
GN Name=PTPRK; Synonyms=PTPK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96279245; PubMed=8663237; DOI=10.1074/jbc.271.28.16712;
RA Fuchs M., Mueller T., Lerch M., Ullrich A.;
RT "Association of human protein-tyrosine phosphatase kappa with members
of the armadillo family.";
RL J. Biol. Chem. 271:16712-16719(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ForeSkin;
RX MEDLINE=97199372; PubMed=9047348; DOI=10.1016/S0378-1119(96)00684-1;
RA Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.;
RT "Molecular cloning and chromosomal localization of a human gene
homologous to the murine R-PTP-kappa, a receptor-type protein tyrosine
phosphatase.";
RL Gene 186:77-82(1997).
CC -I- FUNCTION: Regulation of processes involving cell contact and
adhesion such as growth control, tumor invasion, and metastasis.
CC Forms complexes with beta-catenin and gamma-catenin/plakoglobin.
CC Beta-catenin may be a substrate for the catalytic activity of PTP-
kappa.
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
tyrosine + phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein; at adherens
junctions.
CC -I- TISSUE SPECIFICITY: High levels in lung, brain and colon; less in
liver, pancreas, stomach, kidney, placenta and mammary carcinoma.
CC -I- PTM: This protein undergoes proteolytic processing.
CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 2B subfamily.
CC -I- SIMILARITY: Contains 4 fibronectin type III domains.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -I- SIMILARITY: Contains 1 MAM domain.
CC -I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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CC		
DR	EMBL; Z70660; CAA94519.1; --.	
DR	EMBL; L77886; AAC37599.1; --.	
DR	HSSP; P28827; IRPM.	
DR	Genew; HGNC:9674; FTPRK.	
DR	MIM; 602545; --.	
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	
DR	GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . . ; TAS.	
DR	InterPro; IPK003961; FN III.	
DR	InterPro; IPR008957; FN III-like.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR000998; MAM.	
DR	InterPro; IPR000387; TYR phosphatase.	
DR	InterPro; IPR000242; Tyr_PP.	
DR	Pfam; PF00041; fn3; 2.	
DR	Pfam; PF00047; ig; 1.	
DR	Pfam; PF00629; MAM; 1.	
DR	Pfam; PF00102; Y_phosphatase; 2.	
DR	PRINTS; PR00020; MAMDOWAIN	
DR	PRINTS; PR00700; PTYPHPHTASE.	
DR	PROSITE; PS50853; FN3; 3.	
DR	PROSITE; PS50835; IG LIKE; 1.	
DR	PROSITE; PS00740; MAM_1; 1.	
DR	PROSITE; PS50060; MAM_2; 1.	
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.	
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.	
DR	PROSITE; PS50055; TYR_PHOSPHTASE_Pfp; 2.	
KW	Glycoprotein; Hydroxylase; Immunoglobulin domain; Protein phosphatase;	
KW	Receptor; Repeat; Signal; Transmembrane.	
FT	SIGNAL	1 26 Potential.
FT	CHAIN	27 1439 Receptor-type protein-tyrosine phosphatase kappa.
FT	DNAIN	27 752 Extracellular (Potential).
FT	TRANSMEM	753 774 Potential.
FT	DNAIN	775 1439 Cytoplasmic (Potential).
FT	DMAIN	31 194 MAM.
FT	DMAIN	196 281 Ig-like C2-type.
FT	DMAIN	291 383 Fibronectin type-III 1.
FT	DMAIN	389 485 Fibronectin type-III 2.
FT	DMAIN	490 589 Fibronectin type-III 3.
FT	DMAIN	597 680 Fibronectin type-III 4.
FT	DMAIN	910 1141 Protein-tyrosine phosphatase 1.
FT	DMAIN	1200 1433 Protein-tyrosine phosphatase 2.
FT	ACT_SITE	1082 1082 Phosphocysteine intermediate (By similarity).
FT		
FT	ACT_SITE	1376 1376 Phosphocysteine intermediate (By similarity).
FT		
FT	DISULFID	216 270 Cleavage site (Probable).
FT	SITE	641 644 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	101 101 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	140 140 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	211 211 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	416 416 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	424 424 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	436 436 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	462 462 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	552 552 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	586 586 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	590 590 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	607 607 N-linked (GlcNAC. .) (Potential).
FT	CARBOHYD	690 690 N-linked (GlcNAC. .) (Potential).
FT	CONFLICT	9 L -> V (in Ref. 2).
FT	CONFLICT	158 S -> T (in Ref. 2).
FT	CONFLICT	284 A -> P (in Ref. 2).
FT	CONFLICT	422 T -> S (in Ref. 2).
FT	CONFLICT	572 AEL -> CRT (in Ref. 2).
FT	CONFLICT	715 S -> T (in Ref. 2).
FT	CONFLICT	732 A -> AA (in Ref. 2).
FT	CONFLICT	1366 E -> K (in Ref. 2).
FT	SEQUENCE	1439 AA; 162087 MW; EED529AF7C9FA4451 CRC64;
SQ		

Query Match	99.7%	Score 7688	DB 1	Length 1439				
Best Local Similarity	99.8%	Pred. No. 0						
Matches 1436	Conservative	2	Mismatches	1	Indels	0	Gaps	0

Qy	1	MDTAAALPAFVALLLLSPWPLLSAQOGFSAGGCTFDDPGACDVHDLVDDFEWHV	60
Db	1	MDTAAALPAFVALLLLSPWPLLSAQOGFSAGGCTFDDPGACDVHDLVDDFEWHV	60
Qy	61	SAQPHYLPPEMFGSGYMI VDSDDHPDGEKARLQLPMTKENDTHCIDFSYLLYSQKGLN	120
Db	61	SAQPHYLPPEMFGSGYMI VDSDDHPDGEKARLQLPMTKENDTHCIDFSYLLYSQKGLN	120
Qy	121	GTNLILVRNVKGPLANPIMNVGTGTRDMLRABELAVSTFWPNEYQVITFEAEVSGRSGYI	180
Db	121	GTNLILVRNVKGPLANPIMNVGTGTRDMLRABELAVSSFPWNEYQVITFEAEVSGRSGYI	180
Qy	181	AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNAFTQCIATORDAVHNKLMIORRNGEDIPV	240
Db	181	AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNAFTQCIATORDAVHNKLMIORRNGEDIPV	240
Qy	241	AQTKNINHRRFAASFRLOEVTKTQDLYRCVCTQSERGSGVSNFAQLIVRPPPIAPQOL	300
Db	241	AQTKNINHRRFAASFRLOEVTKTQDLYRCVCTQSERGSGVSNFAQLIVRPPPIAPQOL	300
Qy	301	LGVGPTYLLIQLNANSIIGDGPPIILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYE	360
Db	301	LGVGPTYLLIQLNANSIIGDGPPIILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYE	360
Qy	361	IRVLLTRPBGEGTGLPGPPLITRTKCAEPMRTPTKLKIAIOARRIADVDESIGYNTTRC	420
Db	361	IRVLLTRPBGEGTGLPGPPLITRTKCAEPMRTPTKLKIAIOARRIADVDESIGYNTTRC	420
Qy	421	HTFNVTICVHYFRGHNESKADCLMDPKAQHVNVNHLPPYTNVSLKMLTNPEGRKESEE	480
Db	421	HTFNVTICVHYFRGHNESKADCLMDPKAQHVNVNHLPPYTNVSLKMLTNPEGRKESEE	480
Qy	481	TTIQTDEDVPGVPVKSLQGTSEFNKIFLNKKEPLDPNGIITQYEISYSSIRSPDPAVPV	540
Db	481	TTIQTDEDVPGVPVKSLQGTSEFNKIFLNKKEPLDPNGIITQYEISYSSIRSPDPAVPV	540
Qy	541	AGBPQTVSNLWNSTHVFVMLHPGTTVQPIRASTVKFGFGPATAINTVTTNISAPTLDDYE	600
Db	541	AGBPQTVSNLWNSTHVFVMLHPGTTVQPIRASTVKFGFGPATAINTVTTNISAPTLDDYE	600
Qy	601	GVDAASLNETAATTITVLLRPAQAGAPISAQIVVEELHPHRTKKEAGAMECYQVPVTYQN	660
Db	601	GVDAASLNETAATTITVLLRPAQAGAPISAQIVVEELHPHRTKKEAGAMECYQVPVTYQN	660
Qy	661	AMSGGAPYFAAEPLPGNLPEPAFTVGDNRITQGFWNPPPLAPRKGYNIYFQAMSSVEKE	720
Db	661	AMSGGAPYFAAEPLPGNLPEPAFTVGDNRITQGFWNPPPLAPRKGYNIYFQAMSSVEKE	720
Qy	721	TKTQCVRIATKAATEEPEVITPDAKQTRDVVKIAGISAGILVFTILLVILVILVKKSKLA	780
Db	721	TKTQCVRIATKAATEEPEVITPDAKQTRDVVKIAGISAGILVFTILLVILVILVKKSKLA	780
Qy	781	KKRDAMGNTRQETHMVMNADRSYADOSTLHAEDPLSIITFMDQHNFSPRYENHSATAES	840
Db	781	KKRDAMGNTRQETHMVMNADRSYADOSTLHAEDPLSIITFMDQHNFSPRYENHSATAES	840
Qy	841	SRLLDVPYRLCEGTSPYQTQLHPAIRVADLLQHLINLMKTSDSYGKKEEVSFEGQSA	900
Db	841	SRLLDVPYRLCEGTSPYQTQLHPAIRVADLLQHLINLMKTSDSYGKKEEVSFEGQSA	900
Qy	901	SWDVAKKQDNRAKNRYGNIITAYDHSRVLQPVEDDPSSDYINAWYIDGQRPSHYIATQG	960
Db	901	SWDVAKKQDNRAKNRYGNIITAYDHSRVLQPVEDDPSSDYINAWYIDGQRPSHYIATQG	960
Qy	961	PVHTETVDFWRMTWQEOSACIVMVTNLVVEGRVKCYKWPDDTTEYGDGFKVTCVEMEPLA	1020
Db	961	PVHTETVDFWRMTWQEOSACIVMVTNLVVEGRVKCYKWPDDTTEYGDGFKVTCVEMEPLA	1020
Qy	1021	EYVVRTFTLERRGYNIREVKQHFHTGWPDHGVPYHATGLLSFIRRVKLSNPPSAGPITV	1080

Db 1021 EYVVRTTLERRGYNEIREVKQHFHTGWPDPHGVPYHATGLLSFTRRVKLSNPPSAGSIVV 1080
Qy 1081 HCSAGAGRTGCIYIDIMLMDAEREGVVDIYNCVKALRSRRINNVOPEEQYIFTHDAILE 1140
Db 1081 HCSAGAGRTGCIYIDIMLMDAEREGVVDIYNCVKALRSRRINNVOPEEQYIFTHDAILE 1140
Qy 1141 ACLGGETAIPVCBFAAAYFMIRIDSTQNSHLLKDEFTQTLNSVTPRLQADDCSIACLPN 1200
Db 1141 ACLGGETAIPVCBFAAAYFMIRIDSTQNSHLLKDEFTQTLNSVTPRLQADDCSIACLPN 1200
Qy 1201 HDKNRMDLPPDRCLPFLITIDGESSNYINAAIMDSYROPAAFIYTOYPLNVTXDFWR 1260
Db 1201 HDKNRMDLPPDRCLPFLITIDGESSNYINAAIMDSYROPAAFIYTOYPLNVTXDFWR 1260
Qy 1261 LVYDYGCTSVMLNEVDLSGCGQYWPPEEGMLRYGPIQVECMSCMDCCVINIFRICNL 1320
Db 1261 LVYDYGCTSVMLNEVDLSGCGQYWPPEEGMLRYGPIQVECMSCMDCCVINIFRICNL 1320
Qy 1321 TRPOEGLVMYQQFYQLGWASHREVPVGSKRSLKLLIQVEKWQBEWKEGEGRTIHCINGG 1380
Db 1321 TRPOEGLVMYQQFYQLGWASHREVPVGSKRSLKLLIQVEKWQBEWKEGEGRTIHCINGG 1380
Qy 1381 GRSGMFCAGIVVEMVKRONVDFHVAVKTLRNSKPNMVAPQYRFCYDVALEYLESS 1439
Db 1381 GRSGMFCAGIVVEMVKRONVDFHVAVKTLRNSKPNMVAPQYRFCYDVALEYLESS 1439

RESULT 2

Q86WJ2 PRELIMINARY; PRT; 1440 AA.
ID Q86WJ2
AC Q86WJ2;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mutant receptor type protein tyrosine phosphatase K (EC 3.1.3.48).
GN Name=PTRK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=22679345; PubMed=12794170;
RA Novellino L., Renkvist N., Rini F., Mazzocchi A., Rivoltini L.,
RA Greco A., Deho P., Squarcina P., Robbins P.F., Parmiani G.,
RA Castelli C.;
RT "Identification of a mutated receptor-like protein tyrosine
RT phosphatase 'kappa as a novel, class II HLA-restricted melanoma
RT antigen.";
RL J.Immunol. 170:6363-6370(2003).
DR EMBL; AF533875; AA049502.1; -;
DR HSSP; P28827; IRPM.
DR CG; GO:0016020; C:membrane; IEA.
DR CG; GO:0016787; F:hydrolase activity; IEA.
DR CG; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR CG; GO:0004872; F:receptor activity; IEA.
DR CG; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; Tyr_phosphatase.
DR Pfam; PF00041; fn3.2.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; NAMDOMAIN.
PRINTS; PR00020; NAMDOMAIN.

DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolase; Receptor.
SQ SSQUENCE 1440 AA; 162271 MW; B140BC621878586A CRC64;
Query Match 99.5%; Score 7673.5; DB 2; Length 1440;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1436; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MDTTAAALPAFVALLLLSPWLLGSAQGFSAAGCTFDDGPGACDYHQDLYDDFEVHV 60
Db 1 MDTTAAALPAFVALLLLSPWLLGSAQGFSAAGCTFDDGPGACDYHQDLYDDFEVHV 60
Qy 61 SAQEPHYLPPEMPQGSYMIYDSSDHPDGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120
Db 61 SAQEPHYLPPEMPQGSYMIYDSSDHPDGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120
Qy 121 GTLNILVRNKGPLANPINVTGTRDMLRAELAVSTFWPNEVQVTFEAEVSGRSGYI 180
Db 121 GTLNILVRNKGPLANPINVTGTRDMLRAELAVSTFWPNEVQVTFEAEVSGRSGYI 180
Qy 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAGONATFQCIATGRDAVHNKLMQORNGEDIPV 240
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAGONATFQCIATGRDAVHNKLMQORNGEDIPV 240
Qy 241 AQTKNINHRRAAASFLQEVTKTDQDLYRCVTOSERGSGVSNFAQLIVRPPRIAPQOL 300
Db 241 AQTKNINHRRAAASFLQEVTKTDQDLYRCVTOSERGSGVSNFAQLIVRPPRIAPQOL 300
Qy 301 LGVGPVYLLIQNLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
Db 301 LGVGPVYLLIQNLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
Qy 361 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPTKTLKIAEIQARRIADVWESLGYNITRC 420
Db 361 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPTKTLKIAEIQARRIADVWESLGYNITRC 420
Qy 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPGRKESEE 480
Db 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPGRKESEE 480
Qy 481 TIIQTDDEDVPGVPVKSLQGSTFENKIFLNWKEPLDPNGIITQYEISYSSIRSFDPAPV 540
Db 481 TIIQTDDEDVPGVPVKSLQGSTFENKIFLNWKEPLDPNGIITQYEISYSSIRSFDPAPV 540
Qy 541 AGPPQTVSNLWNSTHVFMHLHGTTVQFFIRASTVKFGFPATAINVTNISAPTLPDYE 600
Db 541 AGPPQTVSNLWNSTHVFMHLHGTTVQFFIRASTVKFGFPATAINVTNISAPTLPDYE 600
Qy 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTVQN 660
Db 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTVQN 660
Qy 661 AMSGGAPYFAAELPPGNLPEPAPFTVGDNRVTQGFNPPPLAPRKGNYIFQAMSSVEKE 720
Db 661 AMSGGAPYFAAELPPGNLPEPAPFTVGDNRVTQGFNPPPLAPRKGNYIFQAMSSVEKE 720
Qy 721 TKTQCVRATK-AATREEPEVIDPAKOTDRVVKIAGISAGILVFILLVILLVKKSL 779
Db 721 TKTQCVRATK-AATREEPEVIDPAKOTDRVVKIAGISAGILVFILLVILLVKKSL 780
Qy 780 AKRKDAMGNTRQEMTHVMVNMADRSYADOSTLHAEDPLSITTFMDQHNFSRYENHSATAE 839
Db 780 AKRKDAMGNTRQEMTHVMVNMADRSYADOSTLHAEDPLSITTFMDQHNFSRYENHSATAE 839

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Db 781 AKRKGAMGNTQSBWTHVMAMDRSYADQSTLHAEDPLSITFMDQHNFSRYENHSATAE 840
Qy 840 SSRLLDVPRLCEGTESPYQGLHPAIRVADILLOHINLMKTSYGFKEEYESFFPGQS 899
Db 841 SSRLLDVPRLCEGTESPYQGLHPAIRVADILLOHINLMKTSYGFKEEYESFFPGQS 900
Qy 900 ASWDVAKKQNRKRNRYNIAYDHSRVLQPVDEDDPSDDYINANYIDGVQRPESHYIATQ 959
Db 901 ASWDVAKKQNRKRNRYNIAYDHSRVLQPVDEDDPSDDYINANYIDGVQRPESHYIATQ 960
Qy 960 GPVHETVDFWRMIWQBSACIVMTNLVLEGRVKCYKWPDDTEVYGDPKVTCVMEPL 1019
Db 961 GPVHETVDFWRMIWQBSACIVMTNLVLEGRVKCYKWPDDTEVYGDPKVTCVMEPL 1020
Qy 1020 AEYVVRFTLRRGYNIREVKQHFHFGWPDHGVPHYATGLLSFIRRVKLSNPPSAGPIV 1079
Db 1021 AEYVVRFTLRRGYNIREVKQHFHFGWPDHGVPHYATGLLSFIRRVKLSNPPSAGPIV 1080
Qy 1080 VHCsAGARTGCIYVIDIMLDMAREGVVDIYNCVKALRSRRINNVOTEEQYIFIHDAI 1139
Db 1081 VHCsAGARTGCIYVIDIMLDMAREGVVDIYNCVKALRSRRINNVOTEEQYIFIHDAI 1140
Qy 1140 EACLGETAIPVCEFKAAFYDMIRIDSTQNSSHLKDEFQTLSVTPRLQAEDCSIACLPR 1199
Db 1141 EACLGETAIPVCEFKAAFYDMIRIDSTQNSSHLKDEFQTLSVTPRLQAEDCSIACLPR 1200
Qy 1200 NHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAFIVTQPLPNTVKDFW 1259
Db 1201 NHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAFIVTQPLPNTVKDFW 1260
Qy 1260 RLVDYDGTCTSVMLNEVDLSQCPQYPEEGMLRVPQIQCSCMSMDCDVINRIFRIN 1319
Db 1261 RLVDYDGTCTSVMLNEVDLSQCPQYPEEGMLRVPQIQCSCMSMDCDVINRIFRIN 1320
Qy 1320 LTRPQEGYLMVQQQYGLGWASHREVPVGSKRFLKLILQVEKQBEWKEGERTIIHCLNG 1379
Db 1321 LTRPQEGYLMVQQQYGLGWASHREVPVGSKRFLKLILQVEKQBEWKEGERTIIHCLNG 1380
Qy 1380 GGRGMFCAIGIVEMVKRQNVVDVFAVKTLRNSKNVWAPRQYRCFYDVALEYLESS 1439
Db 1381 GGRGMFCAIGIVEMVKRQNVVDVFAVKTLRNSKNVWAPRQYRCFYDVALEYLESS 1440

RESULT 3
Q68DT8
AC Q68DT8 PRELIMINARY; PRT; 1440 AA.
ID
AD Q68DT8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686C2268.
GN Name=DKFZp686C2268;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium carcinoma cell line;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaiipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749277; CAH18132.1;
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR00387; TYR phosphatase.
DR InterPro; IPR00242; TYR_PP.
DR Pfam; PF00041; fn3; 2.
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DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPc; 2.
DR SMART; SM00404; PTPc motif; 2.
DR PROSITE; PS00835; IG_Like; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hypothetical protein.
SQ SEQUENCE 1440 AA; 162129 MW; 41BA5B4D6E0C0359 CRC64;

Query Match 99.5%; Score 7670.5; DB 2; Length 1440;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1435; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MDTAAALPAFVALLLSWPILLGSAQGSAGGCTFDDPGACDYHQDLYDDFVWHV 60
Db 1 MDTAAALPAFVALLLSWPILLGSAQGSAGGCTFDDPGACDYHQDLYDDFVWHV 60

Qy 61 SAQEPHYLPPEMPPQGSYMIQDSSDHDPEGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120
Db 61 SAQEPHYLPPEMPPQGSYMIQDSSDHDPEGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120

Qy 121 GTNLILVRVKNKGPLANPIWVTGTGRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180
Db 121 GTNLILVRVKNKGPLANPIWVTGTGRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180

Qy 181 AIDDIQVLSYPCDKSPHFLRGDLGVENVAGQATFQCIATGRDAVHNKLWLQRRNGEDIPV 240
Db 181 AIDDIQVLSYPCDKSPHFLRGDLGVENVAGQATFQCIATGRDAVHNKLWLQRRNGEDIPV 240

Qy 241 AQTKNINHRPFAASFRLOEVTKTDDLYRCVTQSGRSGVSNFAQLIVRPPRIAPOL 300
Db 241 AQTKNINHRPFAASFRLOEVTKTDDLYRCVTQSGRSGVSNFAQLIVRPPRIAPOL 300

Qy 301 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYTKLWHLDPDTEYE 360
Db 301 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYTKLWHLDPDTEYE 360

Qy 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPKTLKIAEIQAARRIAVDWESLGYNITRC 420
Db 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPKTLKIAEIQAARRIAVDWESLGYNITRC 420

Qy 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPGEKSEEE 480
Db 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPGEKSEEE 480

Qy 481 TIQTDEDVPGVPVKSLQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRSDPAVPV 540
Db 481 TIQTDEDVPGVPVKSLQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRSDPAVPV 540

Qy 541 AGPQTYSNLWNSTHVFHMLHPCGTYTQFFIRASTVKGFGPATAINVTNISAFTLPDYE 600
Db 541 AGPQTYSNLWNSTHVFHMLHPCGTYTQFFIRASTVKGFGPATAINVTNISAFTLPDYE 600

Qy 601 GVDASLNETATTTVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTQN 660
Db 601 GVDASLNETATTTVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTQN 660

Qy 661 AMSGGAPYFAAELPPGNLPEPAPFTVDNRTYOGFWNPPLAPRKGYNIYFQAMSSVEKE 720
Db 661 AMSGGAPYFAAELPPGNLPEPAPFTVDNRTYOGFWNPPLAPRKGYNIYFQAMSSVEKE 720

Qy 721 TKTCQVRIATK-AATEPEVIPPAPKQTDRTVVKIAGISAGILVFILLVILLVIVKSKL 779
Db 721 TKTCQVRIATKAAATEPEVIPPAPKQTDRTVVKIAGISAGILVFILLVILLVIVKSKL 780
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QY 780 AKGKQDANGNTRQWTHMNMDSYADQSTLHAEDPLSITFMQHNFSRYENHSATAE 839
 DB 781 AKGKQDANGNTRQWTHMNMDSYADQSTLHAEDPLSITFMQHNFSRYENHSATAE 840
 QY 840 SSRLLDVPRLYCEGTESPYOTGQLHPAIRVADLLQHLNLMKTSYSGFKEYESFFEGQS 899
 DB 841 SSRLLDVPRLYCEGTESPYOTGQLHPAIRVADLLQHLNLMKTSYSGFKEYESFFEGQS 900
 QY 900 ASMDVAKKQONRAKRNIGYIIAYDHSRVILQPVEDDPSSDYINANYIDGQRPISHYIATQ 959
 DB 901 ASMDVAKKQONRAKRNIGYIIAYDHSRVILQPVEDDPSSDYINANYIDGQRPISHYIATQ 960
 QY 960 GPVHETVYDFRMIWQOSACIVMVTNLVEGRVKCYKYPDPDTEVYDGFKVTGVMEPL 1019
 DB 961 GPVHETVYDFRMIWQOSACIVMVTNLVEGRVKCYKYPDPDTEVYDGFKVTGVMEPL 1020
 QY 1020 AEYVVRFTLLRRGYNEIREVKQPHFTGWPDPHGVPHYATGLLSPIRVKLSNPPSAGPIV 1079
 DB 1021 AEYVVRFTLLRRGYNEIREVKQPHFTGWPDPHGVPHYATGLLSPIRVKLSNPPSAGPIV 1080
 QY 1080 VHSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVQTEQYIFIHDAIL 1139
 DB 1081 VHSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVQTEQYIFIHDAIL 1140
 QY 1140 EACLGBETAIPVCEFAKAAFDIMIRIDSQTNSSHLKDEFTLNSVTPRLQAECDSCIAPR 1199
 DB 1141 EACLGBETAIPVCEFAKAAFDIMIRIDSQTNSSHLKDEFTLNSVTPRLQAECDSCIAPR 1200
 QY 1200 NHDKNRMDMLPPDRCLPFLITIDGESSNYINAAALMDSYQPAFIVTQYPLNTVKDFW 1259
 DB 1201 NHDKNRMDMLPPDRCLPFLITIDGESSNYINAAALMDSYQPAFIVTQYPLNTVKDFW 1260
 QY 1260 RLVDYDGTCTSVMLNEVDLSQGCQPYWPEEGMLRYGPIQVECMSCMDCDVINRIFRICH 1319
 DB 1261 RLVDYDGTCTSVMLNEVDLSQGCQPYWPEEGMLRYGPIQVECMSCMDCDVINRIFRICH 1320
 QY 1320 LTRPQGYLWVQFQYLGWASHREVPKGSFKLILQVEKQWBEWKGEGRTIHCING 1379
 DB 1321 LTRPQGYLWVQFQYLGWASHREVPKGSFKLILQVEKQWBEWKGEGRTIHCING 1380
 QY 1380 GGRSGMFCATGIVVEMKRONVVDVHAVKTLRNSKPNVYEAQRFCDVDALEYLESS 1439
 DB 1381 GGRSGMFCATGIVVEMKRONVVDVHAVKTLRNSKPNVYEAQRFCDVDALEYLESS 1440

RESULT 4

PTPK_MOUSE
 ID PTPK_MOUSE STANDARD; PRT; 1457 AA.
 AC P35822;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Receptor-type protein-tyrosine phosphatase kappa precursor
 DE (EC 3.1.3.48) (R-PTP-kappa).
 GN Name=Ptpk; Synonyms=Ptpk;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=RI; TISSUE=Brain;
 RX MEDLINE=93233655; PubMed=8474452;
 RA Jiang Y.P., Wang H., D'Eustachio P., Musacchio J.M., Schlessinger J.,
 RA Sep J.;
 RT "Cloning and characterization of R-PTP-kappa, a new member of the
 RT receptor protein tyrosine phosphatase family with a proteolytically
 RT cleaved cellular adhesion molecule-like extracellular region.";
 RL Mol. Cell. Biol. 13:2942-2951(1993).
 CC -1- FUNCTION: Regulation of processes involving cell contact and
 CC adhesion such as growth control, tumor invasion, and metastasis.
 CC Forms complexes with beta-catenin and gamma-catenin/plakoglobin.

Beta-catenin may be a substrate for the catalytic activity of PTP-kappa.
 -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 -1- SUBCELLULAR LOCATION: Type I membrane protein.
 -1- TISSUE SPECIFICITY: High levels in liver and kidney. Lower levels in lung, brain and heart. Not seen in spleen and testis.
 -1- DEVELOPMENTAL STAGE: Developmentally regulated with highest expression found in developing areas or in areas capable of developmental plasticity.
 -1- PTM: This protein undergoes proteolytic processing.
 -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 2B subfamily.
 -1- SIMILARITY: Contains 4 fibronectin type III domains.
 -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 -1- SIMILARITY: Contains 1 MAM domain.
 -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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 CC EMBL: L10106; AAA40021.1; -.
 DR PIR: A48066; A48066.
 DR HSP: P28827; IRPM.
 DR MGD: MGI:103310; Ptpk.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR000998; MAM.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00629; MAM; 1.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00020; MAMDOMAIN.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00060; FN3; 3.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00137; MAM; 1.
 DR SMART: SM00194; PTPC; 2.
 DR PROSITE: PS00853; FN3; 4.
 DR PROSITE: PS00835; IG LIKE; 1.
 DR PROSITE: PS00740; MAM 1; 1.
 DR PROSITE: PS00660; MAM 2; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE 1; 2.
 DR PROSITE: PS0056; TYR_PHOSPHATASE 2; 2.
 DR PROSITE: PS0055; TYR_PHOSPHATASE PTP; 2.
 KW Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 25 Potential
 FT CHAIN 26 1457 Receptor-type protein-tyrosine phosphatase kappa.
 FT DOMAIN 26 752 Extracellular (Potential).
 FT TRANSMEM 753 774 Potential.
 FT DOMAIN 775 1457 Cytoplasmic (Potential).
 FT DOMAIN 30 193 MAM.
 FT DOMAIN 195 280 Ig-like C2-type.
 FT DOMAIN 290 382 Fibronectin type-III 1.
 FT DOMAIN 388 484 Fibronectin type-III 2.
 FT DOMAIN 489 588 Fibronectin type-III 3.
 FT DOMAIN 589 688 Fibronectin type-III 4.
 FT DOMAIN 922 1158 Protein-tyrosine phosphatase 1.
 FT DOMAIN 1218 1452 Protein-tyrosine phosphatase 2.
 FT ACT_SITE 1100 1100 Phosphocysteine intermediate (By similarity).
 FT ACT_SITE 1394 1394 Phosphocysteine intermediate (By

FT	DISULFID	215	269	similarity).	
FT	CARBOHYD	100	100	Potential.	
FT	CARBOHYD	139	139	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	210	210	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	415	415	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	423	423	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	435	435	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	461	461	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	551	551	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	585	585	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	589	589	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	606	606	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	689	689	N-linked (GlcNAc. . .)	(Potential).
SQ	SEQUENCE	1457 AA;	164185 MM;	19D4B99B7E3E8605 CRC64;	
Query Match					98.2%; Score 7571; DB 1; Length 1457;
Best Local Similarity					97.3%; Pred. No. 0;
Matches 1419; Conservative					13; Mismatches 6; Indels 20; Gaps 4;
Qy	1	MDTAAALPAFVALLLSPLLSGSAQGSAGCTFDDGPGACDHYQDLYDDFEVHVH	60		
Db	1	MD-VAAALPAFVALLLPPLLSGALGQFSAGCTFDDGPGACDHYQDLYDDFEVHVH	59		
Qy	61	SAQEPHYLPPEMPOGSYMIVDSSDHPDCEKARLQ.LPTWKENDTHCIDFSYLLYSQKGLNP	120		
Db	60	SAQEPHYLPPEMPOGSYMIVDSSDHPDCEKARLQ.LPTWKENDTHCIDFSYLLYSQKGLNP	119		
Qy	121	GTNLIVRVNKGPLANPIVNTVGTGRDLRAELAVSTFWNEVQVIFEAESVSGRSGYI	180		
Db	120	GTNLIVRVNKGPLANPIVNTVGTGRDLRAELAVSTFWNEVQVIFEAESVSGRSGYI	179		
Qy	181	AIDDIQVLSYPCDKSPHPLRLGDEVNAGQATFQCIATGRDAVHNLWLQRRNGEDIPV	240		
Db	180	AIDDIQVLSYPCDKSPHPLRLGDEVNAGQATFQCIATGRDAVHNLWLQRRNGEDIPV	239		
Qy	241	AQTNKINHRRFAASFRLEQVTKTDODLYRCVTOSESGVSNFAQLIVREPPRIAPPOL	300		
Db	240	AQTNKINHRRFAASFRLEQVTKTDODLYRCVTOSESGVSNFAQLIVREPPRIAPPOL	299		
Qy	301	LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTVMHLDPDTEYE	360		
Db	300	LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTVMHLDPDTEYE	359		
Qy	361	IRVLLTRPGEQGTGLPGPLITRTKCAEPMPTKTLKIAEIQARRIAVDMESLGVNITRC	420		
Db	360	IRVLLTRPGEQGTGLPGPLITRTKCAEPMPTKTLKIAEIQARRIAVDMESLGVNITRC	419		
Qy	421	HTFNVTICYHYFRGHNESKADCLMDPKAPOHVNVNHLPPYTNVSLKMLTNPGEKRSSE	480		
Db	420	HTFNVTICYHYFRGHNESKADCLMDPKAPOHVNVNHLPPYTNVSLKMLTNPGEKRSSE	479		
Qy	481	TIIOQDEVDVPGVPVKSLQGSFENKIFLNKKEPLDNGIITQVEISYSSIRSFDPAVPV	540		
Db	480	TIIOQDEVDVPGVPVKSLQGSFENKIFLNKKEPLDNGIITQVEISYSSIRSFDPAVPV	539		
Qy	541	AGPPTQVNLWNSTHVFHMLHPGTTGYFFIRASTVKFGFPATAINVTNISAPLDPYE	600		
Db	540	AGPPTQVNLWNSTHVFHMLHPGTTGYFFIRASTVKFGFPATAINVTNISAPLDPYE	599		
Qy	601	GVDSASLNATATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVQN	660		
Db	600	GVDSASLNATATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVQN	659		
Qy	661	AMSGAPYFAAELPPGNLPPAPFTVGDNRITYQGFWMNPLAPRKGNYIYFOAMSSVBEKE	720		
Db	660	ALSGAPYFAAELPPGNLPPAPFTVGDNRITYQGFWMNPLAPRKGNYIYFOAMSSVBEKE	719		
Qy	721	TKTCQVRIATK-AAATEBEVIPPDAKQDTRVVVKIAGISAGILVFILLVILVIVKSKL	779		
Db	720	TKTCQVRIATKAAATEBEVIPPDAKQDTRVVVKIAGISAGILVFILLVILVIVKSKL	779		
Qy	780	AKRKDKAMGNTRQEMTHVMNADRSDYADQSTLHAEDPLSLITFMDQHNFSRPLPNDPLVPT	831		

Db	780	AKRKDKAMGNTRQEMTHVMNADRSDYADQSTLHAEDPLSLITFMDQHNFSRPLPNDPLVPT	839		
Qy	832	-----ENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF	887		
Db	840	AVLDENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF	899		
Qy	888	KEEYESFEGQSASWDVAKDONRKNRYNIIAYDHSRVILQPVDEDPSSDIYANVYI - 946			
Db	900	KBEYESFEGQSASWDVAKDONRKNRYNIIAYDHSRVILQPVDEDPSSDIYANVYI	959		
Qy	947	-----DGYQRPISHYATQGPVHETVDFWRMIWQESACIWMVNLVEVGRVKCYKWPD	1001		
Db	960	IWLRYDGYQRPISHYATQGPVHETVDFWRMIWQESACIWMVNLVEVGRVKCYKWPD	1019		
Qy	1002	DTEVYGDVKVTCVEMEPLAEYVVRTFTLRRGNYNEIREVKQFHFTGHPDHGVPYHATGLL	1061		
Db	1020	DTEVYGDVKVTCVEMEPLAEYVVRTFTLRRGNYNEIREVKQFHFTGHPDHGVPYHATGLL	1079		
Qy	1062	SFIRRVKLSNPPSAGPIVHCSAGAGTGCTCYIVIDIMLMDAERGVVDIYNCVKALRSRR	1121		
Db	1080	SFIRRVKLSNPPSAGPIVHCSAGAGTGCTCYIVIDIMLMDAERGVVDIYNCVKALRSRR	1139		
Qy	1122	INNVQTEEQYIFTHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOFOTLN	1181		
Db	1140	INNVQTEEQYIFTHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOFOTLN	1199		
Qy	1182	SVTPRLQAECDSCIACLRNHDKNRMDLPPDCLPFLITIDGESSNYINAAALMDSYRQP	1241		
Db	1200	SVTPRLQAECDSCIACLRNHDKNRMDLPPDCLPFLITIDGESSNYINAAALMDSYRQP	1259		
Qy	1242	AAFTVTOYPLNTVKDFWRLVYDYGCTSIWMLNEVDLSQCPQYWPEGMRLVGPQIQVEK	1301		
Db	1260	AAFTVTOYPLNTVKDFWRLVYDYGCTSIWMLNEVDLSQCPQYWPEGMRLVGPQIQVEK	1319		
Qy	1302	MSCSMDCDVNIRIFRINLTPQEGYLMVQOFOYLGWASHREVPGSKRSFLKLILQVEKW	1361		
Db	1320	MSCSMDCDVNIRIFRINLTPQEGYLMVQOFOYLGWASHREVPGSKRSFLKLILQVEKW	1379		
Qy	1362	QEBWKEGEGRTIIHCLNGGSGRMFCAIGIVEMVKRQNVVDVFAVKTILNSKPNMVEA	1421		
Db	1380	QEBWKEGEGRTIIHCLNGGSGRMFCAIGIVEMVKRQNVVDVFAVKTILNSKPNMVEA	1439		
Qy	1422	PEQYRFCYDVALEYLESS 1439			
Db	1440	PEQYRFCYDVALEYLESS 1457			
RESULT 5					
PTPM HUMAN					
ID	PTPM_HUMAN	STANDARD;	PRT;	1452 AA.	
AC	P28827;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48) (R-PTP-mu).				
GN	Name=PTPRM; Synonyms=PTPRL1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OK	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;				
RA	Gebblink M.F.B.G., van Eften I., Hateboer G., Suijkerbuijk R.,				
RA	Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.,				
RT	"Cloning, expression and chromosomal localization of a new putative				
RL	receptor-like protein tyrosine phosphatase.";				
RL	FEBS Lett. 290:123-130(1991).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.				
RX	MEDLINE=98010572; PubMed=9346878; DOI=10.1074/jbc.272.44.27505;				

RA Hoffmann K.M., Tonks N.K., Barford D.;
RT "The crystal structure of domain 1 of receptor protein-tyrosine
RT phosphatase mu.";
RL J. Biol. Chem. 272:27505-27508(1997).
CC -1- FUNCTION: May play a key role in signal transduction and growth
CC control.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 2B subfamily.
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; X58288; CAA41226.1; --
DR PIR; S17669; S17669.
DR PDB; 1RPM; X-ray; A/B=879-1156.
DR Genew; HGNC:9675; PTPRM.
DR MIM; 176888; --
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS50853; FN3; 3.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW 3D-structure: Glycoprotein; Hydrolase; Immunoglobulin domain;
KW Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 1452 Receptor-type protein-tyrosine
FT phosphatase mu.
FT FT 21 742 Extracellular (Potential).
FT TRANSMEM 743 764 Potential.
FT DOMAIN 765 1452 Cytoplasmic (Potential).
FT DOMAIN 22 184 MAM.
FT DOMAIN 186 277 Ig-like C2-type.
FT DOMAIN 281 371 Fibronectin type-III 1.
FT DOMAIN 379 477 Fibronectin type-III 2.
FT DOMAIN 482 581 Fibronectin type-III 3.
FT DOMAIN 589 671 Fibronectin type-III 4.
FT DOMAIN 923 1153 Protein-tyrosine phosphatase 1.
FT DOMAIN 1213 1447 Protein-tyrosine phosphatase 2.

FT	ACT_SITE	1095	1095	Phosphocysteine intermediate (By similarity).
FT	ACT_SITE	1389	1389	Phosphocysteine intermediate (By similarity).
FT	DISULFID	206	260	Potential.
FT	CARBOHYD	72	72	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	92	92	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	131	131	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	249	249	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	406	406	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	414	414	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	454	454	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	534	534	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	544	544	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	598	598	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	651	651	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	681	681	N-linked (GlcNAc. .) (Potential).
FT	STRAND	880	881	
FT	TURN	882	884	
FT	HELIX	885	905	
FT	TURN	906	906	
FT	TURN	916	919	
FT	HELIX	921	926	
FT	TURN	930	931	
FT	HELIX	936	938	
FT	STRAND	939	941	
FT	TURN	946	947	
FT	TURN	949	952	
FT	STRAND	953	961	
FT	TURN	962	963	
FT	STRAND	964	971	
FT	HELIX	976	978	
FT	HELIX	979	988	
FT	TURN	989	990	
FT	STRAND	993	996	
FT	TURN	1001	1002	
FT	STRAND	1003	1004	
FT	STRAND	1005	1006	
FT	STRAND	1016	1019	
FT	TURN	1020	1021	
FT	STRAND	1022	1032	
FT	TURN	1033	1034	
FT	STRAND	1035	1044	
FT	TURN	1045	1046	
FT	STRAND	1051	1058	
FT	HELIX	1071	1083	
FT	TURN	1086	1087	
FT	STRAND	1091	1094	
FT	HELIX	1100	1118	
FT	STRAND	1120	1121	
FT	HELIX	1123	1133	
FT	TURN	1135	1136	
FT	HELIX	1141	1155	
SQ	SEQUENCE	1452	AA; 163633 MW; 08175D3595A6C7E0 CRC64;	

Query Match 62.4%; Score 4807; DB 1; Length 1452;
Best Local Similarity 60.8%; Pred. No. 6.8e-313;
Matches 889; Conservative 206; Mismatches 326; Indels 42; Gaps 8;

QY	4	TAAALPAFVALLLLSPWLLGSAQGFAGGCTFDDGPGACDYHQDLYDDPFWVHVSQAQ 63	
DB	3	TLGTCLATLAGLL-----TAAGETPSGGCLFDEPYSTCGYSQSGDDFNWEQVNTL 54	
QY	64	EPHYLPPEMPCQSYMTVDSSDDHPGEKARLQPTMKENDTHCIDPSYLLYSQKGLNPCTL 123	
DB	55	TKPTSDPWWPESGLMLVNASGRPEGARHLLLPQKENDTHCIDPHYFVSSKSNSPPGLL 114	
QY	124	NILVRNKGFLANPIWNVTGTRDWLRAELAVSTFWPNEYQVIFAEVSGRSGYIAID 183	
DB	115	NYTVKVNGLGNPIWNISGDPTRTNRAELAISTFWPFYQVIFEV-ITSGHQGLAID 173	
QY	184	DIQVLSYPCDKSPHFLRLGDEVNAGNATFQCIGATGRDAVHNKMLQRRNGEDIPVAQT 243	

Db 174 EVKVLGHPCTRTPHFLRIQNVENVNAGQPATPQCASIGRTVAGDRLMLQGLDVRDAPLKEI 233
Qy 244 KNIHRRPAASFRLOEVTKTDODLRYCVTQBSRGVSNFPAQLIVRPPRIAPQLLGV 303
Db 234 KVTSSRRFIASFNVTNTKRDAGKYRCMRTEGGVGISYNAELVVKPPVPIAPQLASV 293
Qy 304 GPTVLLIQLNANSIIGDGPITLKEVYRMTSGSTETHAVNAPYKLVHLWLPDPTYEYLRV 363
Db 294 GATVLMVQLNANSINGDGPVAREVEYTAGSGWNRQPDVDSYKIGHLDPDTEYELV 353
Qy 364 LLTRPGEGLTGLPGPPLITRTKCAEPMRTKTLKIAETQARRIAVDWESGLYNITRCHTF 423
Db 354 LLTRPGEGLTGLPGPPLITRTKCAEPMRTKTLKIAETQARRIAVDWESGLYNITRCHTF 423
Qy 424 NVTCYHYFRGHNESKAD--CLMDPDKAPQHVNVHLPDPTVNSVLSKMLITNPEGKESSET 481
Db 414 NLTVHYCYVQGGQBVREVSWDENSHPOHTITNLSPTVTVSVKLLIMNPEGRKESQEL 473
Qy 482 ILOTDEDVPGVPVKSLQGTSPFNKIPLNWKPEPLDPNGILITQVEISYSSIRSFDPAPVPA 541
Db 474 IVQTDDEDLFGAVPTESIQGSTFEKIFLOWREPTQTYGVITLYEITYKAVSSFFDPEIDL 533
Qy 542 GPPQTVSNLMSNTHVFMHLHPGTTTYQFFIRASTVKGFGPATAINVTNISAPTLDPYEG 601
Db 534 NQSGRVSKLGNETHFLFGLYPTGTYFTIRASTAKGFPATNQFTTKISAPMPAYE- 592
Qy 602 VDASLNFTATTITVLLRPAQAKGAPISAYQIVVELHPHRTKRBAGAMECYQVPTVQNA 661
Db 593 LETPLNQDNTVTVMLKPAHSGAPSVYQIVVEBERPRRTKKTTEILKCYVPPIHFQNA 652
Qy 662 MSGGAPYFAELPGLNPELAPFTVGDNRVYQGFNPPPLAPRGVNIYFOAMSSVEKET 721
Db 653 SLNLSQYFAEFPADPSLQAQPFITGDKNTYNGVNTPLPYKSYRIYFOAASRANGET 712
Qy 722 KTQCVRATKAATBEPIVPPAKOTDRVWKIAGISAGILVFILLVILVILVVKSKLAK 781
Db 713 KIDCQVATKGA--TPKVPPEPKQTDHTVKIAGIAGILFVIFLGVLMVKRKLAK 771
Qy 782 KRKAMGNTOEMTHVMNDRSVADQSTLHAEDPLSLTFMDQHNFSRY----- 831
Db 772 KRKETMSSTRQEMTVNWSMDKSAEQGTCNDE--AFSPMDTNLNGRSVSSPSFTMK 828
Qy 832 -----ENHSATAESRLDVRV--LCEGTESPYOTGOLHPAIRVADLLQH 875
Db 829 TNLSTSVNPSYDPETHMTASDSSLVQSHTYKKREPADVPYQVQGLHPAIRVADLLQH 888
Qy 876 INLMKTSYGFKEEYESFFEGQSASVDVAKQONAKNRKYNIIAYDHSRVILQPVBD 935
Db 889 ITQMKCAGYGFKEEYESFFEGQSAPWSAKDENEMKNRYGNIIAYDHSRVRLQITBGD 948
Qy 936 PSSDYINANYIDGYORPSHYIATQGVNHTVYDFWRMTWQBSACIVMVTNLVEGRVKC 995
Db 949 TNSDYINGNYIDGYHRPNHYIATQGMQETTYDFWRVWVHENTASIIWVTNLVEGRVKC 1008
Qy 996 KYKPPDDTEVYDGFVTCVEMEPLEAYVVRFTLERRGVNREIVKQSHFTGWDHGVY 1055
Db 1009 CKYVPPDDTEIYKDIKLTIELLAEYVIRFAVEKRGVHEIREIRHFHTGWDHGVY 1068
Qy 1056 HATGLLSIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIDIMLDMASREGVVDIYNCVK 1115
Db 1059 HATGLLGFVRQVKSPPSAGPLVHCSAGAGRTGCFIVIDIMLDMASREGVVDIYNCVR 1128
Qy 1116 ALRSRRINNVQTEQYIFTHDAILEACLCGETAIPVCEFFKAYFDMIRIDISQTNSSHLK 1175
Db 1129 ELRSRRVNVQTEQYVIFTHDAILEACLCGDSVPASQVRSLSYDMNKLDPQTNSSQIKE 1188
Qy 1176 EFQTLNSVTPRLQAECDGCIACLRNHDKNRPMDLPPDRCLPFLITIDGESSNYNAALM 1235
Db 1189 EFRTLNNVTPTRLVDEDCSIALLPFRNHNKRCMDILPPDRCLPFLITIDGESSNYNAALM 1248
Qy 1236 DSYROPAAFIQVQPLNPTVKDFWRLVDYDGYCTSIWMLNEVDLSQGCQPYWPEGLRYG 1295
Db 1249 DSYKQPSAFIVTQHPLENTVKDFWRLVDYDGYCTSIWMLNEVDVPAQLCQPYWPEGVHRHG 1308

Qy 1296 PIVOECMSCMDCDVINRIENLTPORGYLMVQOFOYLGWASHREVPGSKESFLKLI 1355
Db 1309 PIQVEFVSADLEEDISIRIFRIINAARPDQGYRNVQOQFGLGMPMYRDTPVSKRSFLKLI 1368
Qy 1356 LQVEKQEEWKEGEGRTIIHCLNGGSGRGMFCFCAIGIVVMVKRQNVVDVFAVKTLRNSK 1415
Db 1369 RQVDKQEEYNGEGPTVHVCLNGGSGRTFCAISIVCEMLRHQRTVDVFAVKTLRNNK 1428
Qy 1416 PNWVEAPEQRYFCYDVALEYLES 1438
Db 1429 PNWDLDDQYKFCVVALEYLNS 1451
RESULT 6
ID PTFM MOUSE STANDARD; PRT; 1452 AA.
AC P28828;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)
DE (R-PTP-mu).
GN Name=Ptpm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung.
RX MEDLINE=52008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;
RA Gebbink M.F.B.G., van Etten I., Hateboer G., Suijkerbuijk R.,
RA Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;
RT "Cloning, expression and chromosomal localization of a new putative
RT receptor-like protein tyrosine phosphatase.";
RL FEBS Lett. 290:123-130(1991).
CC -!- FUNCTION: May play a key role in signal transduction and growth
CC control.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Most abundant in lung, less in brain and
CC heart.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 2B subfamily.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58287; CAA41225.1; -;
CC PIR; S17670; S17670.
CC HSSP; P28827; IRPM.
CC MGD; MGI:102694; Ptpm.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR008979; Gal_bind_like.
CC InterPro; IPR003599; Ig-like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR000998; MAM.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00041; fn3; 3.
CC Pfam; PF00047; ig; 1.

Db 909 QLHPAIRVADLLOHITQMKCAEGYFKBEYESFEGQSAWDSAKDENRMKNRYGNIIA 968
 Qy 922 YDHSRVLQPVEDDPSSDIYINANYIDGYQRPSPHYATQGPVHETVYDFWMIWQESACI 981
 Db 969 YDHSRVLQMLEGDNNSDIYINIDGYHPRNHYATQGPVHETVYDFWMIWQESACI 1028
 Qy 982 VMYTNLVEGRVKCYKWPDDTEVYGFKTCVEMEPLEAEVYVTFLLRGRVNEIREVK 1041
 Db 1029 IMYTNLVEGRVKCYKWPDDTEVYGFKTCVEMEPLEAEVYVTFLLRGRVNEIREVK 1088
 Qy 1042 QFHTGWPDPGVPVHATGLLSFTRRVKSLSPPSAGPIVHCSAGAGTGCYVIVIDMLDM 1101
 Db 1089 QFHTGWPDPGVPVHATGLLGFVQVKSPPNAGPLVHCSAGAGTGCYVIVIDMLDM 1148
 Qy 1102 AREGVVDIYVNCVKSLSRRINMVQTEEQYIFHDAILEACLCGETAIPVCEFAAYFDM 1161
 Db 1149 AREGVVDIYVNCVKSLSRRINMVQTEEQYIFHDAILEACLCGETAIPVCEFAAYFDM 1208
 Qy 1162 IRDSQTNLSHLKDFOTLNSVTPRQAEDCSIACLPRNHDKNRFDMLPPDRCLPLIIT 1221
 Db 1209 NKLDQTNSSQIKKEEFTLNVTPTLVEVDCSIALPRNHEKNCRCMDILPPDRCLPLIIT 1268
 Qy 1222 IDGESSNYINAAWLDVSRQPAAFVTOYPLNTVKDFWRLVYDYGCTSIYMLNEVDLSQ 1281
 Db 1269 IDGESSNYINAAWLDVSRQPAAFVTOYPLNTVKDFWRLVYDYGCTSIYMLNEVDLSQ 1328
 Qy 1282 CPQYWPBEGMLRXPQVQECMSMCDVNIIRFICNLTRPOBGLVWQVQFVGLGWASH 1341
 Db 1329 CPQYWPBEGMLRXPQVQECMSMCDVNIIRFICNLTRPOBGLVWQVQFVGLGWASH 1388
 Qy 1342 REVPGSKRSLKILQVKEWQEBWKEGRTIHLNGGGRSGMFCAGIIVEMVQRQNV 1401
 Db 1389 RDTFVSKRSLKILQVKEWQEBWKEGRTIHLNGGGRSGMFCAGIIVEMVQRQNV 1448
 Qy 1402 VDFHFAVKTLSNKNPNAPEQYRCYDVALEYLES 1438
 Db 1449 VDFHFAVKTLSNKNPNAPEQYRCYDVALEYLES 1485

RESULT 8

Q86V60 PRELIMINARY; PRT; 1390 AA.
 AC Q86V60
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE PTPRM protein
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.W., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;

Query Match 61.3%; Score 4726; DB 2; Length 1390;
 Best Local Similarity 62.2%; Pred. No. 1.7e-307;
 Matches 867; Conservative 2%; Mismatches 292; Indels 34; Gaps 7;
 Qy 72 MPOGSMYIVDSDHDPGEKARLQPTMKENDTHCIDPSYLLYSQKGLNPGCTLAILVRVVK 131
 Db 1 MPGSGFNLVNASGRPEGQRAHLLLPQKENDTHCIDPHYFVSKSNPPGLLVYVKNV 60
 Qy 132 GPLANPIWNTGFTGRDMLRAELAVSTFWPNEYQVIFAEVSGSGSYIAIDDIQVLSYP 191
 Db 61 GPLGNPIWNTGFTGRDMLRAELAVSTFWPNEYQVIFAEVSGSGSYIAIDDIQVLSYP 119
 Qy 192 COKSPHFLRLGDEVNAGQATPQTATGRDAVHKLMLQRRNGEDIPVATQKNINHRF 251
 Db 120 CTRTPHFLRIQNVNAGQATPQTATGRDAVHKLMLQRRNGEDIPVATQKNINHRF 179
 Qy 252 AASFLRQEVTKTDODLYRCVQTSERGSYVNAQLVREPRPIAPOLLGVGPTVLLIQ 311
 Db 180 IASFNVTNTKRDAGKYRCMIRTEGGVGSINVAELVVKSPPIAPOLLGVGPTVLLIQ 239
 Qy 312 LNANSIIGDPITLKEVEYRMTSGSWTEVHVNAPYKLMWLDPDTEYERILLTRPGE 371
 Db 240 LNANSINGDPVAREVEVCTAGSNDQPDVSTSYKIGLDPDTEYERILLTRPGE 299
 Qy 372 GTGLPGPPLITRTKCAEMRTPKTKIAEQARIADWESLGYNTTRCHTFNVCYHY 431
 Db 300 GTGSPGALRTKCAEMRTPKTKIAEQARIADWESLGYNTTRCHTFNVCYHY 359
 Qy 432 FRGHNESKAD--CLDMDPKAPQHVHNLPPYTNVSLKMLTNPGEKSEBETIOTDEDV 489
 Db 360 QVGGQGVREEVSWDTEHNSHPQHTITNLSFYTNVSKLILMNPGEKSEBETIOTDEDV 419

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
 SEQUENCE FROM N.A.
 TISSUE=Brain;
 Strausberg R.;

Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051651; AAH51651.1; -
 DR HSSP; P28827; IRPM.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0016787; F-hydrolase activity; IEA.
 DR GO; GO:0004725; P-protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P-protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003599; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000998; MAM.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00629; MAM; 1.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 3.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00853; FN3; 3.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00740; MAM 1; 1.
 DR PROSITE; PS00600; MAM 2; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
 KW Glycoprotein; Hydrolase.

SQ SEQUENCE 1390 AA; 156936 MW; D8173543CDD9F79 CRC64;

Db 264 VTOSRGSGVSNFAELIVKBPPTPIAPPQLLRAGSTVLIILQNTNSIIGDGPVIRKEIEY 323
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Db 324 RMTSGSPWSEVHAVNMQTYKLWHLDPDTEYBISVLLTRPGEGTGLPGPPLISRTKCAEPM 383
Qy 391 RTPKTLKIAEIOARRTAVDSESIGYNTTRFTNTVILCIHYF--RGHNSKACLDMDPK 448
Db 384 RAPKGLAFSIOQRQLTLOWEPLGYNLTRCHTYSVSLCYRYLVGSGNLQNTFRECAKERN 443
Qy 449 APQHVNNHPPYTNVSLMLLTNPGRKSESEETIIODEDVPGVPVVKLSQGTFSFNKIF 508
Db 444 ANRYTIKNLLPYRNHVKLILSNPEGRKEKEVTFTQDEDVPGIASESTFTPLEDMIF 503
Qy 509 LNKWELDPNGIITQVEISYSSIRSFDPAPVAVPGPQTVSNLWNSTHVMHLPHTTYQ 568
Db 504 LKWEPEVPEPGLITQVEISYQSISSDPAVNVPPRRTVSKLRNETVHVFSNLHPGTYL 563
Qy 569 FPIRASTVKGFGATAVNTNITASPLTPDYEGVDASLNETATITVLLRPAQAKGAPIS 628
Db 564 FSVRAETGKGFGQTALTEITNITASPTF-DYGDMPSPGLGSESTITVLLRPAQGRGAPIS 622
Qy 629 AYQIVVEELHPHTKREAGAMECVQVPVTVQNAMSGGAPVYEAELPPGNLPPAPPTVG 688
Db 623 TYQIVVEEDRPKRKIKELGQECFPVPLTFDDHMSRGSVHYGAEPLPASSLTAKPFTVG 682
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Db 802 QSTLODERLCLGFMTHNYSNRQDSSVNVSSLLGSPRRQCKRGKSPVHTGOLHP 861
Qy 866 AIRVADLLQHINLMKTSDSYGPKEEYSEFFEGOSASWDVAKQDNRAKNRYGNIAYDHS 925
Db 862 AVRVDLLQHINQMKTAEGYGFQYEVSEFPEG---WDASK-KDKTKGRQDHVSYDRH 916
Qy 926 RVTLQPVDDPSDYNANVIDYQRPVSHVIAQGPVHETVYDFWMIWQEQSACIVMT 985
Db 917 RVKLHLLGDPNSDYINANYIDGYSRSHFIAQGPQEMVYDFWVWQEHCCSSIVMIT 976
Qy 986 NLYEGRVKCYKWPDDTEYVGFVKTCVMEPLAEYVVTFTLRRGYNEIREVKQFHF 1045
Db 977 KLYEGRVKCKYKWPDDSEMYGDIKILVKSEMLAEYAVRFTALERRGYSARHEVKQFHF 1036
Qy 1046 TGWPDHGVPHATGLLSFIRRVKLSNPPSAGPIVWHCSAGAGRTGCYIVIDIMLMDAERE 1105
Db 1037 TSWPEHGVPHATGLLAFIRVKAFTPPDAGPIVHCSAGTGTGTCYIVLDMVMDAERE 1096
Qy 1106 GVVDIYNVCKALSRINNVQTEQYIFIHDAILEACLCGETAIPVCEFKAAVDFMIRID 1165
Db 1097 GVVDIYNVCKTCSRINNIQTEQYIFIHDAILEACLCGETSIPASEPKPTVKEMVRIE 1156
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Qy 1226 SSNNYINAAIMDSYRQAAFTVTOYPLNTPVKDFWRLVVDYDGTCSIVMLNEVDLSQG--C 1282
Db 1217 SSNNYINAAITDSTYKSAFIVTLHPQNTTDFWRLVVDYDGTCSIVMLNQLNSGSAWPC 1276
Qy 1283 PQWPEGLMYGPIQVECMSCSDCDVINRIFRINLTPORGYLMVQOFOYGLWASHR 1342
Db 1277 LQWPEPGLQHYGMEVEYVSGAEDIVSRLEFRVQNIITLQEGHLMVHRFQYLRWSAYR 1336
Qy 1343 EYDGSXRSFLKLLIYQEKWQEEKKEBGRTHIICLNGGGRSGMFCAGIIVVEMVKQNVV 1402
Db 1337 DTPDSKKSFLHLLAQVERWQKE--SGDGRTVVHCLNGGGRSGTYCASTMILEMIKCHNWA 1394

Qy 1403 DVFAVTKLRNSKNPVWEAPEQYRFCYDVALEYLES 1438
Db 1395 DIFAAKTLRNYKPNVETLEQYHCFYDIALEYLES 1430
RESULT 10
000197
ID 000197 PRELIMINARY; PRT; 1436 AA.
AC 000197;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Receptor protein tyrosine phosphatase hPTP-J precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RC MEDLINE=97223402; PubMed=9070223; DOI=10.1006/bbrc.1997.6004;
RX Wang B., Kishihara K., Zhang D., Hara H., Nomoto K.;
RA "Molecular cloning and characterization of a novel human receptor
RT protein tyrosine phosphatase gene, hPTP-J: down-regulation of gene
RT expression by PMA and calcium ionophore in Jurkat T lymphoma cells.";
RL Biochem. Biophys. Res. Commun. 231:77-81(1997).
DR EMBL; U73727; AAB51343.1; -;
DR PIR; JC5290; JC5290.
DR HSSP; P28827; IRPM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00660; MAM_2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00566; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolase; Receptor; Signal.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 1436 receptor protein tyrosine phosphatase
FT hPTP-J
SQ SEQUENCE 1436 AA; 161092 MW; C05B86FP7A9412D9 CRC64;
Query Match 60.1%; Score 4632; DB 2; Length 1436;
Best Local Similarity 60.1%; Pred. No. 3.6e-301;
Matches 867; Conservative 211; Mismatches 339; Indels 26; Gaps 10;
Qy 6 AAALPAFVALLLSWPLIGSQGQFSAGCTPD---DGFACDHYQDLYDDFEWHVSA 62
Db 4 AQAALVLAITFOLCAP-----ETETPAAGCTFEASDPVPCYSQAQYDDFEQVRI 56

Db	4	AQALVLTALTQLCAP-----ETETPAAGCTFEASDPAPVCEYSOAQYDDFQWBEQVRI	56
Qy	63	QBEHYLPPEMPOGQSYMTIVDSDDHDPGEBKARLQLPTMKENDTHCTIDFYLILYSOKLNPST	122
Db	57	HPGTRAPADLPHGSLYLVMTNSQAPQGRAHVIFQSLSENTHCVQFSYFLYSRDGHSPGT	116
Qy	123	LNILVRVNGKPLANPINVVTGTCGRDMLRAELAVSTFWPNEYQVIFAEVSGGRSGVIAI	182
Db	117	LGVVYRVNGGLPGASVAVNMTGSHGRQWQHAELAVSTFWPNEYQVLFLEALISPRRGYVGL	176
Qy	183	DDIQVLSYPCDKSPHFURLGDVEVNAQONATFOCIATGRDAVHNKMLQORNGEDIPVAQ	242
Db	177	DDIILLISYPCAKAPHSFRLGDVEVNAQONASFCQMAAGRAAEARFLQIQSGALVPAAG	236
Qy	243	TKYNINRRFAASFRLOEVTKTQDLYRCVTCQSERGSGVSNFAQLIVREPPRIAPPOLLG	302
Db	237	VRHISHRRFLATPPLAAVSRAEQDLYRCVSQAPRGAGVSNFAELIVKEPPTPIAPQLLR	296
Qy	303	VGPTYLLIQLNANSIICDGPILLKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYEUR	362
Db	297	AGPTYLLIQLTNWSIICDGPVIRKEIERYMARGPWAHVAVLSQTYKMLHLDPDTEYEIS	356
Qy	363	VLLTRPCEGGTGLPGPPLIIRTKCAEPMRWPKTLKIAEIOARRIADVWESIYGNVITRCHT	422
Db	357	VLLTRPDGGTGRGPPLISRTKCAEPMRWAPKGLAFABEIQAQQLTQWEPGLVNVITRCHT	416
Qy	423	FNVTICYHYFRG--HNESKADCLDMDPKAQHVVNHLPPYTNVLSKMLTNPGRKESEE	480
Db	417	YTVSLCYHYTLGSSHNQTIRECVKTEQGVSRYYITKNLLPYRNHVHVLVLTNPEGRKEGE	476
Qy	481	TIITQTDDEVPVPGVPLQSGTSFENKIFLNWKBPDPNGIITQVEISYSISIRSFDPAPVY	540
Db	477	VTQTQDDEVPGIAAESLUTPLEDMIFLXWEEPOEPNGLIITQVEISYQIESSDPAVNV	536
Qy	541	AGPQTVSNLWNSFHHVFMHLHGTTQYQPIRATSVKGFGPATAINVTNITSAITPLDYE	600
Db	537	PGRRITISIKURNETYHVNFLNHPGTTTYLFSVRARTKGFGQAALTEITTNISAPSF--DYA	595
Qy	601	GVDAISLNETAATTIVLLRPAQAKAPISAYSQIVVVEELPHRTKREAGACMECYQVPVTYQN	660
Db	596	DMSPGLGSENITVLLRPAQGRGAPISVTVQVIVEERARLRREPQGGQCPFPVPLTFEA	655
Qy	661	AMSGGAPYYFAABELPGONPEPPAFVTGDNRTYQGFVNPPLAPRKGYNIYFOAMSSVEKE	720
Db	656	ALARGLVHYFGAELAASSLPEAMPFTVGDNQTVRGFWNPPLPRKAYLIYFQAASHLKGE	715
Qy	721	TKTCQVRIATKAATEEPEVTPDPAKQTDTRVVKTAGISA-GILFPIILLVILVVKSKL	779
Db	716	TRLNCIRIARAKAACKESKRPLEVSQRSSEENGLILGICAGGLAVLILLGAIIVIRKGP	775
Qy	780	AKRKDAMGNTROBMTVMVAMDRSYADQSTLHAEDPLSITFMDQHNFSPRYENHS--AT	837
Db	776	VNMTK--ATVNYRQEKTHMSAVDRSFDTQSTLQEDERLGLSFDWTHGYSYTRGQSRGCVT	834
Qy	838	AESRLLDVPYRLCEGTSPYQTQGLHPAIRVADLLQHIINLMKTSYSGFKEEYESPFEG	897
Db	835	EASLLGGSRRPCGRKGSYPHTQGLHPAVRVADLLQHIINQMKTAEYGFQKEYESPFEG	894
Qy	898	QSAWSVDVAKDQONKAKRYGNIITAYDHSRVLQPVEDDPSSDYINANYIDGYQRPISHYIA	957
Db	895	-----WDATKKDKVKYKSGRQFMPAYDHRHVKLHPMLGDPNADYINANYIDGHRSHNFIA	950
Qy	958	TQGPVHETVYDFWRMIWQESACIVMVTNLVEYGRVKCYKWPDDTEVYGDPKVTCVEME	1017
Db	951	TQGPKEPNVYDFWRMVWQEHSSIVMTIKLVEYGRVKCSRYWPEDSPTYGDIKIMLVKTE	1010
Qy	1018	PLAEYVVRTEFTLERRGYNEIREVKQFHTGWPDRGVPHYATGLISFIRRVKLSNPPSAGP	1077
Db	1011	TLAEYVVRTEFTALERRGYVSARHEVQFHTAWPHEGVPHYATGLLAFIRRVKASTPPDAGP	1070
Qy	1078	IVHCSAGAGRTGCYIIVIDLMDMAEBEGVVDIYNCVKALRSRRINMVQTEQYIFITHDA	1137
Db	1071	IVTHCSAGTRTGCIYVLDMDLMAEBEGVVDIYNCVKILCSRNNMIOTEOQYIFITHDA	1130

DR	PRINTS; PRO0700; PRTYPHPTASE.	
DR	SMART; SM00060; FN3; 3.	
DR	SMART; SM00409; IG; 1.	
DR	SMART; SM00137; MAM; 1.	
DR	SMART; SM00194; PTEC; 2.	
DR	PROSITE; PS00853; FN3; 3.	
DR	PROSITE; PS00060; MAM; 2; 1.	
DR	PROSITE; PS00383; TYR PHOSPHATASE 1; 2.	
DR	PROSITE; PS00056; TYR PHOSPHATASE 2; 2.	
DR	PROSITE; PS00055; TYR PHOSPHATASE PTP; 2.	
KW	Glycoprotein; Hydrolase; Receptor.	
SQ	SEQUENCE 1436 AA; 161199 MW; EFPAAE52C6903F02 CRC64;	
Query Match 59.7%; Score 4602.5; DB 2; Length 1436;		
Best Local Similarity 60.3%; Pred. No. 3.5e-299;		
Matches 855; Conservative 214; Mismatches 329; Indels 19; Gaps 9;		
QY	33 AGCTTDDGPG--ACDYHODLYDDDEWHVHSQAEPHYLPPEMPQGSYMIYVDSDDHDPGE 89	
Db	24 AAGCTFEESADPVVPCFEFSQAQDDFQWEQVRIPHGTRTPEDLPHGAYLMVNASQHTPGQ 83	
QY	90 KARLQLPTMKENDTHCIDFSYLLYSQKGLNPGLTILVRVNGKPLANPIWNVGTGTRDW 149	
Db	84 RAHLIIFQTLSENTHCVQFSYFLYSRDSGSPGLGVYRVNGSPGLSAGAVNMVMTGSHGRW 143	
QY	150 LRALAVSTFWPNEYQVIFEAHSVGGSGYIAIDDIQVLSYPCDKSPHFLRLGDVEYNAG 209	
Db	144 HQELAVSTFWPNEFQVLFALISPDHKGVIIGLDDILLFSYPCAKAPHFSLRGDVEYNAG 203	
QY	210 QNATFOCIATGRAVHNKMLQRNGEDIPVAQTKINHRPAASFLRLQVTKTDQOLYR 269	
Db	204 QNASFCMAAGRAAEAEHFLQSQGLVPAAGVRHISHRRFLATPPLASVGRSEQDLVYR 263	
QY	270 CVTQSERGSGVNSFAOLIIVREPRPTAPOLLGVPGLTYLLIQNLANSIIGDGPILKEVE 329	
Db	264 CVSQAPRGAGVNSFAELIVKEPTPIAPPOLLRAGPTLYLIQNLANSIIGDGPVIRKEIE 323	
QY	330 YRMTSGSWTETHAVNAPTYKMLHLPDTEYEIRVLLTRPGEGLTGLPGPLITRTKCAEP 389	
Db	324 YRMARGFAEVAHVNLQTYKMLHLPDTEYEISVLLTRPGDGTGRPGPLISRTKCAEP 383	
QY	390 MRPYKYLKTAIEQARIADWESLGNITRCHTFNVTICVHYFRG--HNESKADCLDMDP 447	
Db	384 TRAPKGLAFABEIQAROLQWEPGLGNVTRCHTYAVSLCYRYTLGGSHNQITRECVKMER 443	
QY	448 KAPQVNVHLPPVTNYSKMLNPEGRKESEETIQTDEDVPGVPVKSLOQTSFENKI 507	
Db	444 GABRYTKNLLPFRNHRILNPEGRKEGKEVTFQTDDEDVPGGIAASLSLTFPLEDMI 503	
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Db	564 LFSVRARTSGFGQAALETITNISAPSF--DYADMPSPGSESENTITVLLRPAQAGAPI 622	
QY	628 SAYQIVVEELHPRTKEAGAMECYQVPVTVQNASGAPYFAAEPLPGNLPEPAPFTV 687	
Db	623 SVTVQVVEERPRRLRREPGQACFSVPLTFETALARGLVHYFGAELASLSLEAPFTV 682	
QY	688 GDNRTYQGFVNPLAPRKGNIVFYQAMSSVEKETKTQCVRATKAATESEPEVDPAPAKT 747	
Db	683 GDNQTVRGFWNPFLERKAVLIIVQAASHLKGTRLCNIPRIAKACKSKRPLEVSQRS 742	
QY	748 DRVVKIAGISA--GILVPIFILLVILVIVKSKLAKRKDAMGNTRQEMTHVMNMDRSYA 806	
Db	743 EEMGLILGICAGGLAVLILLGALIVIRKGPVNMWK--ATVNVYRQEKTHMMSAVDRSFT 801	
QY	807 DQSTLHAEDPLSTFMDQHNFSRYENHS--ATAESRLLDVRYLCEGTESYQTGQLH 864	
Db	802 DQSTLQEDERGLSFMDAPGYSRPGQRSGVTVASLSLLGSGSPRRRCGRKSGPYHTGQLH 861	
QY	865 PAIRVADLLQHINLMKTSDSYGFKEYESFFEQSASWDAKQDNKRNKRYNIIAYDH 924	
Db	862 PAVRVADLLQHINQMKTAEYGFKEYESFFEQG---WDATKKCKDLKGGQSPVSAYDR 917	
QY	925 SRVILQPVDEDDSSDYINANYIDGYQSPSHYATQGVHETVDFWRMIWQEQSACIVMV 984	
Db	918 HHVKLHPMLADPDADYISANYIDGYSRHNHFIATQGPKEPIYDFWRMWQEQSACIVMI 977	
QY	985 TNLVEVGRVKCYKWPDDTEVYGDQFVTCVEMEPFLAEYVVRTTFLERRGYNEIREVKQFH 1044	
Db	978 TKLVEVGRVKCSRYWEPEDSDMYGDIKITLVKTETLAEYVVRTTFLERRGYNSARHEVRQFH 1037	
QY	1045 FTGWDPHGVPPYHATGLLSFIRRVKLSNPSPSAGIVVHCSAGAGRTGCIYVIDIMLMAER 1104	
Db	1038 FTAMPEHGVPPYHATGLLAFIRRVKASTPPDAGPIVHCSAGTGTGTCYIYVLDVMDLMAEC 1097	
QY	1105 EGVVDLYNCVKALRSRINNMVQTEQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRI 1164	
Db	1098 EGVVDLYNCVKLCSRRVNMVQTEQYIFIHDAILEACLCGETIIPVNEFRATYREMIRI 1157	
QY	1165 DSQTNSSHLKDFQTLNSVTPLQABDCSIACIPLRNHDKNRMDMLPPDORCLPLITIDG 1224	
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QY	1225 ESNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIUMLNEVDLSQG--- 1281	
Db	1218 DPNYINAAALTSYTRSAAFIVTLHPLQSTTPDFWRLVYDYGCTSIUMLNQLQNSAWP 1277	
QY	1282 CQYWEEEGMLRVPLOVECMKSMDCDVINRIFRINLTPRPOEGLVMVQOQYVLGWASH 1341	
Db	1278 CLQYWPEPGRQQGLMEVFVSGTANEDLVSRFVRQNSRLQEGHLLVHRHFOFLRWSAY 1337	
QY	1342 REVPGSKRFLKILQVEKQWKEWKEGEGRTIHLCLNGGGRSGMFCAGIYVWEMVRQNV 1401	
Db	1338 RUTPDSRKAFLHLAEVDKQAE--SGDGRVTVHCLNGGGRSGTFCACATVLEMRCHSL 1395	
QY	1402 VDVFAVKTLRNSKPNMVEAPEQYFCYDVVALEYLES 1438	
Db	1396 VDVFFAAKTLRNVKPNMVEATMDQYHFCYDVVALEYLEA 1432	
RESULT 14		
ID	PTPT MOUSE STANDARD; PRT; 1454 AA.	
AC	Q99M80; Q99M81; Q99M82; Q9JIZ1; Q9JIZ2; Q9JKC2; Q9JLP0;	
DT	10-OCT-2003 (Rel. 42, Created)	
DT	10-OCT-2003 (Rel. 42, Last sequence update)	
DE	Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)	
DE	(R-PTP-T) (RPTP-rho) (mRPTPrho) (RPTPmam4).	
GN	Name=Ptprt;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A. (ISOFORMS 2 AND 5), AND ALTERNATIVE SPLICING.	
RC	STRAIN=C57BL/6J;	
RX	MEDLINE=22730707; PubMed=11423001;	
RA	Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;	
RT	"Genomic organization and alternative splicing of the human and mouse	
RT	RPTPrho genes.";	
RL	BMC Genomics 2:1-1(2001).	
RN	[2]	
RP	ERRATUM.	
RX	MEDLINE=22730717; PubMed=11814386;	
RA	Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;	
RL	BMC Genomics 2:5-5(2001).	
RN	[3]	
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).	
RA	Buchli A.D., Zimmermann D.R., Pfister F., Vaughan L.;	
RT	"RPTPmam4: a fourth member of the NAM family of receptor protein	
RT	tyrosine phosphatases expressed in adult brain.";	


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FT CONFLICT 1076 1076 L -> V (in Ref. 4; AAF82401).
FT CONFLICT 1103 1103 R -> K (in Ref. 1).
FT CONFLICT 1259 1259 F -> L (in Ref. 4; AAF82401).
FT CONFLICT 1266 1266 L -> I (in Ref. 4; AAF82401).
FT CONFLICT 1269 1269 T -> S (in Ref. 4; AAF82401).
SQ SEQUENCE 1454 AA; 163012 MW; C60464F7B423F8A8 CRC64;

Query Match
Best Local Similarity 59.5%; Score 4588.5; DB 1; Length 1454;
Matches 848; Conservative 239; Mismatches 342; Indels 33; Gaps 8;

Qy 1 MDTTAAALPAFVALLLLSPWLLGSAQGSAGCTFDDGPGACDQHDL-YDDESWVH 59
Db 1 MGSJGGLALCLLRLLLLGLQRPPLPGAGAAAGCGSFDHYSCGTSVALGTNGFTWEQ 60
Qy 60 VSAQEPHYLPPEMPQSGYMIYDSSDHPDGEKARLQLPTMKENDTHCIDFSYLLSQKGLN 119
Db 61 INTWEKPLMDPAVPTGFSFMVNSGRASGQKAHLLPLTKENDTHCIDHYFESSRDRSS 120
Qy 120 PGTUNILVRNKGPLANPINVTGTRDMRLABELAVSTFWPNBYQVIFPAEYSGRSGY 179
Db 121 PGALNVTVKVGNGPGQGNPMVNSGVWTEGWVKAELAISTFWPHFYQVIFESVSLKHGYP 180
Qy 180 IATDIOVLSPCDKSPHELELGDVEYNAGONATFOCIATCRDAVHKLMLQORNGEDIP 239
Db 181 IADDEVRLAHPCKAKPHELRQLQNVNNGONATFOCIAGGKWSQHDKMLQWNGRDTA 240
Qy 240 VAQTKNINHRFFAASFRLEQVTKTDQLYRCVCTOSERGSVSNPAQLIVREPPPIAPPO 299
Db 241 LMVTRVNHRRFSATVSADTSQRSISKYRCVIRSDGSGVSNVAILIVPEPTPIAPPE 300
Qy 300 LLGVGPTYLIIQLNANSIIGDPIILKEVEYRMTSGWTEHAVNAPTYKLMLHLDPDTEY 359
Db 301 LLAVGATYLMIKPNANSIIGDPIILKEVEYRTTGTGAETHIVDSPNYKMLHLDPDVEY 360
Qy 360 EIRVLLTRPGEGTGLPGPPLITETKCAEMRTETKLKIAEQARRTAVDWESLGYNITR 419
Db 361 EIRVLLTRPGEGTGLPGPPLITETKCAEMRTETKLKIAEQARRTAVDWESLGYNITR 420
Qy 420 CHTFNVTICYHFRGHNESKADCLMDPKAPQHVNVNHLPPVTVNSLKMILTNPEGRKESE 479
Db 421 CHSVNLTVOQYV--FNQOQYEAEEVLTQTSHTYLRGLRPFMTIRLLLSNPEGRMESE 478
Qy 480 ETIQTDEDVPGVPVVKSLQTSFENKIFLNWKEPLDPNGIITQYEISYSIRSFDPAPV 539
Db 479 ELVVQTEEDVPGVPLESIOGGPEEKIYIQWKPNETNGVITLYEINYKAVGSLDPSAD 538
Qy 540 VAGPPQTVSNLWSTHVFHMLHPGTYTQFIRASTVKGPGDATAIVNTNISAPTLDPY 599
Db 539 LSSQGVKVFKLNRNETHHFLVGLYEGTYSFTIKASTAGFGPPVTTIRATKISAPSMPEY 598
Qy 600 EGVDAASLNATATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVYQ 659
Db 599 D-ADTPLNETDITITVLMKPAQSGAPSVQLVKEERLQKRSRAADIIECESVPVSYR 657
Qy 660 NAMSGGAPYFAAELPGLNPEPAFTVGNRTYQGFNPNPLAPKRGYNIYFOAMSVVEK 719
Db 658 NASNLSLHVFAAELKESNLPVTPFTVGNKTYGWNPLSLPKSYISYFQALSANG 717
Qy 720 ETKTQCVRIATK-----AATEEPFVIPPDAKQTRDVVKIAGISAG 759
Db 718 ETKINCVRLATKAGPMGSAQVTPGTPLCLLTASTQNSNTV-EPEKQVDNVTVMAGVIAG 776
Qy 760 ILVFIALLLVILLVKKSLAKKCKDAMGNTROBMTWNVNMDRSYADQSTLHAEDPLSI 819
Db 777 LLMFIILLGMLTIKRRKLAKQKQKTSQAQREM-GFVASTDKPTAKLGNRNDEGFSS 835
Qy 820 TFMDDQHNFSPRYENHSAATESRLLDV---PRYLCEGTESPYQTQGLHPAIRVADLLQHI 876
Db 836 SSQDVNGFT---DGSRGELSQPLTITQHPYRTCDPVMSYPRDQFQPAIRVADLLQHI 891
Qy 877 NLMKTSDSYGFKEEYEFQGSASWDVAKQONRAKRYGNIAYDHSRVILQPVDEDDP 936

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Db 892 TQMKRGQGYGFKEEYEALPGQQTASWDTAKEDENRNKRNRYGNIISYDHSRVLLVLGDGP 951
Qy 937 SSDYINANYIDGQRPSPHYATQCPVHETVYDFWFRMIWQEOSACIWMVTNLVEVGRVKCY 996
Db 952 HSDYINANYIDGVRPHYATQCPMQETVKDFRMIWQENSASIVMTNLVEVGRVKCV 1011
Qy 997 KYPPDDTEVYDGFVKTCVEMEPLEAYVVRFTFLERRGYNEIREVKQHFTHGPDHGVVPH 1056
Db 1012 RYMPDDTEVYDGIKVTLIETPEPLAEYVIRFTVQKGYHEIRLRFHTFSPDGHGVPCY 1071
Qy 1057 ATGLLSFIRVRVCLSNPPSAGPIVHVCSAGAGRTCTYIVDITMLDAREGVVDVYNCVKA 1116
Db 1072 ATGLLGFVRQVKFLNPPPEAGPIVHVCSAGAGRTCCFIAITMLDMAENEGVVDIFNCVRE 1131
Qy 1117 LRERRINMVQTEEQYIFIHDAILEACLCGETAIPVCEFKAAFYDMIRIDSQTNSSHLKDE 1176
Db 1132 LRAQRVNLVQTEEQYVFWHDAILEACLCGNTAIPVCEFRSLYYNISRLLDPQTNSSQIKDE 1191
Qy 1177 FOTLNSVTPLOAEDCSIACLPRNHDKNRPMDLPPDRCLPFLITIDGESSNYINAAALMD 1236
Db 1192 FOTLNIPTVRPREDCSIGLLPRNHDKNRMDVLPDLRCLPFLITIDGESSNYINAAALMD 1251
Qy 1237 SYRQPAFIYTOYPLNPTVKDFWRLVYDYGCTSIWMLNEVDLSQCCPYWPEEGMLRYGP 1296
Db 1252 SHKQPAFVVTQHPLPNTVADFWRVLFVYDNCSSVVMNLNEMDTAQLCMQYWPKEKTSYGP 1311
Qy 1297 IQVECKSCSMDCDVINRIFRICNLTRPQEGYLMVQQFYQLGWASHRVPVSGSKRSLKLI 1356
Db 1312 IQVEFVSADIDEDIHRIFCINWARPQDGYRIVQHLQYIGWPAYRDTFPSKRSLLKVR 1371
Qy 1357 QVKKQWEKWBKSGRTIHCINGGSGRGMFCAIGIVVEMVKRQNVVDVFAVKTLRNSKP 1416
Db 1372 RLEKQWQYDQREGRTVWVHCLNGGSGRTFCAICSCVCEMIQQQNIIDVFHIVTKLRNKS 1431
Qy 1417 NMVEAPQVYFCYDVALEYLES 1438
Db 1432 NMVETLEQYKFVYEVALEYLSS 1453

RESULT 15
P78399
ID P78399 PRELIMINARY; PRT; 1439 AA.
AC P78399;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Protein tyrosine phosphatase receptor omicron.
GN Name=PTPRO;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98094249; PubMed=9434160; DOI=10.1016/S0378-1119(97)00420-4;
RA Avraham S., London R., Tulloch G.A., Ellis M., Fu Y., Jiang S.,
RA White R.A., Painter C., Steinberger A.A., Avraham H.;
RT "Characterization and chromosomal localization of PTPRO, a novel
RT receptor protein tyrosine phosphatase, expressed in hematopoietic stem
RT cells."
RL Gene 204:5-16(1997).
DR EMBL; U71075; AAC51938.1; -.
DR HSP; P28827; IRPM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal_bind_like.

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